

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 115654

To: Ruixiang Li

Location: REM-4C70 Art Unit: 1646

Wednesday, March 03, 2004

Case Serial Number: 10/060765

From: Beverly Shears Location: Remsen Bldg.

RM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

| Search Notes | | Caller 1 | |
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72 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHBENPYSLLEISTVERGVVSLFGVRSALFV 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 IMALVFLGILVGMVVPSPAGTRANNTLLDSRGWGTLLSRSRAGLAGELAGVNWESGYLVG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 LWVSVLAGLILGACQAHP-----IPDS---SPLLQ----FGGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
               SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%; Score 176.5; DB 4; 29.1%; Pred. No. 1.8e-09; tive 27; Mismatches 52;
                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
ATTORNEY/AGRYI INFORMATION:
NAME: No. 6503886temburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 15: US-09-449-249-15
                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/449,249
FILING DATE: 24-No. 6503886-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 completed: March 2, 2004, 16:09:00
                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 29.1;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Job time : 38.4458 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search
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Chandler, Lois Ann
Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERA
NUMBER OF SEQUENCES: 128
                                                                  45 --RORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 --RORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFL 102
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12 LWALVFLGILVGMVVPSPAGTRANNTLLDSRGWGTLLSRSRAGLAGEIAGVNWESGYLVG 71
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Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYOSEAH 140
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                                                                                                                                                      APPLICANT: Kirschner, Marc W.
APPLICANT: Kinschiner, No. 6399386iyuki
TITLE OF INVENTION: Receptor-Ligand Assay
FILE REFERENCE: HU95-01A2
CURRENT APPLICATION NUMBER: US/09/507,773
CURRENT APPLICATION NUMBER: 08/776,207
PRIOR APPLICATION NUMBER: 08/441,629
PRIOR FILING DATE: 1995-05-15
PRIOR FILING DATE: 1995-05-15
PRIOR PILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09449249 Patent No. 6503886 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Sequence 12, Application US/09507773
Patent No. 6399386
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 198
TYPE: PRI
CRGANISM: Homo Bapien
US-09-507-773-12
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US-09-449-249-15
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US-08-776-207-12
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                                                                                                                                                                                                             33;
                                                                                                                                                                    15.9%; Score 176.5; DB 3; Length 198; 29.1%; Pred. No. 1.8e-09; tive 27; Mismatches 52; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: BILLON, PATRICK J.
APPLICANT: GRUBER, L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STREET: DC
                                                                                                                                                                                                                                                   13 LWVSVLAGLLIGACQAHP-----IPDS---SPLLQ-----FGGQV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                  103 CORPDGALYGSIHFDPEACSFRELLLEDGYNVYOSEAH 140
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PRIOR APPLICATION DATA.
APPLICATION NUMBER: PCT/US95/01790
FILING DATE. 14-FEB-1995
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-UN-1995
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 67/039,045
FILING DATE: 28-FEB-1997
                                                                                                         ; OTHER INFORMATION: /note= "FGF-6" US-08-718-904-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09023082A
Patent No. 6077692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KUBEN, STEVEN M.
JIMENEZ, PABLO
DUAN, D. ROXANNE
RAMPY, MARK **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAMPY, MARK A.
MENDRICK, DONNA
ZHANG, JUN
LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                          Query Match
Best Local Similarity 29.1%
Matches 46; Conservative
                                                    TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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45 --RORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESILLQLKALKPGVIQILGVKTSRFL 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 LWALVFLGILVGMVVPSPAGTRANNTLLDSRGWGTLLSRSRAGLAGEIAGVNWESGYLVG 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LWVSVLAGLLLGACQAHP-----IPDS---SPLLQ-----FGGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
15.9%; Score 176.5; DB 3;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.9%; Score 176.5; DB 3; Best Local Similarity 29.1%; Pred. No. 1.8e-09; Matches 46; Conservative 27; Mismatches 52;
PRIOR DATE: 33-MAY-1997

PRIOR DATE: 23-MAY-1997

PRIOR DATE: 23-MAY-1997

PRIOR DATE: 13-MAY-1997

PRIOR APPLICATION DATA: 406-1997

PRIOR APPLICATION DATA: 13-AUG-1997

PRIOR APPLICATION DATA: 13-AUG-1997

PRIOR APPLICATION NUMBER: US 60/055,561

PRIOR APPLICATION NUMBER: 13-AUG-1997

ATTORNEY AGENT INFORMATION: NAME: STREFFE, ERIC K. REGISTRATION NUMBER: 36,688

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0360008/EKS

TELEPOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600

TELEPHONE: 202-371-2500

INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kirschner, Marc W.
APPLICANT: Kirschner, No. 6680718iyuki
TITLE OP INVENTION: Receptor-Ligand Assay
FILE REFERENCE: HU95-01A2
CURRENT APPLICATION NUMBER: US/08/776,207A
CURRENT FILING DATE: 1997-06-23
EARLIER FILING DATE: 1995-07-19
EARLIER PELICATION NUMBER: 08/441,629
EARLIER PELICATION NUMBER: 08/441,629
EARLIER PELICATION NUMBER: 08/41,629
EARLIER PELICATION NUMBER: 08/295-625
EARLIER PELICATION NUMBER: 08/279,217
EARLIER PELICATION NUMBER: 08/279,217
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 198
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-776-207-12
; Sequence 12, Application US/08776207A
; Patent No. 6080718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOPOLOGY: not relevant TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-023-082A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Patentin Release #1.0, Version #1.30
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Patent No. 6037329
                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REPRENCE/DOCKET NUMBER: 0726:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         not relevant
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: May 12, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (206) 622-4900
                                                                                                                                                                                                                                                                                                 : 198 amino acids
amino acid
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TELEFAX: (206) E82-6031
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                STRANDEDESS: not rel

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-438-439C-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
COUNTRY: USA
      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 36
US-08-718-904-15
                                                                                                                                                                                                                                                                                                 LENGTH:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLEISTVERGVVSLFGVRSALFV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.9%; Score 176.5; DB 2; Length 198; 29.1%; Pred. No. 1.8e-09; trive 27; Mismatches 52; Indels 33.
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Patent No. 5876967

GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Phillip M.
APPLICANT: Macke, Jennifer P.
ITILE OF INVENTION: FIRNOROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,439C
FLING DATE: May 12, 1995
ALTONENEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/046001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                    ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Conservative
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                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                  CORRESPONDENCE ADDRESS
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Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
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                                                                                                                                                         USA
                                                                                                                                                                        ZIP: 92037
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                                                                                                                                                         COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 --RQRYLYTDDAQQTEAHLBIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                   13 INVSVLAGLLIGACOAHP-----IPDS---SPLLO----FGGQV-
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ZIF: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             / Match 15.9%; Score 176.5; DB 2 Local Similarity 29.1%; Pred. No. 1.8e-09; nes 46; Conservative 27; Mismatches 52
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CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: No. 6037329tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
07265/046001
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FILING DATE: 24-SEP-1996
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STRANDEDNESS:
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                                                              US-08-867-471-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- 44
                                                   12 IMALVFLGILVGMVVPSPAGTRANNTLLDSRGWGTLLSRSRAGLAGEIAGVNWESGYLVG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 198;
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13 LWVSVLAGLLLGACQAHP-----IPDS---SPLLQ-----FGGQV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08441629
Parent No. 5766923
GENERAL INFORMATION:
APPLICANT: Kinschner, Marc W.
APPLICANT: Kinschner, No. 5766923iyuki
APPLICANT: Kinschnta, No. 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 AMNSKGRLYATPSFQ-EECKFRETLLPNNYNAYESDLY 166
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                                                                                                                                                                                                                                                                                                                              103 CORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
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MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,217
FILING DATE: 22-UUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granhan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
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amino acid
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US-08-441-629-12
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45 --RORYLYTDDAQOTEAHLEIREDGTVGGAADQSPESILIQLKALKPGVIQILGVKTSRFL 102
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33;
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APPLICANT: Smallwood, Phillip M.
APPLICANT: Macke, Jennifer P
TITLE OF INVENTION: FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 LWVSVLAGLLLGACQAHP-----IPDS---SPLLQ-----FGGQV-
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elem PC compatible
COMPUTER: Elem PC compatible
COMPUTER: Elem PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,471
FILING DATE: 02-JUN-1997
CLASSIFICATION: S34
PRIOR DATE: 02-JUN-1997
RIING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07265/047001
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not relevant
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TELEFAX: 617/678-5099
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Matches 46; Conserv
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PRIOR FILING DATE: 1995-06-05
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                                                                    SEQ ID NO 5
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                                                                                           101 FLCORPDGALYGSIHFDPRACSFREILLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAP-- 158
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rampy, Mark A.
APPLICANT: Rampy, Mark A.
APPLICANT: Rampy, Mark A.
APPLICANT: Bendrick, Donna
APPLICANT: Bussell, Deborah
APPLICANT: Louie, Arthur
ITILE OF INVENTION: Therapeutic Uses of Keratinocyte Growth Factor-2;
FILE REPERBNCE: 1488.1060002
CURRENT APPLICATION NUMBER: US/09/248,998
CURRENT FILING DATE: 1999-02-12
EARLIER FILING DATE: 30-DEC-1998
EARLIER FILING DATE: 31-FEB-1998
MUMBER: OF SEQ ID NOS: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 GGAPRRRKIYC----ATXYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR
                               40 GGAPRREKIYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGR
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                                                                                                                                                                             ---- LPGLPPALPEPPG 179
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15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INTORNATION:
APPLICANT: Alderson, Ralph et al.
TITLE OF INVENTION: Pibroblast Growth Factor 11
FILE REFERENCE: PF184F1
CURRENT APPLICATION NUMBER: US/09/572,406B
CURRENT FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: 60/135,524
PRIOR APPLICATION NUMBER: 09/514,587
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1000-02-28
PRIOR FILING DATE: 1908-06-08
PRIOR APPLICATION NUMBER: 09/693,585
PRIOR FILING DATE: 1998-06-08
PRIOR APPLICATION NUMBER: 09/464,590
                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/09248998
Patent No. 6599879
GENERAL INFORMATION:
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Patent No. 6605441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Ver. 2.0
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US-09-248-998-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 30
US-09-572-406B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Pate
SEQ ID NO 21
LENGTH: 239
                                                                                                                                                                                                                                                                                                               US-09-248-998-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08439725A

| Sequence 14, Application US/08439725A
| Patent No. 56937A1
| GENERAL INFORMATION:
| APPLICANT: Nathans, Jeremy
| APPLICANT: Macke, Philip M.
| APPLICANT: Macke, Philip M.
| APPLICANT: Macke, Jennifer P.
| TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
| TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Fish & Richardson P.C.
| STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
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                                                                                                                                                                              Length 239;
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                                                                                                                                                                                                                           57; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.9%; Score 176.5; DB 1;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52;
                                                                                                                                                                         Query Match 15.9%; Score 177.5; DB 4; Best Local Similarity 29.7%; Pred. No. 1.9e-09; Matches 51; Conservative 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/439,725A
FILING DATE: 12-MAY-1995
CLASSIPICATION: 424
ATTOCNEY AGENT INFORMATION:
NAME: Halle, 1.18a A.
REGISTATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/047001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07265/047001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not relevant
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TELEFAX: 617/678-5099
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NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
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                                                                                    TYPE: PRT
CRGANISM: Homo sapiens
US-09-572-406B-5
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PRIOR APPLICATION DATA:

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APPLICATE: Alderson, Ralph et al.
TITLE OF INVENTION: Fibroblast Growth Factor 15
FILER REFERENCE: PF203P1
CURRENT APPLICATION NUMBER: US/09/564,829
CURRENT APPLICATION NUMBER: 06/132,924
PRIOR APPLICATION NUMBER: 06/132,924
PRIOR APPLICATION NUMBER: 09/425,021
PRIOR FILING DATE: 1999-10-25
PRIOR FILING DATE: 1999-10-25
PRIOR FILING DATE: 1998-10-25
PRIOR FILING DATE: 1998-10-25
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-25
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15.9%; Score 177.5; DB 4;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/229,947
CURRENT FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 43
SOFTWARRE: FASTERQ for Windows Version 3.0
                                                                                             GENERAL INPORMATION:
APPLICANT: Doisher, Theresa A.
APPLICANT: Conklin, Darrell C.
APPLICANT: Raymond, Fenella
APPLICANT: Bukowski, Thomas R.
APPLICANT: Holderman, Susan D.
APPLICANT: Sheppard, Paul O.
TITLE REFERENCE: 96-20C1
                                                                Sequence 35, Application US/09229947 Patent No. 6518236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-564-829-5; Sequence 5, Application US/09564829; Patent No. 6593112; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-229-947-35
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 51; Conserv
                                              US-09-229-947-35
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15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41
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US-09-390-207-18
Sequence 18, Application US/09390207
Patent No. 5654530
GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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APPLICATION NUMBER: US/08/718,904
PILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: No. 6503886temburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                   ); SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-449-249-12
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CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PACENTIN Ver. 2.0
                                                                                                                                                                                                                                                                               LENGTH: 239 amino acids
                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 -----RGPAR-
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; LENGTH: 239
; TYPE: PRT
; ORGANISM: HOMO SADIENB
US-09-390-207-18
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                                                                                                                                         40 GGAPRRRKIYC----ATKYHLQLHPSGRVNGSLENSAYSILBITAVEVGIVAIRGLFSGR
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15.9%; Score 177.5; DB 4; Length 239; 29.7%; Pred. No. 1.9e-09; ative 23; Mismatches 57; Indels 41
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41 GGOVRORYLYIDDAQQTEAHLEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.9%; Score 177.5; DB 3. Best Local Similarity 29.7%; Pred. No. 1.9e-09; Matches 51; Conservative 23; Mismatches 57.
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US-09-368-951-35

Sequence 35, Application US/09368951

Setent No. 6352971

GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Conklin, Darrell C.
APPLICANT: Bukowski, Thomas R.
APPLICANT: Bukowski, Thomas R.
APPLICANT: Hansen, Birgit
SEALIER FILING DATE: 1999-08-05

EARLIER FILING DATE: 1997-10-16

NUMBER OF SEQ ID NOS: 36

SEQ ID NO 35

LENGHH: 239

LENGHH: 239
                      FILING DAYE:
CLASSIPTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,590
FILING DATE: 05-UNI-1995
ATTORNEY AGENT INFORMATION:
NAME: MOLLINS, J. G.
REGISTRATION NUMBER: 325800-438
REGISTRATION NUMBER: 325800-438
TELEFONE: (201) 994-1700
TELEFONE: (201) 994-1744
TELEFONE: (201) 994-1744
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
TENTORY (201) 994-1744
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          325800-438
APPLICATION NUMBER: US/09/093,585
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 239 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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US-09-368-951-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-093-585-11
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Chandler, Lois Ann
Sosnowski, Barbara A.
IITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THER
101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAP-- 158
                                                            101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAP-- 158
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                                                                                                                                                                                           ---LPGLPPALPEPPG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 LWYVSVNGKGRPRRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPG 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.9%; Score 177.5; DB 4; Length 2 Best Local Similarity 29.7%; Pred. No. 1.9e-09; Matches 51; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/449,249
FILING DATE: 24-No., 6503886-1999
CLASSIFICATION: <unimaliar control of the con
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09425021
Fatent No. 6482408
GENERAL INFORMATION:
APPLICANT: Green, John M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Fibroblast Growth Factor 15
FILE REPRENCE: PF203D1
CURRENT FILING DATE: 1999-10-25
FARLIER APPLICATION NUMBER: 09/103,079
EARLIER APPLICATION NUMBER: 09/103,079
EARLIER FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
ILENGTH: 239
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Patent No. 6503886
GENERAL INFORMATION:
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ORGANISM: Homo sapiens
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US-09-449-249-12
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STATE: N
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Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STEET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GRITZ, REINBR L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
NAME: NO. 6037329tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-631
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 239 amino acide TENGTH: 239 amino acide STRANDEDMESS: single TOPOLOGY: unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "FGF-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09023082A Patent No. 6077692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JIMENEZ, PABLO
DUAN, D. ROXANNE
RAMPY, MARK A.
MENDRICK, DONNA
ZHANG, JUN
NI, JIAN
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                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR 100
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Patent No. 6110893
GENERAL INFORMATION: FIREARY
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: FIREABLAST GROWTH FACTOR-11
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1488.0360008/EKS
FILING DATE: 05-JUN-1995
PRIOR PAPLICATION DATE:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATE:
APPLICATION DATE:
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY AGENT INFORMATION:
NAME: STEFFFE, ERIC K.
NAME: STEFFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 239 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6 BECKU
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US-09-093-585-11
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SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Greene, John M.
TITLE ROSEN, Craig M.
TITLE OF INVENTION: Fibroblast Growth Factor 15
FILE REFERENCE: PF203D1
CURRENT APPLICATION NUMBER: US/09/103,079A
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 08/462,169
EARLIER FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
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29.7%; Pred. No. 1.9e-09;
Live 23; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 -----RGPAR------FLP----
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ZIP: 981.04-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Conservative
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STATE: Washington
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Best Local Similarity
Matches 51; Conserva
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPILICATION NUMBER: US/08/207,412B
FILING DATE: 08-MAR-1994
CLASSIFICATION: 435
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29.7%; Pred. No. 1.9e-09;
iive 23; Mismatches 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Mismatches
                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Ferraro, Gregory D
REGISTRATION UNBER: 35,134
REFERENCE/DOCKET NUMBER: 325800-100
TELECOMMUNICATION INFORMATION:
TELEPHANE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity
Matches 51; Conserva
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Matches 51; Conserv
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US-08-951-822-35
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Sequence 12, Application US/08718904
Patent No. 6037329
GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Scanowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPI
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 GGAPRRKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGR
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                                                                                              --LPGLPPALPEPPG 179
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                                                                  101 FLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
40 GGAPRRKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGR 95
                                                                                                                        159 RGP----ARFLPLPGLPPALPEPPGILAPQPPDVGSSDPLSNVGPSQGRSPSYAS 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/464,590A
FILING DATE: 05-UN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                Sequence 11, Application US/08464590A
Patent No. 5763214
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J. G.
REGISTRATION NUMBER: 30,073
REFRENCE/DOCKET NUMBER: 3258;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 994-1704
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: lin
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RESULT 16 US-08-462-169B-11 ; Sequence 11, Application US/08462169B

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41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQLLGVKTSR 100
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Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41.
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APPLICANT: Hu, Jing-Shan
TITLE OF INVENTION: Fibroblast Growth Factor-10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Garella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SAPPLICANT: John Greene and Craig A. Rosen
TITLE OF INVENTION: Fibroblast Growth Factor-15
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWARI & OLSTEIN
                                                                                                         ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325800-441 (PF203)
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM ES/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,169B
FILING DATE: 05 JUN 95
CLASSIFICATION: 514
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Patent No. 5817485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 239 AMINO ACIDS TYPE: AMINO ACID
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STATE: N.
COUNTRY:
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E: Fish & Richardson P.C.
4225 Executive Square, Suite 1400
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STRANDEDNESS: not relevant
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MOLECULE TYPE: protein
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; LENGTH: 245
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-28
                     STREET: 422
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       ADDRESSEE:
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US-09-390-207-28
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                                                                                                                                             COUNTRY:
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                                                      GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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APPLICANT: Nathans, Jeremy
APPLICANT: Stallwood, Phillip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBROBIAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: ACTOR-2 AND METHODS OF USE
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.1%; Score 179; DB 2; Length 245; 28.8%; Pred. No. 1.4e-09; tive 30; Mismatches 78; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALIZED CONTO COMPUTER REPORTS.

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/867,471 FILING DATA: CLASSITCATION DATA: APPLICATION NUMBER: 08/439,725 FILING DATE: 12-MAY-1995 ATTORNEY AGENT INFORMATION: NAME: Haile, Lisa A. REGISTRATION: NUMBER: 38,347 REGISTRATION NUMBER: 38,347 R
                                                                                                                                                                                                                                                                                                                                          SSEE: Fish & Richardson P.C.
I: 4225 Executive Square, Suite 1400
La Jolla
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       Sequence 11, Application US/08867471 Patent No. 5872226
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Patent No. 5876967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 07.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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Matches 51; Conserva
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STREET: 42
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US-08-438-439C-7
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41 GGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR 100
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Patent No. 6504530
GENERAL INPORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-31
CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT FILIG DATE: 1999-09-07
NUMBER OF ISEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,439C
FILING DATE: May 12, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REFERENCE/DOCKET NUMBER: 07265/046001
TELEPHONE: 619/678-5070
TELEFRAX: 619/678-5070
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Best Local Similarity 28.8%; Pred. No. 1.4e-09;
Matches 51; Conservative 30; Mismatches 78
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40 GGAPRRKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGR 95
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CITY: La Jolla
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US-08-439-725A-11
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Sequence 7, Application US/09417721
Patent No. 6451303
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Whitehouse, Martha J.
APPLICANT: Wavanaugh, Michael W.
APPLICANT: Kavanaugh, Michael W.
TITLE OF INVENTION: Administering
FILE REPERENCE: 1296/12169USO5
CURRENT APPLICATION NUMBER: US/09/417,721
CURRENT FILING DATE: 1999-10-13
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
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1 Similarity 38.3%; Pred. No. 4e-12;
49; Conservative 27; Mismatches 43; Indels 9.
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                                                                                                                                                              APPLICANT: DOBERT, S.
APPLICANT: JOBERT, S.
APPLICANT: Glocher, S.
APPLICANT: Glocher, S.
APPLICANT: Glocher, S.
TITLE REFERENCE: GENET. 054PR2
CURRENT APPLICANTON: USTS and Encoded Human Proteins.
FILE REFERENCE: GENET. 054PR2
CURRENT APPLICANTON NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4031
LENGTH: 134
                                       181 ----LAPQPPDVGSSDPLSMV-GPSQGRSPSY 207
                                                                                                                                Sequence 4031, Application US/09621976
Patent No. 6639063
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Best Local Similarity 28.8%
Matches 51; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 240
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122 NGYDVYHS 129
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-621-976-4031
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                               101 FLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
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                                                                                                                                        40 GGAPRRRKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGR
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APPLICANT: Smallwood, Philip M.
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
APPLICANT: Macke, Jennifer P.
APPLICANT: Macke, Jennifer P.
APPLICANT: Macke, Jennifer P.
AND MATHODS OF USE
NUMBER OF SEQUENCES: 15
OORRESPONDENCE ADDRESS:
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16.1%; Score 179; DB 1; Length 245;
Best Local Similarity 28.8%; Pred. No. 1.4e-09;
Matches 51; Conservative 30; Mismatches 78; Indels
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APPLICATION NUMBER: US/08/439,725A FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Fish & Richardson P.C.
4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/047001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08439725A Patent No. 5693775 GENERAL INFORMATION:
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US-08-867-471-11

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68 TVGGAADQSPESILIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELL 127
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                                                                                                                                                                                                                                                                                              Transmembrane Polypeptides and Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 216;
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36.3%; Pred. No. 5.2e-18;
:ive 27; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Secreted and Transmembrane Intil REPERERNE: 10466-11.

TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TILE REPERENCE: 10466-11.

TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/902,775A CURRENT FILING DATE: 2001-07-10

PRIOR PELICATION NUMBER: PC/1050/04414

PRIOR FILING DATE: 1999-07-26

PRIOR PELICATION NUMBER: US 60/145,698

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-15

PRIOR PELING DATE: 1999-10-15

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-06

PRIOR PELING DATE: 1999-12-07

PRIOR PELING 
                                                                                                                                                         Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                        Pan, James
Paoni, Nicholas F.
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Best Local Similarity 36.33
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-902-775A-59
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 VVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRXLCMGADGKWQGLLQXSEBDCAFBEBI 126
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                                                                                PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
                                                         APPLICATION NUMBER: PCT/US99/20944
           PCT/US99/20594
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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US-09-905-125A-59
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US-09-902-775A-59
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LENGTH: 216
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26; Gaps

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Ferrara, Napoleone
Filvaroff, Blen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
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Mather, Jennie P.
                                                                                                                                                                           Conservative
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Eaton, Dan L.
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                                                                                                                                    Query Match
Best Local Similarity
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US-09-905-125A-59
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APPLICANT:
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-06

PRIOR PILING DATE: 1999-07-06

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-89

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/23089
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84
                                LEIREDGTVGGAADQSPESKLOLK 84
                                                                                                                                                                                                                                                                                                                                                                                                 Godowski, Paul J.
Grimaldi, Christopher J.
Grimaldi, Christopher J.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Rather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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; Sequence 59, Application US/09907794A
; Patent No. 6635468
LEIREDGTVGGAADQSPESLLQLK
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                   Gerber, Hanspeter
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Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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127 RPDGYNVYRSEKHRLPVSLSSAKQ-RQLYKNRG---FLPLSHFLPMLPMVPEEPEDLRGH 182
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                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                      Length 216;
                                                                                                                                                                                                                                                                               23.8%; Score 265; DB 4; Length 21. 36.3%; Pred. No. 5.2e-18; trive 27; Mismatches 82; Indels
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CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR PELICATION NUMBER: PCT/USO/04414
PRIOR PELICATION NUMBER: PCT/USO/04414
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR PLING DATE: 1999-07-07
PRIOR PLICATION NUMBER: US 60/145,698
PRIOR PLICATION NUMBER: US 60/145,698
PRIOR PLICATION NUMBER: US 60/145,222
PRIOR PLICATION NUMBER: US 60/146,222
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER 05 SEQ ID NOS: 423
; SEQ ID NO 59
; LENGTH: 216
; TYPE: PRT
; ORGANIGM: Homo sapiens
US-09-907-794A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 59, Application US/09905125A Patent No. 6664376
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Grimaldi, Christopher J.
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RESULT 5
9-09-621-976-5213
; Sequence 5.213, Application US/09621976
; Patent No. 6639063
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LOCATION: -28...1
NAME/KEY: UNSURE
LOCATION: 57
OTHER INFORMATION: Xaa = Ala, Pro
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al Similarity 80.7%;
146; Conservative
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98.8%;
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Best Local Similarity 98.8
Matches 83; Conservative
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Best Local S:
Matches 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 GLWVS-VLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVG
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Patent No. 6504530
GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Ribroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE PATENTIN Ver. 2.0
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                                                                                                                                                                                 Query Match

86.2%; Score 959; DB 4; Length 181;
Best Local Similarity 99.4%; Pred. No. 1.8e-85;
Matches 180; Conservative 0; Mismatches 1; Indels
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CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 181
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Best Local Similarity 78.9°
Matches 157; Conservative
                                                                                                        TYPE: PRT
GRGANISM: Homo sapiens
US-09-390-207-5
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LENGTH: 210
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TS-09-390-207-6
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US-09-390-207-4
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GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                  Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Indels
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APPLICANT: Dumas Mine Edwards, J.B.
APPLICANT: Dumas Mine Edwards, J.B.
APPLICANT: Johert, S.
TITLE OF INVENTION: EST6 and Encoded Human Proteins.;
FILE REFERENCE: GENSET. 054 PR.2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO $213
LENGTH: 85
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Pred. No. 9.2e-35;
0; Mismatches 1.
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Pred. No. 1.8e-65;
9; Mismatches 26
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LENGTH: 209
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| / cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
| / cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
| / cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-390-207-6
US-09-621-976-5213
US-09-621-976-5213
US-09-905-125A-59
US-09-905-125A-59
US-09-621-976-4031
US-08-417-721-7
US-08-439-725A-11
US-08-438-439C-7
US-08-867-471-11
US-08-867-471-11
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US-09-023-082A-21
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US-09-103-079-11
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US-09-368-951-35
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US-09-229-947-35
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Maximum Match 100%
Listing first 45 summaries
                                                                     sw model
                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                       US-10-060-765-4
1113
1 MDSDETGFEHSGLWVSVLAG.
                                                                     protein search, using
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CSFREILLEDGYNVYQSEAHGLPLHIPGNKSPHRDPAPRGPARFLPLPGLPPAPPEPPGI 180
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5, Appli
10, Appl
                                    1 MDSDETGFEHSGLWVSVLAGILLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thomason, Arlen
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09390207
Patent No. 6504530
GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INFORTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
CURRENT APPLICATION NUMBER: US/09/390,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1106; DB 4;
Pred. No. 1.2e-99;
0; Mismatches 1;
US-09-564-829-5

US-09-248-998-21

US-09-24-168-5

US-08-439-725A-14

US-08-471-14

US-08-877-471-14

US-08-438-439C-10

US-08-438-439C-20

US-08-138-439C-10

US-08-138-139

US-09-1023-092-15

US-09-507-773-12

US-09-507-773-12

US-09-507-773-12

US-09-507-773-12

US-09-449-249-15

US-09-449-249-15

US-09-48-988-14

US-09-48-988-14

US-09-48-98-14

US-09-48-98-14

US-09-48-98-14

US-09-48-98-14

US-09-48-98-14

US-09-48-98-14

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US-09-48-98-14

US-09-48-98-14

US-09-417-721-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09390207; Patent No. 6504530; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.4%;
Best Local Similarity 99.5%;
Matches 208; Conservative
   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-2
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inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which are useful for detecting the presence of tumour in a mammal which compared to the sample of calls taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample of is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour, olon tumour, breast tumour, prostate tumour, rectal tumour or useful as molecular weight markers for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful configuration animals or knock-out animals which are useful configuration animals or knock-out animals which are useful configuration animals or knock-out animals which are useful substitution and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide. \mathcal{S}

Sequence 208 AA;

1, l; Gaps Query Match
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1;

1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 60

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CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180 121

2, 2004, 16:04:50 Search completed: March Job time: 128.4 secs

17-APR-2003

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480. 26-AUG-2002; 2002US-00227873 (GETH) GENENTECH INC. WPI; 2003-644807/61. N-PSDB; ADD06259

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

useful New PRO polypeptides and nucleic acids encoding the polypeptides, in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.

Claim 11; SEQ ID NO 78; 314pp; English.

CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in cusful for stimulating the proliferation of or gene expression in cusful for stimulating the proliferation of for propagation are useful for stimulating the proliferation of differentiation of chondrocyte for stimulating the proliferation of differentiation of chondrocyte calls. PRO357, PRO355, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (INF)-care useful for stimulating the release of tumour necrosis factor (INF)-care useful for stimulating the release of tumour necrosis factor (INF)-care useful for stimulating the PRO337, PRO363, PRO351, PRO1080, PRO1134, PRO126, PRO1136, PRO1136, PRO1137, PRO1134, PRO1134, PRO1134, PRO1134, PRO1134, PRO1134, PRO1134, PRO1334, PRO1134, PRO1334, PRO133 invention describes an isolated PRO (secreted and transmembrane) transmembrane PRO polypeptide.

Sequence 208 AA;

Gapa 1; 98.7%; Score 1098.5; DB 7; Length 208; 99.5%; Pred. No. 8.6e-91; cive 0; Mismatches 0; Indels 1; Conservative Query Match Best Local Similarity 208; Best Loca Matches

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à В ò

61 LEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120

121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGPPALPEPPGI 180

120 CSFRELLLEDGYNVYQSEAHGLPLHFPGNKSPHRDFARRFLFLFGLPPALPEPPGI 179 180 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS P ò

RESULT 40

Ŕ ADC77779 standard; protein; 208

ADC77779;

(first entry) 01-JAN-2004 Novel human secreted and transmembrane protein PRO10196.

release; Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; oclon tumour; prostate tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;

Homo sapiens.

gene therapy

US2003088066-A1

08-MAY-2003

13-AUG-2002; 2002US-00219466

01-JUN-2001; 2001WO-US017800.

29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Goddard A, Godowski PJ; shan JF, Watanabe CK, Wood WI; Gerritsen ME, Goddard Smith V, Stephan JF, Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-657980/62. N-PSDB; ADC77778 One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, or for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody, e.g. cancer.

Claim 11; Fig 78; 314pp; English.

The invention describes an isolated PRO (secreted and transmembrane)
cuseful for stimulating the proliferation of or gene expression in
cuseful for stimulating the proliferation of or gene expression in
pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
for stimulating the proliferation or differentiation of chondrocyte
cells. PRO357, PRO355, PRO1355, PRO1365 polypeptide are useful
for stimulating the proliferation or differentiation of chondrocyte
cells. PRO317, PRO357, PRO1355, PRO1366 or PRO1419, PRO214,
alpha from human blood. PRO982, PRO1357, PRO1306, PRO1419, PRO214,
PRO1478, PRO1137, PRO526, PRO363, PRO357, PRO1301, PRO1411, PRO1119,
PRO1478, PRO1114, PRO1126, PRO1196, PRO1192, PRO1244, PRO1309,
PRO1343, PRO1310, PRO1367, PRO1309, PRO1474, PRO1341, PRO1309,
PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1411, PRO1367,
PRO1940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
stimulating the proliferation of normal human dermal fibroblasts cells.
PRO5940, PRO5725, PRO7164, or PRO7425 polypeptide are useful for

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The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyce cells. PRO327, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO331, PRO357, PRO125, PRO136 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (INF)-alpha from human blood. PRO982, PRO357, PRO356, PRO3306, PRO1419, PRO1419, PRO1414, PRO183, PRO8247, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers, for treating arthritis and tumor.
                                                                                                                                   CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                       60 LEIREDGIVGGAADQSPESILQLKALKPGVIQILGVKISRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) - alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                    LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen ME, Goddard A, Godowski P
Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                          181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                180 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 208
                                                                                                                                                                                                                                                                                                                                ADC78025 standard; protein; 208 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001; 2001WO-US017B00.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-765529/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADC78024
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09-APR-2002;
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PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1126, PRO1336, PRO1343, PRO1336, PRO1336, PRO1343, PRO1336, PRO1343, PRO1343, PRO1346, PRO1356, PRO1343, PRO1343, PRO1343, PRO1344, PRO1356, PRO1843, PRO1928, PRO1948, PRO1944, PRO1944, PRO1943, PRO1944, PRO1943, PRO1944, PRO1944, PRO1943, PRO1944, PRO1944, PRO1943, PRO1944, PRO1944, PRO1943, PRO1944, PRO1943, PRO1944, PRO1943, PRO1944, PRO1943, PRO1944, PRO1943, PRO1944, PRO1952, PRO1948, PRO1948, PRO1948, PRO1949, PRO1949, PRO1948, PRO1948, PRO1949, PRO1948, PRO1949, PRO1948, PRO1948, PRO1949, PRO1949, PRO1948, PRO1949, PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.7%; Score 1098.5; DB 7; Length 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted and transmembrane protein PRO10196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane PRO polypeptide.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 208 AA;
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ID ADD
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179

US2003073816-A1 Homo sapiens

. PJ; « Wood WI;

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polypeptide (1). rkuyst, rkulley, rkulley, carterior of cr gene expression in caseful for stimulating the proliferation of or gene expression in pericyte cells. PRO257, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO257, PRO255, PRO1305 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF) are useful for stimulating the release of tumour necrosis factor (TNF) are useful for stimulating the release of tumour necrosis factor (TNF) pro157, PRO357, PRO351, PRO1035, PRO1080, PRO1419, P tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue liver tumour or as therapeutic agents. A polyancleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful for generating useful reagents. PRO357, PRO252, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and polypeptide (I) PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are transmembrane PRO polypeptide.

Sequence 208 AA;

61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180 53 1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGGVRQRVLYTDDAQQTEAH 60 LEIREDGIVGGAADQSPESILQLKAIKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH Gaps 1; DB 7; Length 208; Pred. No. 8.6e-91; 0; Mismatches 0; Indels Query Match

Best Local Similarity 99.5%; Pred. No. 8.6eMatches 208; Conservative 0; Mismatches LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 121 181 g ð 셤 g à ò

ADC47150 standard; protein; 208 (first entry) 18-DEC-2003 ADC47150; RESULT 37

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Novel human secreted and transmembrane protein PRO10196.

Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation;

The invention describes an isolated PRU (secreted and transmemorane)

CC polypoptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypoptide are useful for stimulating the proliferation of or gene expression in useful for stimulating the proliferation of or gene expression in constitution the proliferation of or gene expression in pericyte cells. PRO357, PRO125, PRO1136, PRO136 or PRO1419 polypoptide are useful for stimulating the proliferation or differentiation of chondrocyte calpha from human blood. PRO982, PRO3136, PRO1366 or PRO1419, PRO1419, PRO1314, PRO1316, PRO1316, PRO1316, PRO1319, PRO1314, P tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO259, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy. Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; tumour; The invention describes an isolated PRO (secreted and transmembrane) dermal fibroblast cell differentiation inhibitor; tumour; lung colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; Claim 11; Fig 78; 308pp; English. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480. 13-AUG-2002; 2002US-00219070. 25-JUL-2000; 2000US-0220666P. Desnoyers L, (GETH) GENENTECH INC WPI; 2003-801246/75. N-PSDB; ADC47149 JS2003105288-A1. Grimaldi JC, Homo sapiens gene therapy 05-JUN-2003 Baker KP,

transmembrane PRO polypeptide.

Gaps Ή, Score 1098.5; DB 7; Length 208; Pred. No. 8.6e-91; 0; Mismatches 0; Indels 1; 98.7%; Conservative Query Match Best Local Similarity Matches 208; Conserv

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Novel
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transmembrane PRO polypeptide
                                                   Sequence 208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated PRO (secreted and transmembrane)

C polypeptide (I). PRO982, PRO1180, PRO1187 or PRO1292 polypeptide are
polypeptide (I). PRO982, PRO1180, PRO1292 or PRO1292 polypeptide are
cuseful for stimulating the proliferation of of on gene expression in
perioryte cells. PRO357, PRO725, PRO1250, PRO1216 or PRO419 polypeptide
cells. PRO211, PRO357, PRO725, PRO1136, PRO1419 polypeptide
are useful for stimulating the release of tumour necrosis factor (INP)-
are useful for stimulating the release of tumour necrosis factor (INP)-
cells. PRO3131, PRO356, PRO351, PRO1083, PRO1130, PRO1181,
PRO1134, PRO1256, PRO1056, PRO1051, PRO1195, PRO1196, PRO1196,
PRO1184, PRO1136, PRO1186, PRO1195, PRO1197, PRO1197, PRO1196,
PRO1286, PRO1139, PRO1186, PRO1196, PRO1197, PRO1197, PRO1197,
PRO1987, PRO3928 or PRO10056 polypeptide are useful for
PRO1987, PRO5929, PRO188, PRO1197, PRO1197, PRO1197, PRO1326,
PRO1987, PRO5929, PRO188, PRO1197, PRO1197, PRO1197, PRO1197,
PRO1987, PRO5929, PRO188, PRO1197, PRO1198, PRO4341, PRO326,
PRO1987, PRO5929, PRO7186, PRO1197, PRO1197, PRO1197, PRO1197,
PRO1987, PRO5929, PRO7186, PRO1197, PRO1198, PRO4322,
PRO5939, PRO5929, PRO7186, PRO1197, PRO1197, PRO1197, PRO1197,
PRO1987, PRO5929, PRO7186, PRO1198, PRO1197, PRO1198, PRO4302,
PRO5931, PRO5929, PRO7186, PRO1198, PRO1198, PRO4302, PRO4408,
PRO5931, PRO5929, PRO7186, PRO1198, PRO1198, PRO4302, PRO4408,
PRO5931, PRO5932, PRO7198, PRO1198, PRO4302, PRO4408,
PRO5931, PRO5932, PRO7198, PRO1198, PRO4302, PRO4408,
PRO5931, PRO5938, PRO1198, PRO1198, PRO1198, PRO4302, PRO4408,
PRO5931, PRO5938, PRO1198, PRO1198, PRO4302, PRO4408,
PRO5931, PRO5939, PRO5039, PRO5009, PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski PJ;
rk. Wood WI;
                                                                                                                                                             release;
                                                                                     protein; PRO; cytostatic; vulnerary;
                                                                                                          antiarthritic; periotte cell proliferation; perioty cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha chondrocyte cell differentiation; tumour necrosis factor alpha (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung colon tumour; breast tumour; prostate tumour; rectal tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerritsen ME, Goddard A, Godowski F
Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                          liver tumour; tissue typing; chromosome mapping; gene mapping;
                                      human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 78; 315pp; English
                                                                                             transmembrane
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09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2002; 2002US-00232231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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                                                                                                  secreted and
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                                                                                                                                                                                                                                                                                                                                                                                                 JS2003088071-A1
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                   60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPPEA 119
                                                                                                                                                                                                                                                                                 180
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Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNR) -alpha release; dermal fibroblast cell proliferation; cell proliferation; colon tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; issue typing; chromosome mapping; gene mapping;
                                                                                                                                 1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                 CSFRELLLEDGYNVYQSEAHGLFLHLPGNKSPHRDPAPRGPARFLFLPLPGLPPALPEPPGI
                                                                                                                                                                                61 LEIREDGTVGGAADOSPESLLOLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                       1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New PRO polypeptide for use as molecular weight markers for protein electrophoresis purposes and for detecting the presence of tumor in
                                            Gaps
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Watanabe CK,
DB 7; Length 208;
                                               Indels
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Score 1098.5; DB 7;
Pred. No. 8.6e-91;
0; Mismatches 0;
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Smith V, Stephan JF,
                                                                                                                                                                                                                                                                                                                                                                                  LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                               180 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC47405 standard; protein; 208 AA.
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2002; 2002US-00232233
    Query Match
Best Local Similarity 99.5%;
Matches 208; Conservative
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Grimaldi JC, Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                            181
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tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue liver tumour. (I) is useful as molecular weight markers, for tissue useful or as therapeutic agents. A polyamucleotide (II) encoding (I) is useful for generating transgenic animals or knock-out animals which are useful for generating useful reagents. PRO357, PRO252, PRO1572 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.
is indicative of the presence of tumour in the mammal. The tumour is lung
                      8X8888888888XX
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Sequence 208 AA;

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120
                                                                                                                             60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                 121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                 59
                                                        9
                                                                             1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                             61 LEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                     1 MDSDETGFEHSGLWWSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                             Gaps
                             ۲,
 DB 7; Length 208;
Score 1098.5; DB 7; Length
Pred. No. 8.6e-91;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                            LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
  Query Match

Best Local Similarity 99.5%;
Matches 208; Conservative
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Novel human secreted and transmembrane protein PRO10196. ADC49027 standard; protein; 208 (first entry) 18-DEC-2003 ADC49027; RESULT 34

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release; human, secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) -alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;

gene therapy

US2003088070-A1 Homo sapiens

28-AUG-2002; 2002US-00230260 08-MAY-2003.

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, (GETH) GENENTECH INC

WPI; 2003-801155/75 N-PSDB; ADC49026

and nucleic acids encoding the polypeptides, useful New PRO polypeptides and nucleic acids encoding the polypeptides, in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.

Claim 11; SEQ ID NO 78; 315pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
cc useful for stimulating the proliferation of or gene expression in
perioryte cells. PRO357, PRO225, PRO1272 or PRO4405 polypeptide are useful
for stimulating the proliferation or differentiation of chondrocyte
cc ells. PRO313, PRO525, PRO1155, PRO1306 or PRO1419 polypeptide
are useful for stimulating the release of tumour necrosis factor (TNF)are useful for stimulating the release of tumour necrosis factor (TNF)cr PRO127, PRO337, PRO525, PRO531, PRO1306, PRO1141, PRO1414,
PRO1330, PRO1347, PRO1365, PRO1065, PRO1069, PRO1075, PRO1069, PRO1141, PRO1141,
PRO1347, PRO1340, PRO1347, PRO1365, PRO1444, PRO1411, PRO1414, PRO1341,
PRO1366, PRO1367, PRO1367, PRO1369, PRO1474, PRO1414, PRO1414,
PRO1367, PRO1928, PRO4341, PRO1801, PRO1089, PRO1274, PRO1340, PRO1366,
PRO1867, PRO1928, PRO4341, PRO1801, PRO4333, PRO1344, PRO1326,
PRO1867, PRO1928, PRO186, PRO11091, PRO4333, PRO1346, PRO4326,
CC PRO940, PRO6679, PRO986, PRO1079, PRO1488, PRO4322, PRO5425,
PRO181, PRO225, PRO7154, or PRO7435 polypeptide are useful for
CC PRO940, PRO6725, PRO7154, or PRO7435 polypeptide are useful for
CC Inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC Inhibiting the proliferation of normal human dermal fibroblast
CC Involves comparing the presence of tumour, PRO5788, PRO4332, etc.,
CC Involves comparing the presence of tumour in ammal. The tumour is lung
CC Involves comparing the presence of tumour, rectal tumour or
CC the PRO polypeptides in the test sample as compared to the control sample
CC Involves comparing the presence of tumour, rectal tumour or
CC Typing, color tumour, breast tumour, prostate tumour, rectal tumour or
CC Typing, color tumour, breast tumour, prostate tumour, rectal tumour or
CC Typing, color presence and gene mapphing or gene therapeutic agents. PRO495 polypeptide
CC Sercening us transmembrane PRO polypeptide.

Sequence 208 AA;

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120 180 59 60 LEIREDGIVGGAADQSPESLLQLKALKPGVIQILGGVKTSRFLCQRPDGALYGSLHFDPEA CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSSPLLQFGGQVRQRYLYTDDAQQTEAH LEIREDGTVGGAADQSPESLLQIKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 7: DB 7; Length 208; Indels Score 1098.5; DB 7; Pred. No. 8.6e-91; 0; Mismatches 0; 98.7%; Query Match
Best Local Similarity 99.5
Matches 208; Conservative 61 121

LAPQPEDVGSSDPLSMVGPSQGRSPSYAS 208 ADC49544 standard; protein; 208 AA. RESULT 35 ADC49544 EXXXE 셤

181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209

ð d Š 18-DEC-2003 (first entry)

ADC49544;

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them. The PRO polypucleotides encoding them. The PRO polypucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, retain tumour or liver tumour, in a mammal, for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood, for stimulating the proliferation of differentiation of conditoryte cells, for stimulating the proliferation of or gene expression in perioyte cells or for stimulating the proliferation of or gene expression in perioyte cells or for stimulating the proliferation of normal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating anticense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which markers and in generating probes. The PRO polypeptides, or anti-PRO markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, such as perioyte-associated tumours and home and/or cartilage antibodies, such as perioyte-associated tumours and home and/or cartilage antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated PRO polypeptide useful for tissue typing, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.
                                                                                                                                                                                                                                                                                                               Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 78; 308pp; English.
             2000WO-US023328.
2000WO-US030873.
2000US-0253646P.
                                                                                                                                                              25-MAY-2001; 2001WO-US017092.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
                                                                         2000WO-US032678.
2000US-00747259.
2000WO-US034956.
                                                                                                                                            28-FEB-2001; 2001WO-US006520
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Matches 208; Conservative
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Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
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                                                                                                  20-DEC-2000;
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                                                                                01-DEC-2000;
                                                     28-NOV-2000;
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1; Gaps 98.7%; Score 1098.5; DB 7; Length 208; 99.5%; Pred. No. 8.6e-91; Pred. No. 8.6e-91; 0; Mismatches 0; Indels

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LEIREDGIVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPGGALYGSLHFDPEA 119 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPG1 179 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120 121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180 09 1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 59 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 9 120 셤 ð g

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ADC49828 standard; protein; 208 AA. RESULT 33 ADC49828

ADC49828;

(first entry) 18-DEC-2003 Novel human secreted and transmembrane protein PRO10196

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy

Homo sapiens.

US2003088064-A1.

08-MAY-2003.

14-AUG-2002; 2002US-00219075.

25-JUL-2000; 2000US-0220605P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Wood WI Goddard A, Godowski PJ; phan JF, Watanabe CK, W Gerritsen ME, Goddard Smith V, Stephan JF, ķ, Desnoyers I Grimaldi JC, Baker

WPI; 2003-801154/75. N-PSDB; ADC49827.

ĸ New secreted and transmembrane PRO polypeptide useful for preparing medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody, e.g. cancer.

Claim 11; SEQ ID NO 78; 314pp; English.

Life invention unsuscribed an isolated fro (sected and Laimmentaine) polypeptide (I). PR0982, PR01812 or PR01329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PR0357, PR02259, PR01272 or PR04405 polypeptide are useful for stimulating the proliferation of differentiation of chondrocyte cells. PR0357, PR0725, PR01155, PR01306 or PR01419 polypeptide are useful for stimulating the release of tumour necrossis factor (TMP)-care useful for stimulating the release of tumour necrossis factor (TMP)-care useful for stimulating the release of tumour necrossis factor (TMP)-care useful for stimulating the release of tumour necrossis factor (TMP)-care useful for stimulating the PR0357, PR01037, PR01036, PR01419, PR01419, PR01186, PR01181, PR01881, PR018881, PR018888881, PR01 The invention describes an isolated PRO (secreted and transmembrane)

us-10-060-765-4.rag

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LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC21797 standard; protein; 208
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2000US-0219556P
2000US-0220585P
2000US-0220605P
2000US-022067P
2000US-022064P
2000US-0220634P
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2000US-0222425F.
2000US-0227133F.
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2000US-0212901P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO polypeptide #39.
                                                                                                                                                                         Query Match
Best Local Similarity 99.5
Matches 208; Conservative
                                                                                                                                              Sequence 208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynucleotides encoding them. The PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosenosis or bioreactors. They are particularly useful for diagnostics, biosenosis or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMP)-alpha from human lood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells or for stimulating the proliferation of or gene or normal human dermal fibrollasts. The PRO nucleic acids are useful as normal human dermal fibrollasts. The PRO nucleic acids are useful as antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which
                                                                                                                         CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                    LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                             60 LEIREDGIVGGAADOSPESLLOLKALKPGVIQILGVKTSRFLCORPDGALYGSLHFDPEA 119
                Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
  MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                Human, PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, or for preparing a medicament for treating
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Smith V, Stephan JF,
                                                                                                                                                                                  180 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 208
                                                                                                                                                                  LAPOPPDYGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                             ADC36807 standard; protein; 208 AA.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                             Human PRO polypeptide #39.
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Grimaldi JC, Gurney AL,
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ADC36807
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may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sporte injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.7%; Score 1098.5; DB 7; Length
99.5%; Pred. No. 8.6e-91;
iive 0; Mismatches 0; Indels
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The invention describes an isolated PRO (secreted and transmembrane)

co polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

cols. PRO357, PRO235, PRO1272 or PRO405 polypeptide are useful

cor stimulating the pro116eration of of gene expression in

periotyc cells. PRO357, PRO725, PRO1306 or PRO1419 polypeptide

cols. PRO231, PRO357, PRO725, PRO1306 or PRO1419 polypeptide

cols. PRO231, PRO357, PRO725, PRO1306, PRO1419, PRO214,

pro147, PRO3137, PRO526, PRO531, PRO1908, PRO1419, PRO1411,

PRO147, PRO3137, PRO526, PRO1059, PRO531, PRO1060, PRO1412,

PRO147, PRO3137, PRO1305, PRO1305, PRO1073, PRO1244, PRO1314,

PRO1307, PRO1307, PRO1305, PRO1305, PRO1073, PRO1412, PRO1412,

PRO148, PRO13130, PRO1305, PRO1005, PRO1173, PRO1411, PRO1412,

PRO148, PRO1307, PRO1305, PRO1186, PRO1197, PRO1411, PRO1412,

PRO148, PRO1307, PRO1305, PRO1109, PRO1437, PRO1411, PRO1412,

PRO1307, PRO1307, PRO1305, PRO1109, PRO1437, PRO1412,

PRO143, PRO1525, PRO7154, PRO11001, PRO4333, PRO144, PRO1322,

PRO143, PRO525, PRO7154, Or PRO1005 polypeptide are useful for

PRO523, PRO5725, PRO7154, Or PRO7152, PRO1469, PRO4408,

PRO5724, PRO5725, PRO7154, Or PRO7152, PRO1714, PRO5778, PRO4408,

PRO141, PRO5725, PRO7154, Or PRO7152, PRO1714, PRO5778, PRO4408,

PRO5724, PRO5725, PRO7154, Or PRO7425 polypeptide are useful for detecting the presence of tumour in ammal which ammal which

are useful for detecting the presence of tumour incental tumour or

contain the PRO polypeptides in the test sample as compared to the control sample of

in a test sample of cells taken from the mammal, and a control sample of

in a test sample of cells taken from the mammal, The tumour is lung

contain cells of the same cell type, where a higher level of expression of

the PRO polypeptides in the test sample as compared to the control sample

contain cells of the same cell type, where a higher level of expression of

the PRO polypeptides in the test sample as compared (II) encoding (II)

colspeptides are sample of cells taken from the mammal, and a c

CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180 61 LBIREDGTVGGAADQSPESILIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH Query Match 98.7%; Score 1098.5; DB 7; Length 208; Best Local Similarity 99.5%; Pred. No. 8.6e-91; Matches 208; Conservative 0; Mismatches 0; Indela 1. 181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 208 transmembrane PRO polypeptide. Sequence 208 AA; 121 120 180 원 g ò 8 셤 ð d à

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Gaps

ADB72969 standard; protein; 208 AA. (first entry) 04-DEC-2003 ADB72969 ADB72969
ID ADB7
XX ADB7
XX ADB7
DT 04-D
DT 04-D
XX B huma
KW anti

Novel human secreted and transmembrane protein PRO10196.

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation;

chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNE)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping gene therapy

Homo sapiens

US2003092887-A1.

12-AUG-2002; 2002US-00218956. 15-MAY-2003.

29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-777258/73. N-PSDB; ADB72968 Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers, for treating arthritis, tumor.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (I). PR0982, PR01160, PR01187 or PR01129 polypeptide are useful for stimulating the proliferation of or gene expression in periotyte cells. PR0357, PR0229, PR01272 or PR04405 polypeptide are useful for stimulating the proliferation of differentiation of chondrocyte cells. PR0357, PR0725, PR01155, PR01196 or PR01419 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PR0331, PR0982, PR0353, PR01255, PR01306 or PR04419, PR0419, PR0214, PR0247, PR0337, PR0526, PR0363, PR0537, PR0725, PR01306, PR0419, PR01419, PR0214, PR0247, PR0337, PR0526, PR0363, PR01083, PR01244, PR01340, PR01349, PR01340, PR01340, PR01340, PR01341, PR01360, PR01344, PR01360, PR01344, PR01360, PR01343, PR01376, PR01360, PR01383, PR01344, PR01360, PR01383, PR01343, PR01380, PR01381, PR01380, PR01 tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO257, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

Sequence 208 AA;

ï Gaps Ξ; DB 7; Length 208; Indels 98.7%; Score 1098.5; DB 7; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Conservative Similarity Matches 208; Query Match Best Local S

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Matches
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Transmembrane polypeptides and polypublecetides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours fe.g. huma tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene capression in pericyte cells or for stimulating the proliferation of or gene or probes, in chromosome and gene mapping, in generating are useful as hybridisation probes, in chromosome and gene mapping, in generating cantisense RNA and DNA, in preparing PRO polypeptides by recombinant centionogy, in generating transgenic animals or knock-out animals which reagents, in gene therapy, in chromosome identification, as chromosome condition which is responsive to the PRO polypeptides, or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the re-
CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated PRO polypeptides, useful for tissue typing, gene therapy, molecular weight markers in protein electrophoresis, and for treating
                                                                                                                                                                                                             Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breat; prostate; rectum; liver; tumour necrosis factor-alpha; TNP-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
                             209
                                                      208
                                            LAPQPPDVGSSDPLSWVGPSQGRSPSYAS
                              LAPOPPDVGSSDPLSMVGPSQGRSPSYAS
                                                                                                                    ADB84699 standard; protein; 208 AA.
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02-MAR-2000; 2000WO-US005841.
01-JUN-2001; 2010WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                      (first entry)
                                                                                                                                                                                             Human PRO polypeptide #39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis and tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
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Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                                                                                                                                                                                                                                                  61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
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differentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                 1;
                                                                                                                                       Length 208;
                                                                                                                                                                                    Indels
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                                                                                                                                          DB 7;
                                                                                                                                     Score 1098.5; DB 7;
Pred. No. 8.6e-91;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB83814 standard; protein; 208
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2001WO-US021066.
2002US-00119480.
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208; Conservative
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                                                                                                    Sequence 208 AA;
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29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                 Query Match
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ADB87117 standard; protein; 208 AA 04-DEC-2003 (first entry) Human PRO polypeptide #39 Sequence 208 AA; 121 181 ADB87117; 180 RESULT 27 ADB87117
ID ADB6
XX
AC ADB6
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XX
DT 04-I
XX
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The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (1). PRO982, PRO1160, PRO1187 or PRO129 polypeptide are
polypeptide (1). PRO982, PRO1160, PRO1187 or PRO129 polypeptide are
cc useful for stimulating the proliferation of or gene expression are
cc lis. PRO317, PRO329, PRO3120, PRO419 polypeptide are useful
cc ells. PRO317, PRO357, PRO7125, PRO1190 polypeptide
are useful for stimulating the release of tumour necrosis factor (TNP)
are useful for stimulating the release of tumour necrosis factor (TNP)
cr pro1134, PRO3136, PRO9126, PRO91095, PRO91095, PRO1191, PRO1141, PRO1130,
PRO1134, PRO1136, PRO1186, PRO1192, PRO1197, PRO1141, PRO1191,
PRO1137, PRO1137, PRO1186, PRO1192, PRO1197, PRO1141, PRO1191,
PRO1193, PRO9136, PRO9136, PRO9106, PRO1193, PRO1194, PRO1192,
PRO1184, PRO11928, PRO9136, PRO9106, PRO1193, PRO1194, PRO1192,
PRO1184, PRO11928, PRO9136, PRO9106, PRO1193, PRO1194, PRO1192,
PRO1184, PRO11928, PRO9134, PRO1106, PRO1193, PRO1194, PRO1192,
PRO1184, PRO11928, PRO9134, PRO1106, PRO1193, PRO1194, PRO1192,
PRO1184, PRO11928, PRO9134, PRO1106, PRO1192, PRO1194, PRO1192,
PRO1184, PRO11928, PRO9134, PRO1106, PRO1192, PRO1194, PRO1192,
PRO1184, PRO11928, PRO9194, PRO1106, PRO1192, PRO1194, PRO1192,
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PRO1184, PRO11928, PRO9194, PRO1197, PRO1194, PRO1192,
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PRO1194, PRO11928, PRO9194, PRO1194, PRO1192, PRO1194, PRO9192, PRO9194,
PRO1194, PRO1195, PRO9194, PRO1195, PRO1194, PRO9194, PRO9
Claim 11; Fig 78; 308pp; English.
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CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180 120 CSFREILLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 179 61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 1 MDSDETGFEHSGIWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH Gaps ا : DB 7; Length 208; Score 1098.5; DB 7; Length Pred, No. 8.6e-91; 0; Mismatches 0; Indels LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 208 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 98.7%; Query Match Best Local Similarity 99.5 Matches 208; Conservative

120

9 59

CSFRELLLEDGXNVYQSBAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180 60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPBA 119 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120 1 MDSDETGFEHSGLWYSYLAG-LLGACQAHPIPDSSPLLQFGGGVRQRYLYTDDAQQTEAH MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH Score 1098.5; DB 7; Length 208; Pred. No. 8.6e-91; 0; Mismatches 0; Indels 1; 98.78; Matches 208; Conservative Similarity Н 61 121 Query Match Best Local ਨੋ 셤 à Dp ð

Sequence 208 AA;

7;

Gaps

1;

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them. The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF) -alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene cormal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating transgenic animals which may be used in the development and screening of therapeutically useful reagents, in generating probes. The PRO polypeptides by recombinant reagents, in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing medicament for treating a methodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which servers and in the development and propess or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which servers and surgeness and the properties or anti-PRO condition which servers and surgeness and servers and surgeness and servers and surgeness and servers and server antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as Wood WI; molecular markers for protein electrophoresis, and in tissue typing. sequence represents a human PRO polypeptide of the invention. Human, PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic. One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, o hybridization probes in chromosome and gene mapping. Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, W claim 11; Fig 78; 314pp; English. 01-JUN-2001; 2001MO-US017800. 29-JUN-2001; 2001MO-US021066. 09-APR-2002; 2002US-00119480. 13-AUG-2002; 2002US-00219479. Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, (GETH) GENENTECH INC. WPI; 2003-657981/62. N-PSDB; ADB87116 US2003088067-A1 Homo sapiens. 08-MAY-2003. 1;

Gaps

1;

DB 7; Length 208;

9 59 119 180 179

us-10-060-765-4.rag

RESULT 25 ADB84945

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Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers in protein electrophoresis, for treating
condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducting the redifferentiation of chondrocytes. PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release (TNF) alpha release, dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; tumour; lung tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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Smith V, Stephan JF, Watanabe CK,
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                                                                                                                                                                                                                                                                                                Score 1098.5; DB 7; Lengtl:
Pred. No. 8.6e-91;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human secreted and transmembrane protein PRO10196.
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
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nes 208; Conservative
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                                                                                                                                                                                                                                                    Sequence 208 AA;
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09-APR-2002;
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Grimaldi JC,
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                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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transmembrane polypeptides) and the PRO polymucleotides encoding them.

The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumnours (e.g. lung tumnour, colon tumnour, brast tumnour, prostate tumnour, rectal tumnour necrosis factor (TMP)-alpha from human blood, for stimulating the proliferation or differentiation of conductoryte cells, for stimulating the proliferation of or gene expression in pericyte cells or for stimulating the proliferation of or gene normal human dermal fibroblasts. The PRO nucleic acids are useful as normal human dermal fibroblasts. The PRO nucleic acids are useful as normal human dermal fibroblasts may proparing to hypeptides by recombinant antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals of therapeutically useful reagents, in generating probes. The PRO polypeptides, or anti-PRO markers and in generating probes. The PRO polypeptides, or anti-PRO markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a matibodies, are useful for preparing a medicament for treating a
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Wood WI;
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Smith V, Stephan JF, Watanabe CK,
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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release;

Godowski PJ;

Wed Mar

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are useful for stimulating the release of tumour necrosis factor (TNF)-
alpha from human blood. PRO362, PRO357, PRO725, PRO1306, PRO1419, PRO214,
PRO247, PRO337, PRO526, PRO363, PRO5619, PRO1806, PRO1419, PRO1414,
PRO1478, PRO1134, PRO8126, PRO1106, PRO1909, PRO1071, PRO1411, PRO1309,
PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1374, PRO1340,
PRO1387, PRO1376, PRO1347, PRO1340, PRO1474, PRO1340, PRO1340,
PRO1887, PRO4936, PRO494, PRO4333, PRO3444, PRO4322,
PRO1887, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
stimulating the pro11feration of normal human dermal fibroblasts cells.
PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells.
                                                                                                                                                                                                                                                                                                                                                                                             polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of calls taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue tryping, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful is useful leagents. PRO327, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ransmembrane PRO polypeptide
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Sequence 208 AA;

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120
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                                                                                                                                                                                  60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                                                                                 59
                                                                                                           1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                    LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                                                                                                                                                            121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI
                                                                           1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                       1; Gaps
98.7%; Score 1098.5; DB 7; Length 208; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                         LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                               208
                                                                                                                                                                                                                                                                                                                                             LAPOPPDVGSSDPLSMVGPSQGRSPSYAS
     Query Match
Best Local Similarity 99.5
Matches 208; Conservative
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Novel human secreted and transmembrane protein PRO10196 ADB78297 standard; protein; 208 (first entry) 04-DEC-2003 ADB78297; RESULT 24

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Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiathritic; perioyte cell proliferation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; chongone mapping; gene mapping; gene therapy

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1129 polypeptide are useful for stimulating the proliferation of or gene expression in useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO225, PRO1155, or PRO4105 polypeptide are useful for stimulating the proliferation of or gene expression in cells. PRO31, PRO357, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood. PRO982, PRO3137, PRO1305, PRO1419, PRO1314, PRO1317, PRO1305, PRO1181, PRO1181, PRO1181, PRO1181, PRO1181, PRO1182, PRO1181, PRO1881, PRO1981, PRO1981 tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue ryping, or as therapeutic agents. A polymucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful is useful leagents. PRO357, PRO259, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and Wood WI; New isolated PRO polypeptide useful for tissue typing, gene therapy, amolecular weight markers in protein electrophoresis, and for treating the invention describes an isolated PRO (secreted and transmembrane) Godowski PJ; Goddard A, Goucher TR. Watanabe CK, Gerritsen ME, Goddard Smith V, Stephan JF, Claim 11; Fig 78; 308pp; English transmembrane PRO polypeptide. 01-JUN-2001; 2001MO-US017800. 29-JUN-2001; 2001MO-US021066. 09-APR-2002; 2002US-00119480. 13-AUG-2002; 2002US-00219478. Desnoyers L, (GETH) GENENTECH INC. WPI; 2003-765495/72. N-PSDB; ADB78296. Sequence 208 AA; US2003092889-A1 Homo sapiens. Baker KP, De Grimaldi JC, 15-MAY-2003

1; Gaps 98.7%; Score 1098.5; DB 7; Length 208; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Indels 1; Query Match Best Local Similarity 99.5 Matches 208; Conservative

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61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120

%\$GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

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antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
proliferation;
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Homo sapiens.

US2003088068-A1

08-MAY-2003

13-AUG-2002; 2002US-00219481

01-JUN-2001; 2001MO-US017800. 29-JUN-2001; 2001MO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Wood WI; Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, W Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-657982/62. N-PSDB; ADB80673 One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or hybridization probes in chromosome and gene mapping.

Claim 11; Fig 78; 305pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I) PRO982, PRO1160, PRO1197 or PRO1329 polypeptide are

colsusful for stimulating the proliferation of or gene expression in

perioryce cells. PRO357, PRO222, PRO1272 or PRO4405 polypeptide are useful

cor stimulating the proliferation of differentiation of chondrocyte

cells. PRO31, PRO357, PRO72, PRO1155, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)
cells. PRO31, PRO357, PRO357, PRO725, PRO1106, PRO1419, PRO214,

PRO130, PRO3134, PRO326, PRO3105, PRO3176, PRO1244, PRO1116, PRO1186,

PRO143, PRO337, PRO1126, PRO1186, PRO1197, PRO1141, PRO1309,

PRO143, PRO337, PRO136, PRO1186, PRO1197, PRO1141, PRO1309,

PRO136, PRO1381, PRO357, PRO1186, PRO1197, PRO1411, PRO1309,

PRO136, PRO1381, PRO356, PRO1186, PRO1193, PRO1444, PRO13124,

PRO1364, PRO327, PRO9836 or PRO1086, PRO1273, PRO1444, PRO1312,

PRO1364, PRO529, PRO9836 or PRO10805 polypeptide are useful for

cryptogrides such as PRO6004, PRO4333, PRO3444, PRO3414,

PRO523, PRO375, PRO7184, PRO19197, PRO1486, PRO432,

CROMINIATING the proliferation of normal human dermal fibroblast cells.

CROMINIATING the proliferation of normal human dermal fibroblast cells.

CROMINIATION of the proliferation of normal human dermal fibroblast cells.

CROMINIATION of the proliferation of normal human dermal fibroblast cells.

CROMINIATION of the proliferation of normal human dermal fibroblast cells.

CROMINIATION of the proliferation of normal human dermal fibroblast cells.

CROMINIATION of the proliferation of normal human dermal fibroblast cells.

CROMINIATION of the same cell type, where a higher level of expression of the above PRO polypeptides in the test sample of cells taken from the mammal, and a control sample tumour, breast tumour, prostate tumour, rectal tumour of tumour, breast tumour, prostate tumour, rectal tumour of tumour, breast tumour, prostate tumour, rectal tumour of the mammal properties of suseful for transing beneful transmembrane PRO polypeptide.

Sequence 208 AA;

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO359, PRO229, PRO122 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO351, PRO355, PRO1155, PRO1306 or PRO1419 polypeptide

Claim 11; Fig 78; 308pp; English.

arthritis and tumors.

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                                                                                                                                             60 LEIREDGTVGGAADQSPESILQIKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                            human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                               1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGGVRQRYLYTDDAQQTEAH
                                                                     1 MDSDETGFEHSGLWVSVIAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                            61 LEIREDGTVGGAADQSPESILIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                                                                                                                CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGI
                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated PRO polypeptides useful as molecular weight markers in protein electrophoresis, useful for tissue typing, and for treating
                  DB 7; Length 208;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted and transmembrane protein PRO10196.
Score 1098.5; DB ',
                               Pred. No. 8.6e
0; Mismatches
                                                                                                                                                                                                                                        181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                         180 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 208
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                  98.7%;
99.5%;
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Grimaldi JC, Gurney AL,
                                 Best Local Similarity 99.5
Matches 208; Conservative
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                     Query Match
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Claim 11; Fig 78; 315pp; English

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 invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the invention
                                                                                                                                                                                                                                                                             LEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                                                                                                                                                                                                                                                     LEIREDGIVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPBA 119
                                                                                                                                                                                                                                                                                                                                                                     CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; prostate tumour; prostate tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                     1 MDSDETGFEHSGLWVSVLAGLILGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                 Gaps
cytostatic activities through the stimulation of
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                                                                                                                                                Score 1098.5; DB 7; Length 208;
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0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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99.5%;
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Grimaldi JC, Gurney
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N-PSDB; ADB83567.
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Best Local Similarity
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                                                                                                                  Sequence 208 AA;
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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1229 polypeptide are

to useful for stimulating the proliferation of or gene expression in

pericyte cells. PRO327, PRO222, PRO11272 or PRO4405 polypeptide are useful

for stimulating the proliferation or differentiation of chondrocyte

cells. PRO3131, PRO325, PRO1185, PRO1186 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNR)-

alpha from human blood. PRO982, PRO3157, PRO1260, PRO1419, PRO214,

PRO125, PRO1181, PRO9126, PRO1186, PRO1192, PRO1244, PRO1411, PRO1412,

CC PRO1025, PRO1181, PRO1186, PRO1192, PRO1244, PRO1274, PRO1318,

CC PRO1286, PRO137, PRO1305, PRO1305, PRO1274, PRO1274, PRO13138,

CC PRO1887, PRO328, PRO4341, PRO1801, PRO4333, PRO3444, PRO4322,

CR STIMULATING the proliferation of normal human dermal fibroblasts cells.

CR STIMULATING the proliferation of normal human dermal fibroblasts cells.

CR STIMULATING the proliferation of normal human dermal fibroblast cells.

CR STORO980, PRO6708, PRO7184, or PRO7425, PO19Peptide are useful for

stimulating the proliferation of normal human dermal fibroblasts cells.

CR STORO980, PRO6704, PRO491, PRO7778, PRO3488, PRO4322, PRO4788, PRO1184, PRO1378, PRO4322, PRO5725, PRO7788, PRO1544, or PRO7425, PRO1784, PRO3778, PRO3784, PRO5778, PRO5778,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO465 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CSFREILLIEDGYNVYQSEAHGIPIHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
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Pred. No. 8.6e-91;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted and transmembrane protein PRO10196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.5
Matches 208; Conservative
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Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;

180

60 LEIREDGIVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119

61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA

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Human membrane bound receptor/protein PRO10196 amino acid sequence.

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ABJ72096 standard; protein; 208

RESULT 20 ABJ72096 16-OCT-2003 (first entry)

ABJ72096;

Human, PRO, membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; oytotoxic factor; addifferentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.

2000WO-US005004. 2000WO-US005841. 2001WO-US017800. 2001WO-US021066.

24-FEB-2000; 02-MAR-2000; 01-JUN-2001;

09-APR-2002; 2002US-00119480

29-JUN-2001;

(GETH) GENENTECH INC.

99US-0146222P.

28-JUL-1999;

29-AUG-2002; 2002US-00232224.

US2003065147-A1.

03-APR-2003

Homo sapiens.

121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI

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acute lung injury; acute respiratory distress syndrome;
multiple organ dysfunction syndrome; sepsis;
chronic obstructive pulmonary disease; emphysema; chronic bronchitis;
panorcatitis; ischaemia; multiple trauma; tissue injury;
haemorrhagic shock; immune-mediated organ injury; shock; renal failure.
                                                                                mortality, morbidity, fibroblast growth factor 21; FGF-21; antinfilammatory, respiratory, antibacterial; immunosupressive; vasotropic, haemostatic; nephrotropic; glucose level regulator; glucose uptase stimilator; insulin sensitivity enhancer; systemic inflammatory response syndrome; respiratory distress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.7%; Score 1098.5; DB 7; Length 208; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Indels 1;
                                                              Human fibroblast growth factor 21 SEQ ID NO:1.
ADA37038 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                           08-JAN-2003; 2003WO-US000010.
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                                           (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 208 AA;
                                                                                                                                                                                                                              WOZ003059270-A2
                                                                                                                                                                                                           Homo sapiens
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                                           20-NOV-2003
                                                                                                                                                                                                                                                                                                                                           Heuer JG,
                       ADA37038;
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The present invention describes a method for the reduction of mortality and morbidity in critically ill patients, which involves the administration of fibroblast growth factor 21 (FGF-21) (1). (1) has antinflammatory, respiratory, antibacterial, immunosuppressive, vasotropic, heemostatic and nephrotropic activities, and an insulin solution elevation regulator. a glucose uptake stimulator, and an insulin ensity enhancer. (1) can be used in the manufacture of a medicament for the reduction of morbidity and mortality in critically ill patients suffering from systemic inflammatory response syndrome (SIRS), respiratory distress, acute lung injury, response syndrome (SIRS), respiratory distress, acute lung injury, acute respiratory distress syndrome, multiple organ dysfunction syndrome, sepsis and chronic cobstructive pulmonary disease (e.g. emphysema and chronic bronchitis). The SIRS includes pancreatitis, isothemia, multiple trauma and tissue injury, haemorrhagic shock, immune-mediated organ injury, shock and renal disease. STAT regulates glucose levels in response to sepsis; reduces morbidity and mortality that occurs in critically ill patients, and stimulates glucose uptake and enhances insulin sensitivity. The present sequence represents the human FGF-21 amino acid sequence, which is given in the exemplification of the present invention.
Use of fibroblast growth factor 21 for reduction of mortality and morbidity in patients suffering from e.g. systemic inflammatory response syndrome and acute respiratory distress syndrome.
                                                                                                                                                                                                                                                             Disclosure; Page 15-16; 22pp; English.
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This invention relates to one hundred and twenty two novel nucleic acids encoding human PRO membrane bound proteins or receptors. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate printenance. The information is often transmitted by secreted printenance. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor liquand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Fig 78; 315pp; English.
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Grimaldi JC, Gurney AL,
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N-PSDB; ABT43920.
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1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 60
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1;

Conservative

208;

Matches

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60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel isolated PRO protein encoding nucleic acid. The nucleic acid of the invention may be useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a useful in a mammal. Furthermore, the molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells, the release of tumour necrosis factor (TNF)-alpha from human blood, the proliferation or differentiation of chordrocyte cells and for inhibiting the proliferation of normal human dermal fibroblast cells. Finally, the molecules may be utilised during gene therapy. The current sequence is that of the human PRO protein of the invention
                                                                                                                                                                                                                                                                                                       A, Godowski PJ;
Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte; tumour necrosis factor; proliferation; differentiation; gene therapy; dermal fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                       New PRO protein encoding nucleic acid, useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence tumor in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.7%; Score 1098.5; DB 6; Length 208; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted/transmembrane polypeptide PRO 10196.
                                                                                                                                                                                                                                                                                                       Gerritsen ME, Goddard A,
Smith V, Stephan JF, Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Fig 78; 324pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; protein; 208
                                                                                                                                                                         26-AUG-2002; 2002US-00227884.
                                                                                                                                                                                                          01-JUN-2001; 2001WO-US017800.
                                                                                                                                                                                                                        29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                           Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
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Best Local Similarity
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N-PSDB; ABT44547
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                                                                                                         US2003027988-A1.
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                                                                           Homo sapiens
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AC ABO3
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The invention relates to an isolated nucleic acid encoding a PRO polypeptide. Nucleic acids that encode PRO can be used to generate either transgenic animals or knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy for replacing defective gene, in chromosome identification, as chromosome markers, or in generating probes to isolate till length PRO cDNA. The PRO polypeptides are useful for chondrocyte stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation and for detecting the presence of tumour in an mammal. The PRO polypeptides are useful as molecular markers for protein electrophoresis and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing, Anti-PRO antibodies are useful in diagnostic assays for pro and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents the amino acid sequence of a human secreted/transmembrane PRO polypeptide
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                                                                                                                                                                                                                                                                                                                                                             Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes.
              gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.7%; Score 1098.5; DB 6; Length 208; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0; Indels 1;
          Human, chondrocyte stimulation, TNF-alpha stimulation, gene
human dermal fibroblast stimulation, tumour, tissue typing,
affinity purification.
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                                                                                                                                                                                                             28-AUG-2002; 2002US-00230338
                                                                                                                                                                                                                                                               29-JUN-2001; 2001WO-US021066
09-APR-2002; 2002US-00119480
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Best Local Similarity 99.5
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                 Baker KP, Desnoyers
Grimaldi JC, Gurney
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                                                                                                                                US2003044934-A1
                                                                                              Homo sapiens
                                                                                                                                                                    06-MAR-2003
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120

9 59

Gaps

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179

RESULT 19 ADA37038 13

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Homo sapiens
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AC ABJ7
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DT 06-1
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                                                                                                                                                                                                                                                                            The present sequence represents human fibroblast growth factor 21 (FGP-21). FGF-21 is located to chromosome 19, more specifically to 19q13.1-qter. The present invention describes a method for treating a mammal exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal for obesity which comprises administering to the mammal a composition comprising FGF-21 which has at least 95% amino acid sequence dientity to the 20% amino acid sequence given in ABP96156. Also described: (1) inducing an increase in glucose uptake in adipocyte cells by administering FGF-21 to induce an increase in glucose uptake, and (2) manufacturing a medicament for treating type 1 diabetes, type 2 diabetes or obesity in a mammal using FGF-21 having 95% amino acid sequence identity to ABP96156. FGF-21 has antidiabetic and anorectic activities. The method is useful for treating a mammal exhibiting type 2 or 1 diabetes or for treating a mammal exhibiting type 2 or 1 diabetes or for treating a mammal for obesity. The method is preferably useful for treating humans exhibiting type 1 or type 2 diabetes, and for treating domestic animals for obesity per 1 or type 2 diabetes, and for treating domestic animals for obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                    Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or obesity, by administering composition comprising fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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                                                                                                                                   Shiyanova TL;
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                                                                                                                                    Kharitonenkov A,
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                                                                                                                                                                                                                                                          Claim 3; Fig 1; 32pp; English
                                                                2001US-0308702P.
2002US-0347991P.
                                       22-JUL-2002; 2002WO-US021290
                                                                                                                                   Glasebrook AL, Hammond LJ,
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208; Conserv
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                                                                                                                                                                            N-PSDB; ABZ79797
                                                                   30-JUL-2001;
10-JAN-2002;
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                13-FEB-2003.
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Best Local Si
Matches 208;
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The invention relates to a novel isolated nucleic acid encoding a fully defined PRO polypeptide. The molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells or the release of TMF-alpha from human blood. Other possible uses include the stimulation or inhibition of chondrocyte proliferation or differentiation, the stimulation of human dermal fibroblast cell proliferation and the detection of the presence of a tumour within a mammal. Furthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or a medicament for detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding for a PRO protein, useful for the manufacture of a medicament for diagnosing or treating tumors or for measuring or detecting expression of an associated gene.
                                                                                                                                                                                                                                                                                                                                                                            Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
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09-APR-2002; 2002US-00119480.
                                                                                                                       28-AUG-2002; 2002US-00230414
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Best Local Similarity 99.5%;
Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   Desnoyers L, C, Gurney AL,
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                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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US2003050448-A1
                                                                                                                                                                                                                                                                                                                                                                                                                    Grimaldi JC,
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                                                              13-MAR-2003
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tully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122 nucleotide sequences. The RNO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are community breast tumour, prostate tumours (e.g. lung tumour, or liver tumour) in a mammal, for stimulating the release of TNF-alpha from human blood, or commal human dermal fibroblast proliferation of fiferentiation of chondrocyte cells, for stimulating proliferation of pericyte cells, or for modulating normal human dermal fibroblast proliferation. The RNO nucleic acid or polypeptide is also useful in drug screening, particularly as targets or arthritis or wounds. The RNO polypeptides are useful in drug screening, particularly as targets for the presence of these diseases, and in the diagnostic determination of the presence of these diseases. The RNO polypeptides are useful as molecular weight markers, or for cheromosome contential in drug screening, particularly as targets indentification. The RNO genes are useful as hybridiation probes, or for screening libraries of human cond, genomic DNA or mRNA. The RNO genes may also be used in gene therapy, particularly for replacing a defective consuments and the sequence of a novel human secreted and transmembrane RNO polypeptide.
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Sequence 208 AA;

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120 CSFREILLEDGYNVYQSEAHGLPLHPGNKSPHRDPAPRGPARFLPLPGLPPALPEPGT 179
                                                                                                                        LEIREDGTVGGAADOSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                                                                                           121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
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                                                                                         1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                            1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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Score 1098.5; DB 6; Length 208; Pred. No. 8.6e-91; 0; Mismatches 0; Indels 1;
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ABU82086 standard; protein; 208 AA. (first entry) 25-JUN-2003 RESULT 14 ABU82086

Novel human secreted and transmembrane protein PRO10196

Human; secreted and transmembrane protein; PRO; cardiant; cytostatic; antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertroph; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; atterial restenosis; rhemarcid arthritis; angins; mycardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.

Homo sapiens

US2003088063-A1

Human; fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter; diabetes; obesity; antidiabetic; anorectic; type 2 diabetes; type 1 diabetes.

WO2003011213-A2

Homo sapiens.

Human fibroblast growth factor 21 protein SEQ ID NO:2.

(first entry)

12-MAY-2003

ABP96156;

ABP96156 standard; protein; 208 AA

08-MAY-2003

12-AUG-2002; 2002US-00219003

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60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDFEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, agerelated macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, ungina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 179
                                                                                                                                       Godowski PJ;
~ Wood WI;
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                                                                                                                                                                                                                                                                          One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
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                                                                                                                                                        Gerritsen ME, Goddard A, Godowski P. Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 98.7%; Score 1098.5; DB 6; Length al Similarity 99.5%; Pred. No. 8.6e-91; 208; Conservative 0; Mismatches 0; Indels
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            25-JUL-2000; 2000US-0220664P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                          Desnoyers L,
                                                                                                                  (GETH ) GENENTECH INC.
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N-PSDB; ACA68535.
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Grimaldi J
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arthritis; wound
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Grimaldi JC,
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                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                60 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, PRO polypeptide, secreted and transmembrane protein, anti-PRO antibody; diagnostic assay, gene expression, tumour; cytostatic.
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phan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                     1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                 1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                             LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                                                                                                                                                                                                                                             CSFRELLLEDGYNVYOSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                     Сарв
                                                                                                   1;
                                                            Length 208;
                                                                                                   Indels
                                                              DB 5;
                                                            Score 1098.5; DB 5;
Pred. No. 8.6e-91;
0; Mismatches 0;
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Smith V, Stephan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                          180 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 208
                                                                                                                                                                                                                                                                                                                                                                                             LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU80777 standard; protein; 208 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-2000; 2000US-022063BP.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-2002; 2002US-00230163
                                                                              ilarity 99.5%;
Conservative
                                                              98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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                                                                                    al Similarity
208; Conserv
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                          Sequence 208 AA;
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                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSFRELLLEDGYNVYOSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of
directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted and transmembrane protein; PRO; cytostatic; antiarthritic; osteopathic; gene therapy; INF-Agonist-Alpha; chondrocyte stimulator; fibroblast modulator; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour; oolon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; bone disorder; cartilage disorder; sports injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                        1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRKLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                             LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                                                                                                                                                                                                                       1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                       Length 208;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted and transmembrane protein PRO10196.
data for this patent was obtained in electronic format USPTO web site at segdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                          DB 6;
                                                                                                                                                          98.7%; Score 1098.5; DB 6; 99.5%; Pred. No. 8.6e-91; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO33743 standard; protein; 208
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                            Conservative
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N-PSDB; ACD68631.
                                                                                                                                                                                           Local Similarity
nes 208; Conserv
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Wounds in a mammal
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The invention relates to an isolated human polypeptide (1) for zFGF11 (a fibroblast growth factor), and the encoding polymucleotide (II). (I) and (II) are used in methods of the invention stimulating proliferation of mesenchymal cells, detecting the presence of zfGF11 in a biological sample, detecting the presence of FGFRIIC in a biological sample and stimulating proliferation of osteoblastic lineage cells. The polypeptides, nucleic acid and/or antibodies of the invention may be used in treatment of deseneration, amyotrophic lateral sclerosis, cerebrovascular stroke, neuropathy associated with diabetes mellitus, neural cell development or deseneration, amyotrophic lateral sclerosis, cerebrovascular stroke, neuropathy associated with lack of maintenance of neuronal development. Molecules of the nervous system or lack of neuronal development. Molecules of the invention may also be useful for improving cardiac function and for promoting wound healing of the epidermis. The present sequence represents the amino acid sequence of
                                                                                      Human; fibroblast growth factor; FGF; zFGF11; mesenchymal cell; FGFRIIIc; osteoblastic lineage cell; diabetes mellitus; neuropathy; neural cell development; amyotrophic lateral sclerosis; cerebrovascular stroke; neuronal differentiation; congenital disorder; nerrous system disorder; cardiac function; wound healing.
                                                                                                                                                                                                                                                                                                                28. .208
/note= "Mature fibroblast growth factor homologue,
zFGF11. This sequence is specifically claimed in claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide for zFGFI1 (fibroblast growth factor) useful in treatment of disorders associated with diabetes mellitus, neural cell development or degeneration, amyotrophic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 98.7%; Score 1098.5; DB 5; Length Best Local Similarity 99.5%; Pred. No. 8.6e-91; Matches 208; Conservative 0; Mismatches 0; Indels
                                                  Human fibroblast growth factor (FGF) homologue, zFGF11.
                                                                                                                                                                                                                                                                               1. .27
/label= Signal_sequence
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 1; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-2000; 2000US-0174526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JAN-2001; 2001US-00755695
                  05-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerebrovascular stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CONK/) CONKLIN D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen Z;
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N-PSDB; ABK91310.
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                                                                                                                                                                                                                                                                                                                     Protein
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The present invention relates to new extracellular messenger polypeptides and polynucleotides encoding them. XMES is useful in the diagnosis, treatment and prevention of neurological disorders (e.g. epilepsy, stroke, or Alzheimer's disease), autoimmune/inflammatory disorders (e.g. encoders), acquired immune deficiency syndrome, AIDS, Addison's disease, or allergies), developmental disorders (e.g. renal tubular acidosis, anaemia or Chring's syndrome), endocrine disorders (e.g. hypophysectomy, aneurysm or vascular malformation), and cell proliferative disorders (e.g. cancer), and in the assessment of the effects of exogenous or compounds on the expression of nucleic acid and anino acid sequences of extracellular messengers. XMES may also be used in the treatment of viral, bacterial, fungal, parasitic, protozoal and helminthic infections, trauma, disorders associated with hypopituitarism, the properthyroidism or gonadal steroid hormones, and pancreatic disorders such as type I or type II diabetes mellitus. The XMES may be used for somatic or germine gene therapy. The present sequence is human XMES-3 protein
                                                                                                                                                                                                                                                                                                                                                                           Human; extracellular messenger; neurological disorder; epilepsy; XWES-3; Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke; acquired immune deficiency syndrome; AIDS; Addison's disease; cytoetatic; developmental disorder; anaemia; Cushing's syndrome; endocrine disorder; vascular malformation; cell proliferative disorder; gene therapy; cancer; neuroprotective; trauma; hypopicuitarism; hypothyroidism; antihelminthic; hyperthyroidism; gonadal steroid hormone; pancreatic disorder; nootropic; diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial; antiviral; antifungal; parasitic; protozoal; allergy.
                     120 CSFREILLEDGYNVYQSEAHGLPIHILPGNKSPHRDFAPRGPARFLPLPGLPPALPEPPGI 179
121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
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S, Hafalia A;
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Lu Y, Baughn MR, Duggan BM, Lee
                                                                                                                                                                                                                                                                                                                                                Human extracellular messenger (XMES)-3 protein.
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                                                                                                   180 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS
                                                                                LAPOPPDVGSSDPLSMVGPSQGRSPSYAS
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                                                                                                                                                                                                                       AAE17601 standard; protein; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-2000; 2000US-0210233P.
23-JUN-2000; 2000US-0213465P.
14-NOV-2000; 2000US-0249019P.
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                                                                                                                                                                                                                                                                                                          (first entry)
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n Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              не А,
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                                                                                  181
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DB 5; Length 208;

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sclerosis, cerebrovascular stroke, neuropathy associated with lack of sclerosis, cerebrovascular stroke, neuropathy associated with lack of maintenance of neuronal differentiation and congenital disorders of the nervous system or lack of neuronal development, promoting angiogenesis and wound healing, for revascularisation in eye, complications related to poor circulation such as diabetic food ulcers, improving cardiac function, modulating surfactant production in the lung epithelium, to reduce damage to the tissue caused by ischaemia or ischaemia-reperfusion events, particularly in the heart or brain and for inducing skeltal amuscle neogenesis and/or hyperplasia, kidney regeneration and/or for treating of systemic and pulmonary hypertension. Antagonists of 2FGFII are useful for inhibiting disorders associated with kidney epithelium
                                                                                                                                                                                                                                                                                                                                                             LEIREDGTVGGAADQSPESILLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                                                                                                                                                                                                                                                                                                                               CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPDPGLPPALPEPPGI 180
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                                                                                                                                                                                                                                                                                                                       1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGGGVRQRYLYTDDAQQTRAH 59
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, secreted protein, PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.
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                                                                                                                                                                                                                                     DB 4; Length 208;
                                                                                                                                                                                                                                     Score 1098.5; DB 4; Length
Pred. No. 8.6e-91;
0; Mismatches 0; Indels
or degeneration,
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mellitus, neural cell development
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2000US-0220607P.
2000US-0220624P.
2000US-0220638P.
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                                                                                                                                                                                                                                       98.78;
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                                                                                                                                                                              such as glomerulonephritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                     Local Similarity
les 208; Conserv
                                                                                                                                                                                                          Sequence 208 AA;
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22-AUG-2000;
23-AUG-2000;
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25-JUL-2000;
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25-JUL-2000;
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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in perioyre cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. PAU833713 represent human PRO protein sequences of the invention
                                                                                                                                                                                                                                                                                                                                                     One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or liver tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LEIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
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Smith V, Stephan JF, Watanabe CK, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 78; 359pp; English.
                                                            2000WS-00747259
2000WG-US034956.
2001WG-US0066520.
2001WS-00816744.
2001WS-00816744.
2001WS-00854208.
                2000WO-US030873.
2000US-0253646P.
                                                2000WO-US032678
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Best Local Similarity 99.59
Matches 208; Conservative
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N-PSDB; ABK33574.
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                                                              20-DEC-2000;
20-DEC-2000;
20-PEB-2001;
21-MAR-2001;
22-MAR-2001;
10-MAY-2001;
10-MAY-2001;
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                10-NOV-2000;
28-NOV-2000;
01-DEC-2000;
24-AUG-2000;
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Human; fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis; proliferation, mesenchymal cell; osteoblastic lineage cell; osteoblassis; chromosomal disorder; chondroarcoma; atherosclerosis; obesity; fracture, bone formation; diabetes mellitus; neural cell development; angiogenesis; amyotrophic lateral sclerosis; cerchrovascular stroke; neuropathy, ulcer; congenital disorater, wound healing; cardiac function; glomerulonephitis; surfactant production; anorectic; ischaemia; neogenesis; hyperplasia;
CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zFGF11 protein. zFGF11 gene is located on chromosome 19. zFGF11 is useful for stimulating proliferation of mesenchymal cells, osteoblastic lineage cells. zFGF11 is useful for identifying chromosomal disorders associated with abnormal expression of zFGF11 protein. zFGF11 is also useful for stimulation, inhibition or proliferation of myocytes, smooth muscle cells, adipocytes, chondrocytes, neural tube-derived stem cells, neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel zFGF11 polypeptide and polynucleotide, a member of fibroblast growth factor family, for stimulating proliferation of mesenchymal, osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is human fibroblast growth factor (FGF) homologue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crest stem cells and neuronal progenitors, pancreatic cells, prostate-
derived cells and endothelial cells and inhibiting chondrosarcomas,
atherosclerosis, restenosis and obesity. Stimulation of osteoblasts
results in bone formation useful for treating bone defects, fractures,
osteoporosis and other deficiencies in bone structure and formation.
zFGFI1 is useful for treating disorders associated with diabetes
                                                                                                                                                                                                                                                                                                                                                          Human fibroblast growth factor (FGF) homologue, zFGF11 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Heparin binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surfactant production, anorectic; ischaemia; n
hypertension; cytostatic; vasotropic; therapy.
                                                                                                                          181 LAPOPPDVGSSDPLSMVGPSOGRSPSYAS 209
                                                                                     LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
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label= Signal_peptide
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                                                                                                                                                                                                                                     AAE05078 standard; protein; 208
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N-PSDB; AAD09151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel sbgFGF-19a polypeptide, a member of fibroblast growth factor family and polynucleotides encoding them useful for diagnosing, treating stroke, psoriasis, cancer, atherosclerosis, rheumatoid arthritis and cirrhosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Human; sbgFGF-19a; fibroblast growth factor; stroke; cancer; psoriasis; traumatic brain injury; cerebral ischemia; atherosclerosis; rhenumatic brain injury; cirrhosis; sarcoldosis; wound repair; idiopathic pulmonary fibrosis; tumour development; accordent; vaccine developmental disorder; skeletal disorder; acrocephaly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human shgFGF-19a polypeptide. The polypeptide is a member of fibroblast growth factor family of polypeptides. The polymucleotides and polypeptides are useful in the treatment of diseases such as stroke, traumatic brain injury, cerebral ischemia, cancer, atherosclerosis, rheumatoid arthritis, cirrhosis, psoriasis, sarcoidosis, idiopathic pulmonary fibrosis, tumour developmental disorders, skeletal disorders, wound repair, and acrocephaly. They are also useful as vaccines for inducing an immunological response in a mammal
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                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a human sbgFGF-19a polypeptide.
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Pred. No. 1.8e-91;
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The present sequence is that of human JAFFA, a novel member of the fibroblast growth factor family. Analysis of rare sequences in the Milennium datebase led to the identification of an expressed sequence tag from a buman prostate tumour library which coded for a novel typothetical signal peptide. Further analysis led to the identification of JAFFA, The invention provides JAFFA polypeptides, polymoleocides and anti-JAFFA antibodies. It also provides antisense mucleic acid molecules, recombinant expression vectors, host cells and transgenic animals. JAFFA proteins may be useful for developing novel diagnostic and therapeutic proteins may be useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders such as cancers and other disorders which demonstrate ABO(H) blood group disorders and for controlling cellular proliferative and/or differentiative disorders. The JAFFA conclein may be used to treat and/or diagnose a variety of immune disorders such as autoimmune disease and multiple sclerosis. The proteins may also be used to screen for naturally occurring JAFFA substrates, to screen for drugs or compounds which modulate JAFFA antibodies, which can be used to detect and isolate JAFFA proteins, regulate the bioavailability of JAFFA proteins and modulate JAFFA activity.
                                                                                                                                                                                                                   Isolated JAFFA nucleic acid molecules which encode novel fibroblast growth factor family members (JAFFA) are useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders such as
                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 1; 137pp; English.
99US-00444165
                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                      WPI; 2001-355881/37.
N-PSDB; AAF90326, AAF90327.
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22-NOV-1999;
                                                                                                    Khodadoust MM;
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0 120 61 LEIREDGTVGGAADQSPESILQIKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120 9 9 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA CSFREILLEDGYNVYOSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI Gaps 0; 99.4%; Score 1106; DB 4; Length 209; 99.5%; Pred. No. 1.8e-91; ive 0; Mismatches 1; Indels (LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209 Local Similarity 99.5 es 208; Conservative 61 181 181 Query Match 121 Matches g g ð g à g Š

Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes; inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis; renal tubule damage; gastrointestinal abnormality; wasting syndrome; neurodegenerative disease; haematopoietic cell reconstitution; cachexia; Human Fibroblast Growth Factor-like (FGF-like) polypeptide. AAU00957 standard; protein; 209 AA (first entry) 24-MAY-2001 AAU00957; AAU00957 RESULT

The sequence represents a fibroblast growth factor-like (FGF-like)

polypeptide. FGF-like protein and its associated nucleic acid play a role
in modulating body growth, maturation or life-span. They are also usseful
for treating, preventing or ameliotating disorders such as cirrhosis,
inflammatory bowel disease, mucositis, Crohn's disease, diabetes,
cobseity, gastrointestinal abnormalities, neurodegenerative diseases,
damage to renal tubules as a result of acute tubular necrosis,
camage to renal tubules as a result of acute tubular necrosis,
haematopoietic cell reconstitution following chemotherapy, wasting
syndromes (e.g., cancer associated cacheria), damage to the corneal
cepithelium, lens or retinal tissue, multiple sclerosis, myopathies, short
steture, delayed maturation, excessive growth (e.g. acromegaly),
conchopulmonary dysplasia, acute respiratory distress syndrome, tumours
cof the eye or other tissues, atherosclerosis, hypercholesterolemia,
cof the eye or other tissues, atherosclerosis, hypercholesterolemia,
cof the eye or other tissues, atherosclerosis, decreased stamina, decreased
cardiac function, immune system dysfunction, cancer, Parkinson's disease,
senile dementia, Alzheimer's disease, and decreased cognitive function chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy; multiple sclerosis; short stature; delayed maturation; excessive growth; acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia; androgen target organ abnormality; respiratory distress syndrome; stroke; cancer; atherosclerosis; hypercholesterolaemia; osteoporosis; baldness; desteoathritis; muscle atrophy; sarcopenia; withles; increased fatigue; decreased stamina; decreased function; immune system dysfunction; parkinson's disease; Alzheimer's disease; decreased cognitive function; Novel isolated fibroblast growth factor-like polypeptide useful for treating, preventing or ameliorating cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease, diabetes, obesity, stroke and "Mature human FGF-like protein" "Signal peptide" Location/Qualifiers Claim 13; Fig 2; 138pp; English. 07-SEP-1999; 99US-00391861. 23-AUG-2000; 2000US-00644052. 05-SEP-2000; 2000WO-US024373 .209 /note= senile dementia; human. /note= WPI; 2001-226743/23. (AMGE-) AMGEN INC. N-PSDB; AAS00779 Sequence 209 AA; WO200118172-A2 Thomason AR, Homo sapiens osteoporosis 15-MAR-2001 Peptide Protein

LEIREDGIVGGAADQSPESILQIKALKPGVIQILGVKISRFLCQRPDGALYGSLHFDPEA 120 61 LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120 9 9 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTBAH 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 0 99.4%; Score 1106; DB 4; Length 209; 99.5%; Pred. No. 1.8e-91; Indels 0; Mismatches fatches 208; Conservative Sest Local Similarity 19 Query Match

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The invention relates to fibroblast growth factor (FGF)-like polypeptides and nucleic acid molecules encoding such polypeptides. Sequences of the invention are useful for treating, preventing or ameliorating a medical condition. They are useful for treating dermal wounds, epidermolysis, bullosa, male pattern alopecia, gastric ulcer, duodenal ulcer, erosive gastritis, oesophaguist, oesophagual reflux disease, inflammatory bowel disease, crohn's disease, radiation- or chemotherapy-induced gut toxicity, hyaline membrane disease, necrosis of the respiratory compitions, pulmonary fibrosis, chepatic cirrhosis, toxic insults to the liver, fulminant liver failure, viral hepatitis, mucositis, multiple sclerosis and other currhosis, toxic insults to the liver, fulminant liver failure, viral hepatitis, uncositis, multiple sclerosis and other currhosis, toxic insults to the liver, fulminant liver failure, bronchopulmonary dysplasia, acute respiratory distress syndrome or other currhosis modulating of the eye or the other tissues and organs. Cromorhopulmonary dysplasia, ecute respiratory distress syndrome or other currhosis, modulating differentiating or meliorate skin aging, promoting and skeletal muscle cells, preventing or ameliorate skin aging, preventing or and skeletal muscle cells, preventing or and differentiation of neuronal cells, disporytes the active distress and differentiation of neuronal cells, and differentiation of neuronal cells, disporytes or the context of the
                                                                                                               CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haematopoietic cells and bone marrow cells and maintaining organs before transplantation and for supporting cultures of primary cells and tissues. Sequences of the invention are also used in gene therapy and as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibroblast growth factor; FGF-like protein; wound healing; bullosa; epidermolysis; erosive gastritis; inflammatory bowel disease; ulcer; oesophagitis; Crohn's disease; hyaline membrane disease; emphysema; pulmonary fibrosis; hepatic cirrhosis; liver failure; angiogenesis; multiple sclerosis; neurodegenerative disease; lung abnormality; viral hepatitis; respiratory distress syndrome; tumour; skin aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel fibroblast growth factor-like polypeptide useful for treating, ameliorating and/or preventing dermal wounds, gastric ulcer, Crohn's disease and pulmonary inflammation.
                                                                                                                                                                                          LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                         LAPQPPDVGSSDPLSMVGPSQGRSPSYAS
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                                                                                                                                                                                                                                                                                                                                                                               AAE18826 standard; protein; 209
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                                                                                                                                                                                                  CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                             The present sequence is human FGF-21 protein which is a member of the FGF family
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note= "predicted casein kinase II phosphorylation site"
                                                                                                       1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH 60
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/note= "protein kinase C predicted phosphorylation site"
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/note= "protein kinase C predicted phosphorylation site"
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                                                         Length 209;
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                                                          Score 1113; DB 5;
Pred. No. 4.3e-92;
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re= "N-myristoylation"
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/note= "N-myristoylation"
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/label= Mature_protein
                                                                                                                                                                                                                                                  LAPOPPDVGSSDPLSMVGPSQGRSPSYAS
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                 AAB82351 standard; protein; 209
                                                           100.0%;
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                                                                                   Conservative
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/note= "1
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                                                           Query Match
Best Local Similarity
Matches 209; Conserv
                                     Sequence 209 AA;
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standard; protein; 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-2000; 2000JP-00213385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000; 2000JP-00240398
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                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                             Human FGF-related protein.
                   Best Local Similarity 100.
Matches 209; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-448752/48.
N-PSDB; ABK52425.
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les 209; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21). For proteins regulate growth and differentiation of a variety of cell types. FGF-21 nucleic acids and polypeptides are useful for treating diseases and disorders characterised by inadequate numbers of hepatic cells, preferably cirrhosis of the liver. They may also be used in the treatment of infertility, impotence, and testicular cancer, as well as leukemia, lymphoma, autoimmune disease, or proliferative disorders of the
                                                                                                                               120
                                                                                                                                                                                               180
                                                                                                                                                   LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                                                                                                                          CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid molecule useful for treating disease, e.g. infertility,
                                                                                                                                                                                                                                                                                                                                                                               Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation; hepatic cell; cirrhosis; infertility; impotence; testicular cancer; leukemia; lymphoma; autoimmune disease; thymus proliferative disorder.
                                                                                                  1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
                                                                                                                                                                                      1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of human fibroblast growth factor-21 (FGF-21).
the FGF family
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                                           Length 209;
                                                              Indels
some members of
                                         Score 1113; DB 4;
Pred. No. 4.3e-92;
; Mismatches 0;
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 amino acid sequences of
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                                          100.0%;
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11-MAY-2000; 2000US-0203633P.
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                                                                                                                                                                                                                                                                                              AAB68417 standard; protein;
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                                                                Conservative
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                                                     Local Similarity
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                      Sequence 209
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njuries, burns, thrombosis, arteriosclerosis, hepatopathy, pancreopathy,
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                                                                                                                                                                                                                                                                                                                       LETREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA
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                                                                                                 1 MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, injury, burn, thrombosis, arteriosclerosis, pancreopathy,
hepatopathy, FGF-related protein.
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100.0%; Pred. No. 4.3e-92;
tive 0; Mismatches 0;
100.0%; Score 1113; DB 4; 100.0%; Pred. No. 4.3e-92;
                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            209
                                                                                                                                                                                                                                                                                                                                                                                                                           LAPOPPDVGSSDPLSMVGPSQGRSPSYAS
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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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OM protein - protein search, using sw model

Run on:

ritle:

1 MDSDETGFEHSGLWVSVLAG......SSDPLSMVGPSQGRSPSYAS 209 US-10-060-765-4 1113 score: Perfect

BLOSUM62 Scoring table: Sequence:

1586107 segs, 282547505 residues Gapop 10.0 , Gapext 0.5 Searched: 1586107 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* 1: genesemining geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* ٠. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2004s:*

geneseqp2003as:* geneseqp2003bs:*

STIMMARTES

| LEG | Description | Aag65667 Human fib | 7 Amino | Human | Aae18826 Human FGF | 1 Human | Human | Aab83951 Amino aci | 8 Human | Human | Abg32358 Human fib | Human | | | Novel | Abp96156 Human fib | Human | Abj72394 Human PRO | Human | Ada37038 Human fik | | | Adb80674 Novel hun | Novel] | Adb78297 Novel hum | Adb84945 Human PRO |
|-----------|----------------|--------------------|----------|----------|--------------------|----------|----------|--------------------|----------|----------|--------------------|----------|----------|----------|----------|--------------------|----------|--------------------|----------|--------------------|----------|----------|--------------------|----------|--------------------|--------------------|
| SUMMAKIES | GI. | AAG65667 | AAB68417 | AAU79289 | AAE18826 | AAB82351 | AAU00957 | AAB83951 | AAE05078 | AAU83630 | ABG32358 | AAE17601 | ABU80777 | AB033743 | ABU82086 | ABP96156 | ABJ72266 | ABJ72394 | ABO34289 | ADA37038 | ABJ72096 | ADB83568 | ADB80674 | ADB73215 | ADB78297 | ADB84945 |
| | DB | 4 | 4 | Ŋ | ហ | 4 | 4 | 4 | 4 | Ŋ | S | Ŋ | 9 | 9 | 9 | 9 | 9 | ø | 9 | ~ | 7 | 7 | 7 | 7 | 7 | 7 |
| | Length | 209 | 209 | 209 | 209 | 209 | 209 | 209 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 |
| d | Query Match | 100.0 | 100.0 | 100.0 | 100.0 | 99.4 | 99.4 | 99.4 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 7.86 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 |
| | | 1113 | 1113 | 1113 | 1113 | 1106 | 1106 | 1106 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 |
| | ω <u>.</u> | | U | m | 4 | Ŋ | ų | 7 | 89 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 |

| Novel | Adb87117 Human PRO | Human | Adb83814 Novel hum | Novel 1 | Human | Adc21797 Human PRO | Adc49828 Novel hum | Novel | Adc49544 Novel hum | | Novel | Adc78025 Novel hum | Novel | Novel | Add50742 Novel hum | Novel] | Add50469 Human PRO | Add50223 Human PRO | Add51234 Novel hum |
|----------|--------------------|----------|--------------------|----------|----------|--------------------|--------------------|----------|--------------------|----------|----------|--------------------|----------|----------|--------------------|----------|--------------------|--------------------|--------------------|
| | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | |
| ADB78051 | ADB87117 | ADB84699 | ADB83814 | ADB72969 | ADC36807 | ADC21797 | ADC49828 | ADC49027 | ADC49544 | ADC47405 | ADC47150 | ADC78025 | ADD06260 | ADC77779 | ADD50742 | ADD50988 | ADD50469 | ADD50223 | ADD51234 |
| 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | , | 1 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 |
| 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 |
| 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 98.7 | 7.86 | 7.86 |
| 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 | 1098.5 |
| 36 | 27 | 20 | 200 | 0 | ; ;- | 100 | 1 6 | 34 | 5 | 36 | 37 | 38 | 6 | 40 | 41 | 42 | 43 | 44 | 45 |
| | | | | | | | | | | | | | | | | | | | |

ALIGNMENTS

Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic; fat deposition; vulnerary; antiulcer; dermatological; anoretic; antidiabetic; antiinflammatory; cytostatic; hepatic; virucide; neuroprotectant; pulmonary; gene therapy; vaccine; human. Human fibroblast growth factor (FGF)-21. AAG65667 standard; protein; 209 AA (first entry) 07-JAN-2002 AAG65667; RESULT 1 AAG65667

WO200172957-A2. Homo sapiens.

04-OCT-2001.

02-APR-2001; 2001WO-IB000664. 31-MAR-2000; 2000US-00540118.

(ITOH/) ITOH N.

Itoh N;

WPI; 2001-611623/70.

New human nucleic acid encoding fibroblast growth factor-like peptide, useful for treatment and diagnosis of e.g. wounds and inflammatory bowel disease.

Disclosure; Fig 3; 172pp; English.

viral The invention provides human nucleic acids encoding fibroblast growth factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by etandard recombinant methodology and are mitogenic for a wide range of cells, inducing differentiation and proliferation, and inhibiting deposition of fat. The FGF-like polypeptides, polynucleotides and specific antibodies and modulators are useful for treating a very wide range of diseases and conditions, e.g. wounds, ulcers, skin aging, obesity, diabetes, alopecia, inflammatory bowel disease, emphysema, viral hepatitis, multiple solerosis, respiratory distress syndrome, tumors of the eye, etc., also for maintaining organs before transplant and supporting culture of primary cells and tissues. Sequences AAG65647-67

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                         OM protein - protein search, using sw model
                                                                                       Run on:
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Gapop 10.0 , Gapext 0.5 US-10-060-765-7 86 1 RQRYLYTDDAQQTEAH 16 **BLOSUM62** Scoring table: Title: Perfect score: Sequence:

389414 segs, 51625971 residues Searched: Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:/
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep: Issued Patents AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | ŭ | 5213, Ap | 5, Appli | 2, Appli | 6, Appli | 4, Appli | 14225, A | 4355, Ap | 28, Appl | 28391, A | 10181, A | 7, Appli | | 4224, Ap | 396, App | 14221, A | - | 5569, Ap | 16, Appl | _ | 20, Appl | 15, Appl | 2, Appli | 2, Appli | 2, Appli | 31483, A | 3993, Ap | 2086, Ap |
|---|---|--------------------|-----------------|-----------------|-----------------|-----------------|----------------------|---------------------|------------------|----------------------|----------------------|-----------------|-----------------|--------------------|-------------------|----------------------|----------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-----------------|-----------------|----------------------|---------------------|--------------------|
| | Description | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Seguence | Sequence | Sequence | Sequence | Sequence | Sequence | Seguence | Sequence | Sequence | Seguence | Sequence |
| | El | US-09-621-976-5213 | US-09-390-207-5 | US-09-390-207-2 | US-09-390-207-6 | US-09-390-207-4 | US-09-489-039A-14225 | US-09-107-532A-4355 | US-09-171-461-28 | US-09-252-991A-28391 | US-09-489-039A-10181 | US-09-147-236-7 | US-09-522-474-7 | US-09-621-976-4224 | US-09-634-238-396 | US-09-489-039A-14221 | US-09-489-039A-10731 | US-09-134-001C-5569 | US-08-089-397A-16 | US-07-603-133B-17 | US-07-603-133B-20 | US-08-089-397A-15 | US-08-157-005-2 | US-08-747-863-2 | US-09-565-864-2 | US-09-252-991A-31483 | US-09-134-001C-3993 | US-09-540-236-2086 |
| | DB | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4, | 4 | 4 | 4 | 4 | 4 | 4 | マ | ٣ | Н | Н | ო | - | m | 4 | 4 | 4 | 4 |
| | Length | 85 | 181 | 209 | 181 | 210 | 479 | 137 | 1121 | 152 | 366 | 735 | 735 | 136 | 164 | 285 | 526 | 557 | 747 | 116 | 176 | 776 | 2396 | 2396 | 2396 | 310 | 317 | 318 |
| ф | Query Match | 100.0 | 100.0 | 100.0 | 87.2 | 87.2 | 55.8 | 48.8 | 47.7 | 46.5 | 46.5 | 45.3 | 45.3 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 43.0 | 43.0 | 43.0 |
| | Score | 86 | 98 | 86 | 75 | 75 | 48 | 42 | 41 | 40 | 40 | 39 | 39 | 38 | | 38 | 38 | 38 | | | 38 | 38 | 38 | 38 | 38 | 37 | 37 | 37 |
| | Result No. | | 1 6 | lm | 4 | ហ | 9 | 7 | 80 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |

| Sequence 5499, Ap | Sequence 29, Appr Sequence 29728, A | Sequence 6926, Ap | Sequence 3, Appli | Sequence 3, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 21514, A | Sequence 12, Appl | Sequence 3716, Ap | Sequence 288, App | Sequence 4500, Ap | Seguence 4626, Ap | Sequence 4652, Ap | Sequence 8159, Ap | Seguence 3429, Ap | Seguence 13575, A |
|---------------------|--|---------------------|-------------------|-------------------|-------------------|-------------------|----------------------|-------------------|---------------------|--------------------|---------------------|--------------------|---------------------|---------------------|---------------------|----------------------|
| US-09-543-681A-5499 | US-09-352-990-28 US-09-252-991A-29728 | US-09-543-681A-6926 | US-08-785-048-3 | US-08-996-799-3 | US-08-785-048-2 | US-08-996-799-2 | US-09-252-991A-21514 | US-07-603-133B-12 | US-09-134-001C-3716 | US-09-198-452A-288 | US-09-134-001C-4500 | US-09-328-352-4626 | US-09-134-000C-4652 | US-09-543-681A-8159 | US-09-134-001C-3429 | US-09-489-039A-13575 |
| 4 (| J 4. | 4 | Н | N | н | 7 | 4 | н | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 |
| 338 | 400 | 497 | 547 | 547 | 553 | 553 | 635 | 775 | 1335 | 789 | 82 | 249 | 308 | 347 | 383 | 208 |
| 43.0 | 443.0 | 43.0 | 43.0 | 43.0 | 43.0 | 43.0 | 43.0 | 43.0 | 43.0 | 42.4 | 41.9 | 41.9 | 41.9 | 41.9 | 41.9 | 41.9 |
| 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 36.5 | 36 | 36 | 36 | 36 | 36 | 36 |
| 28 | 3 23 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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Gaps
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      Sequence 5213. Application US/09621976
; Batent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: GLORET, S.
; TITLE OF INVENTION: GENSET.054 PRZ
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SIGNAL
LOCATION: -28...1
NAME/KEY: UNSURE
LOCATION: 57
OTHER INFORMATION: Xaa = Ala, Pro
NAME/KEY: UNSURE
LOCATION: 52
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US-09-621-976-5213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.(
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-09-621-976-5213
                                                                                                                                                                                                                                                                           SEQ ID NO 5213
LENGTH: 85
                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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1 RORYLYTDDAQQTEAH 16 45 RQRYLYTDDAQQTEAH 60 g

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US-09-390-207-5
; Sequence 5, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371 CURRENT APPLICATION NUMBER: US/09/390,207 CURRENT FILING DATE: 1999-09-07 NUMBER OF SEQ ID NOS: 41

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Query Match
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US-09-390-207-6
US-09-390-207-6
; Sequence 6, Application US/09390207
; Parent No. 6504530.
; GENERAL INFORMATION:
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REPERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
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0
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APPLICANT: Thomson, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
FILE REFERENCE: 99-371
CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 86; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indel8
                                                                                                                                 Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 75; DB 4; Length 181; Pred. No. 2.3e-05; 0; Mismatches 2; Indels
                                                                                                                                                                     0; Indela
                                                                                                                                 Score 86; DB 4; ]
Pred. No. 3.1e-07;
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                       RESULT 3
US-09-1390-207-2
; Sequence 2, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
                                                                                                                               Query Match
Best Local Similarity 100.0%; Pr
Matches 16; Conservative 0;
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Best Local Similarity 87.5%;
Matches 14; Conservative
                                                                                                                                                                                                             1 RORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                 17 RORYLYTDDAQQTEAH 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-09-390-207-2
                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-5
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RESULT 5

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RESULT 6
US-09-489-039A-14225
US-09-489-039A-14225
Sequence 14225, Application US/09489039A
Fatent No. 6610836
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ALD AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1909-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR PILING DATE: 1999-01-29
SEQ ID NO 14225
LENGTH: 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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| Sequence 4, Application US/09390207
| Sequence 4, Application US/09390207
| Patent NO. 6504530
| GENERAL INFORMATION:
| APPLICANT: Thomason, Arlen
| TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
| TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
| FILE REFERENCE: 99-371
| CURRENT APPLICATION NUMBER: US/09/390,207
| NUMBER OF SEQ ID NOS: 41
| SOFTHARE: PatentIn Ver. 2.0
| SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.2%; Score 75; DB 4; Length 210; 87.5%; Pred. No. 2.7e-05; tive 0; Mismatches 2; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4355, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 RORYHPGDDROOPOAH 475
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RORYLYTDDAQQTEAH 16
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                              r TYPE: PRT
CORGANISM: Mus musculus
US-09-390-207-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 10; Conserva
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US-09-107-532A-4355
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## Sequence 28391, Application US/09252991A

| Sequence 28391, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICATION:
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US/09/252,991A
| CURRENT FILING DATE: 1999-02-18
| PRIOR FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| SEQ ID NO 28391
| LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10181, Application US/09489039A

Patent NO. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: DIEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1099-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 10181

LENGTH: 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.5%; Score 40; DB 4; Length 152; 63.6%; Pred. No. 17;
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Patent No. 6316251
GENERAL INFORMATION:
APPLICANT: TONOUCHI, Nacto
APPLICANT: TSUCHIDA, Takayasu
APPLICANT: YOSHINAGA, Fumihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                   731 RÓQFRYADDPEÓBE 744
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                              1 RORYLYTDDAQOTE 14
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129 WRDDAPQTESH 139
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Matches 7; Conserv
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US-09-489-039A-10181
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US-09-252-991A-28391
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US-09-147-236-7
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Sequence 28, Application US/09171461

Sequence 28, Application US/09171461

Sequence 28, Application US/09171461

Septicant: Baker, Adam

APPLICANT: Cotten, Matthew

APPLICANT: Chicce, Matthew

APPLICANT: Chicce, Robert

APPLICANT: Chicce, Robert

APPLICANT: Chicce, Robert

APPLICANT: Chiccen Embryo Lethal Orphan (CELO) Virus

TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO)

CURRENT APPLICANTON NUMBER: US/09/171,461

CURRENT FILING DATE: 1999-01-12

CURRENT FILING DATE: 1999-01-12

SARLIER FILING DATE: 1997-04-18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 28

LENGTH 1121

LENGTH 1121
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Best Local Similarity 50.0%; Pred. No. 99;
Matches 7; Conservative 3; Mismatches 4; Indels
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Pred. No. 6.9;
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US-09-171-461-28
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...137
SEQUENCE DESCRIPTION: SEQ ID NO: 4355:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLGGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.8%;
54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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108 YIYTDESDETE 118
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Gaps

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4; Indels

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Score 38; DB 4; Length 136;
Pred, No. 33;
    APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                             CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4224
LENGTH: 136
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COCATION: (1)...(164)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-634-238-396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 396, Application US/09634238 Patent No. 6544772
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Havukkala, Ilkka J.
Bloksberg, Leonard, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Lactobacillus rhamnosus
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Dekker, James
Christensson, Anna C.
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Best Local Similarity 53.8
Matches 7; Conservative
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23 FLYTDEAMRVRFH 35
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                 ; NAME/KEY; SIGNAL
; LOCATION: -41..-1
US-09-621-976-4224
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APPLICANT: TONOUCHI, Nacto
APPLICANT: TONOUCHI, Takayasu
APPLICANT: TSUCHIDA, Takayasu
APPLICANT: TAHARA, Nacki
APPLICANT: THARRA, Nacki
APPLICANT: TAKARI, Takahisa
TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
FILE REFRENCE: 6537-011-0PCT
CURRENT APPLICATION NUMBER: US/09/522,474
CURRENT FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-10-09
APPLICANT: TAHARA, Naoki
APPLICANT: HAYASHI, Takahisa
TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
FILE RFERENCE: 6537-011-0PCT
CURRENT APPLICATION NUMBER: US/09/147,236A
CURRENT APPLICATION NUMBER: PCT/JP97/03633
EARLIER APPLICATION NUMBER: PCT/JP97/03633
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 12
SOFTHARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 735
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70.0%; Pred. No. 1.4e+02;
tive 1; Mismatches 2; Indels
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70.0%; Pred. No. 1.4e+02;
tive 1; Mismatches 2; Indels
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Patent No. 6639063
GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09522474
Patent No. 6573076
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                          ORGANISM: Acetobacter xylinum
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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US-09-621-976-4224
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LENGTH: 735
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Sequence 14221, Application US/09489039A;
Patent No. 6610836;
GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
APPLICANT: Holland, Ross
APPLICANT: O'TOOLE, Paul W.
APPLICANT: O'TOOLE, Paul W.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polymucleotides, materials incorporating
CURRENT FILLING: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTRARE: FaatSEQ for Windows Version 4.0
SEQ ID NO 396
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 164;
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Pred. No. 40;
3; Mismatches
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Gaps
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APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 747;
  Length 557;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 2006-1888

ZIP: 2006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/089,397A
FILING DATE: US-JUL-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.2%; Score 38; DB 3; I 42.9%; Pred. No. 2.1e+02; ative 3; Mismatches 5;
44.2%; Score 38; DB 4; I
ilarity 60.0%; Pred. No. 1.5e+02;
Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 29311-20003.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                           APPLICANT: SABARA, MARTA I.J.
APPLICANT: FRENCHCK, PATRICK J.
APPLICANT: FOTTER, ANDREW A.
APPLICANT: 10AZ, MOHEMMAD X.
APPLICANT: GILCHRIST, JAMES E.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ROTAVIRUS VACCINES
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                      Sequence 16, Application US/08089397A
Patent No. 6086880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/07603133B Patent No. 5298244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| || | :: ||
299 QYTYTRDGEEVTAH 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RYLYTDDAQQTEAH 16
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Matches 6; Conservative
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MOLECULE TYPE: protein
                                                                                                                                           522 rbbrekrkah 531
                                                                                               7 TDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: DC
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 19
US-07-603-133B-17
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                                                Matches
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Requence 5669, Application US/09134001C

Retent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: BUIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PERICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
FRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10731
LENGTH: 526
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  TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14221
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.2%; Score 38; DB 4; Length 526; 54.5%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                            44.2%; Score 38; DB 4; Length 285; 46.2%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.4e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10731, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                    TYPE: PRT

ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                      4 YLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 16
US-09-489-039A-10731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-489-039A-10731
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Gaps

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Score 38; DB 3; Length 776; Pred. No. 2.2e+02; 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CODYTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/089,397A

FILING DATE: 07-UUL-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: SABARA, MARTA I.J.
APPLICANT: FRENCHICK, PATRICK J.
APPLICANT: POTTER, ANDREW A.
APPLICANT: 1JAZ, MOHAWAD K.
APPLICANT: GILCHKIST, JAMES B.
APPLICANT: REDMOND, WARK J.
TITLE OF INVENTION: ROTAVIRUS VACCINES
NUMBER OF SEQUENCES: 24
REFERENCE/DOCKET NUMBER: 9313-0004.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/08089397A Patent No. 6086880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: ADLER, REID G.
REGIETRATION UNDRER: 30,988
REPERENCE/DOCKET UNDRER: 2931:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAK: (202) 887-1501
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.28;
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                               302 QYTYTRDGEEVTAH 315
                                                    TELERAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
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                                                                                                                                         : 776 amino acids
AMINO ACID
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Best Local Similarity 42.99
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                                                                                                                                                                                              , MOLECULE TYPE: protein US-07-603-133B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-089-397A-15
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US-08-089-397A-15
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ADRESSE: NOTAVIRAL DISEASE
ADRESSE: Morrison & Foerster
SADRESSE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length //v, Pred. No. 2.2e+02;
                                                                                                           COUNTRY: C. ZIP: 94025
COUNTRY: C. ZIP: 94025
COMPUTER READABLE FORM: BLODG/WG disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION NUMBER: 33,208
ATTORNEY/ASENT INFORMATION:
REFERENCE/DOCKET NUMBER: 9313-0004.00
FEFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 17:
TELECOMMUNICATION 17:
TELECOMMUNICATION 17:
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CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                               STREET: 545 Middlefield Road, Suite 200 CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 20, Application US/07603133B ; Patent No. 5298244 ; GENERAL INFORMATION:
                                             Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RObins, Roberta L.
REGISTRATION NUMBER: 33,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 QYTYTRDGEEVTÁH 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
    NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-603-133B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-603-133B-17
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OF THE MYSTERY SWINE DISEASE,
                 APPLICANT: Mocrman, Robertus J
APPLICANT: Mocrman, Chokanna J
APPLICANT: Mellenberg, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 525 South 300 East
STREET: 525 South 300 East
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meulenberg, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISE
VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.2%; Score 38; DB 3; Length 2396; 54.5%; Pred. No. 7.2e+02; Live 3; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:

RIGHS APPLICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/157,005

FILING DATE: 26-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 91201398.4

FILING DATE: 06-JUN-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92200781.0

FILING DATE: 18-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92200781.0

FILING DATE: 05-JUN-1992

ATOMNEY AGENT THORPHATION:

ANAMA: THORNEY ADDITED
                                                                                                                                                                                                                                                                             ZIP: 84111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: WINDOWS95
SOFTWARP: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wensvoort, Gert
Terpstra, Catharinus
Pol, Johannes M
Moorman, Robertus J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09565864 Patent No. 6455245 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: TUTTER, Allen C.
REGISTRATION NUMBER: 33041
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (801) 532-1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (801) 531-9168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2396 amino acids
Pol, Johannes M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||:: |: |
2278 YTDDSRYTQDH 2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-747-863-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 YTDDAQQTEAH 16
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Best Local Similarity
Matches 6; Conserv
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TELEFAX: (8
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US-09-565-864-2
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                                                                                                                                                                                           APPLICANT: Wensvort, Gert
APPLICANT: Terpstra. Catharinus
APPLICANT: Terpstra. Catharinus
APPLICANT: Pol, Johannes M
APPLICANT: Moorman, Robertus J
APPLICANT: Moulenberg, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
TITLE OF INVENTION: VACINE COMPOSITIONS AND DIAGNOSTIC KITS
TITLE OF INVENTION: VACINE COMPOSITIONS AND DIAGNOSTIC KITS
TITLE OF INVENTION: VACINE ADDRESSE:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STRIE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,005
FILING DATE: 26-NOV-1993
CLASSIFICATION: 424
PRICA APPLICATION DATA:
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
PRICA APPLICATION DATA:
APPLICATION NUMBER: EP 92200781.0
FILING DATE: 18-MAR-1992
PRICA APPLICATION DATA:
APPLICATION NUMBER: P 92200781.0
FILING DATE: 05-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: MOCAN, THOMBER: 44819
TELECOMMUNICATION INPORMATION:
TELEFRAM: (212) 917-9550
TELEFAX: (212) 315-1931
TELEFAN: (212) 315-1931
TELEFAN: 2396 amino acide
LENGTH: 2396 amino acide
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                                                                                                                         Sequence 2, Application US/08157005
Patent No. 5620691
GENERAL INFORMATION:
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            302 QYTYTRDGEEVTAH 315
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2278 YTDDSRYTQDH 2288
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Best Local Similarity 54.5
Matches 6; Conservative
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US-08-747-863-2
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Gaps

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Sequence 3993, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERENCE:
TITLE OF INVENTION:
FILE REPERENCE:
GURRENT APPLICATION WUMBER: US/09/134,001C
GURRENT FILING DATE: 1998-08-13
FRIOR FILING DATE: 1997-11-08
FRIOR FILING DATE: 1997-11-08
FRIOR FILING DATE: 1997-08-14
FRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3993
LENGTH: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CAID
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2086
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Gaps
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Indels
9
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53.3%; Pred. No. 1.2e+02;
tive 3; Mismatches 4
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Pred. No. 1.2e+02;
1; Mismatches 5
  Mismatches
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Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Staphylococcus epidermidis US-09-134-001C-3993
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294 RQGNIYTGDTQNTNSN 309
                                               1 RORYLYTDDAQQTEAH 16
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Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
    7; Conservative
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US-09-540-236-2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-543-681A-5499
                                                                                                                                                                                    US-09-134-001C-3993
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    Matches
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US-09-252-991A-31483

is Sequence 31483, Application US/09252991A

is Sequence 31483, Application US/09252991A

patent No. 6551795

igeneral information:
    APPLICANT: Marc J. Rubenfield et al.
    APPLICANT: Marc J. Rubenfield et al.
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
    TITLE OF INVENTION: NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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Pred. No. 7.2e+02;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/565,864
FILING DATE: 05-May-2000
CLASSIFICATION DATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/157,005
FILING DATE: cUNKNOWN-
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
FILING DATE: 18-MAR-1992
APPLICATION NUMBER: P 92200781.0
FILING DATE: 18-MAR-1992
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 06-JUN-1992
                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Moran, Thomas F
REGISTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 44819
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPHONE: (212) 315-1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: procein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-565-864-2
       STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2396 amino acids
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.0%;
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54.5%;
                                                                                               ZIP: 10112
COMPUTER READABLE FORM:
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2278 YTDDSRYTQDH 2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                    STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 YTDDAQQTEAH 16
                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 310
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APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: UNCORTICS AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 4; Length 497;
Pred. No. 2e+02;
4; Mismatches 3; Indels
                        Length 400;
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; Sequence 3, Application US/08785048
; Patent No. 5762246
; GENERAL INFORMATION:
APPLICANT: Hodgeon, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5762246el tRNA Synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                     Score 37; DB 4; Le
Pred. No. 1.6e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,048
FILING DATE: 17-JAN 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P31355-3
                                                                                                                                                                                                                                                                                                                                                  Sequence 6926, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                   295 EQYLYRRAADDGQHACQPRTEAH 317
                                                                                                                                           2 QRYLY---TDDAQ-----QTEAH 16
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APPLICATION NUMBER: 9601099.6
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38,891
                           Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
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REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 QRYIVTDSIKETK 272
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                                                                                                                                                                                                                                                                                                                          US-09-543-681A-6926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 6926
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43.0%; Score 37; DB 4; Length 338;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 7; Indels
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; Patent No. 6255090
; GENERAL INFORMATION:
APPLICANT: Famodu, Layo O.
; APPLICANT: Paraclaki, Antoni
TITLE OF INVENTION Plant Aminoacyl-tRNA Synthetase
; FILE REFERENCE: BB-1191
; CURRENT FILING DATE: 1999-0'-14
; EARLIER APPLICATION NUMBER: US/09/352,990
; CURRENT FILING DATE: 1999-0'-14
; EARLIER APPLICATION NUMBER: 60/092,866
; EARLIER APPLICATION OF CONTROL OF CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.0%; Score 37; DB 3; 146.7%; Pred. No. 1.5e+02;
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
LENGTH: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 REVYLYTDSRKDKPYH 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 ORGLWFDDPERPECH 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ORYLYTDDAQOTEAH 16
                                                                                                                                                                                                                                                  TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Synechocystis sp. US-09-352-990-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RORYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-29728
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                                                                                                                                                                                                                          43.0%; Score 37; DB 1; Length 547; 60.0%; Pred. No. 2.2e+02; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08996799
Patent No. 5965416
GENERAL INPORMATION:
APPLICANT: Hadgeon, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5965416el tRNA Synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P31355-3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/785,048
FILING DATE: 17-JAN-1997
APPLICATION NUMBER: 9601099.6
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 547 amino acids TYPE: amino acid
                                                                   INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 547 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610-270-5090
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MOLECULE TYPE: peptide
                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                        512 TDDIEKTKAH 521
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43.0%;

Query Match Best Local Similarity

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                                                                                                                                           Sequence 2, Application US/08785048
Patent No. 576246
GENERAL INFORMATION:
APPLICANT: Hodgeon, John
TITLE OF INVENTION: No. 5763246el tRNA Synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5965416el tRNA Synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,048
FILING DATE: 17-JAN-1997
CLASSIFICATION NATA:
APPLICATION NUMBER: 9601099.6
FILING APPLICATION DATA:
APPLICATION NUMBER: 9601099.6
FILING DATE: 13-JAN-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
ATTORNEY, AGENT THORMATION:
NAME: GAMMI, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08996799; Patent No. 5965416; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P:
TELECOMMUNICATION INFORMATION
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                   STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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518 TDDIEKTKAH 527
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512 TDDIEKTKAH 521
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7 TDDAQQTEAH 16
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                                                                                                                             US-08-785-048-2
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                                                                                                    APPLICANT: Referency, Mark J.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Parker, Michaell D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
43.0%; Score 37; DB 1; Le
Best Local Similarity 42.9%; Pred. No. 3.2e+02;
Matches 6; Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3716, Application US/09134001C Patent No. 6380370
                                                                                                                                                                               Sequence 12, Application US/07603133B Patent No. 5298244 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RODIOS, RODETCA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313:
TELECHONE: (415) 327-7250
TELEFAX: (415) 327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 327-2951
TELEX: 706141
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 775 amino acids
                                                 | |:|: ||
254 RHRHLHADDFADRPAH 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 QYTYTRDEEEVTAH 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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US-09-134-001C-3716
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## Sequence 215195
## GENERAL INFORMATION:
## TITLE OF INVENTION:
## TITLE OF INVENTION:
## TITLE OF INVENTION:
## ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## TITLE OF INVENTION:
## TITLE OF INVENTION:
## ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## CURRENT APPLICATION NUMBER: US/09/252,991A
## CURRENT APPLICATION NUMBER: US/09/252,991A
## PRIOR FILING DATE: 1998-02-18
## PRIOR FILING DATE: 1998-07-27
## PRIOR FILING DATE: 1998-07-27
## NUMBER OF SEQ ID NOS: 33142
## SEQ ID NO 21514
## LENGTH: 635
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43.0%; Score 37; DB 4; Length 635;
Best Local Similarity 43.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.0%; Score 37; DB 2; Length 553; 60.0%; Pred. No. 2.2e+02; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FSESESO EN Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,799
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                        PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/785,048
FILING DATE: 17-JAN-1997
APPLICATION NUMBER: 961089.6
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 37-JUL-1996
APPLICATION NUMBER: 9861587
REGISTRATION NUMBER: 938 991
REFERENCE/DOCKET NUMBER: P31355-3
TELECOMMUNICATION INPORMATION:
TELEFHONE: 610-270-4478
TELEFAX: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P31355-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 553 amino acids
                                                                                                                    ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0°
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518 TDDIEKTKAH 527
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US-09-252-991A-21514
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                                                                                                     USA
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Search completed: March 2, 2004, 16:09:01
Job time : 3.86667 secs
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| Sequence 4500, Application US/09134001C
| Patent No. 6380370
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al Amino ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: GTC-007
| CURRENT APPLICATION NUMBER: US 60/064,964
| PRIOR APPLICATION NUMBER: US 60/065,779
| PRIOR APPLICATION NUMBER: US 60/055,779
| PRIOR FILING DATE: 1997-08-14
| NUMBER OF SEQ ID NOS: 5674
| LENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 288, Application US/09198452A;
Parent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverint ERFERENCE: 9710-003, OFFICE OFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                   43.0%; Score 37; DB 4; Length 1335; 43.8%; Pred. No. 5.7e+02; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
41.9%; Score 36; DB 4; Length 82;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4500
                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     629 RYLYSDEEKEEALAQEETH 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 RYLYTDDAQ----QTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|:|||||| ::
107 KQQSLSTDDANQNQTN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RORYLYTDDAQQTEAH 16
    PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3716
LENGTH: 1335
                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
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US-09-134-001C-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 39
US-09-198-452A-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-198-452A-288
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1 RORYLYTDDAQO 12 : |: | || || ||

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March 2, 2004, 15:51:42; Search time 87.0833 Seconds (without alignments) 757.244 Million cell updates/sec
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1113
1 MDSDEIGFEHSGLWVSVLAG......SSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1017041 segs, 315518202 residues
                                                                                                                OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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1: SP_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_numan:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mnc:*
9: sp_organelle:*
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1: sp_organel:*
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Result Accre Match Length DB ID Description

1 1106 99.4 209 4 QBN683 QBN683 QBN683 MQBN683 MQBN80 GBN180 GB

| Q9est9 rattus norv Q9dfc9 brachydanio Q9iai6 gallus gall Q7zzu4 gallus gall Q8nf90 homo sapien Q9nf90 homo sapien Q95112 sus scrofa Q9pvy1 xenopus lae Q8r4x0 rattus norv Q809096 mus musculu Q8vcy9 mus musculu Q9erg5 mus musculu | Q86yn7 homo sapien Q91a15 gallus gall Q8nfi9 homo sapien Q95k97 macaca fasc Q96k94 meleagris g Q80k94 meleagris g Q80k97 meleagris g Q81k97 ciona intes Q951k7 mustela vis Q951k7 mustela vis | Q90y71 xenopus lae |
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| Q9EST9 Q9DFC9 Q9IA16 Q7ZZN4 Q8W6A2 Q9W6A2 Q95112 Q95112 Q9FVY1 Q8R4X0 Q8R4X0 Q8VCY9 Q9ERQS | Q86YN7 Q91A15 Q91A15 Q95K97 Q95K97 Q96F59 Q80454 Q42407 Q9N1B9 Q81A9 Q81A9 Q81A9 | Q90Y71 |
| 113 13 13 13 11 11 11 11 11 | 4 4 4 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 | 13 |
| 212 191 234 208 208 208 211 252 245 | 252 253 253 208 204 207 212 212 213 214 218 218 218 218 218 218 | 111 |
| 4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4. | 11111111111111111111111111111111111111 | 11.9 |
| 160 159.5 159.5 157.5 157.5 153 153 153 153 153 153 | 15.0 148.5 150 147.5 147.5 147.5 144.5 141.5 1338 1336 | 132 |
| 22222222222222222222222222222222222222 | 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 4 4 5 4 5 |
| | | |

ALIGNMENTS

| SUL N68 | 683 | PRELIMINARY; | NARY; | PRT; | | 209. AA. | | | | |
|---|--|---|-------------------|-----------------|---------------|-----------------------------------|--|--------------|--------|-----|
| AC 08N6 DT 01-0 | QBN683; 01-OCT-2002 01-OCT-2002 | (TrEMBLrel. | | | d) equence | Created) Last sequence update) | | | | |
| 10 10 10 10 10 10 10 10 10 10 10 10 10 1 | 01-OCT-2003 | (TrEMBLrel. | rel. 25, | Last | nnotat | annotation update) | re) | | | |
| | Fibroblast growth factor 21 | growth fa | actor 21 | | | | | | | |
| OS Home | Homo sapiens (Human). Rukarvota: Metazoa: Chordata: | s (Human, Wetazoa: |). Chordat | | iata; | Craniata; Vertebrata; | ta; Eutel | Euteleostomi | i, | |
| _ | Mammalia, Butheria, Primates; | utheria; | Primate | | rrhini | Catarrhini; Hominidae; | dae; Homo. | , | | |
| DN NCB | NCBI_TAXID=9606; [1] | 4000 | | | | | | | | |
| | SEQUENCE FROM N.A. | OM N.A. | | | | | | | | |
| | TISSUE=Lung; | •• | | | | | | | | |
| RA Str | Strausberg R.; | R. ; | | | • | | | | | |
| | Submitted (I | (DEC-2001) to the EMBL/GenBank/DDBJ databases |) to the | EMBL/G | enBank | /DDBJ da | cabases. | | | |
| DR EMB | EMBL; BC018404; AAH18404.1; | 404; AAH | 18404.1; | | | | | | | |
| | GO; GO:0008083; F:growth factor activity; IEA. | 083; F.g | rowth fa | actor ac | tivity | ; IEA. | | | | |
| | erPro; I | PR008996 | ; Cytok | 111. 21 11.K | ď. | | | | | |
| | InterPro; IPR002348; 1L1 HBGF. | PR002348 | 1111 ' | 3GF. | | | | | | |
| | Pfam; PF00167; FGF; 1. | 67; FGF; | 1. | | | | | | | |
| | PRINTS; PR00262; ILIHBGF. | 0262; IL | IHBGF. | | | | | | | |
| | ProDom; PD000831; ILL HBGF; | 00831; I | LI_HBGF; | | | | | | | |
| SO SEO | SMAKT; SMUU442; FGF; SEQUENCE 209 AA; | 442; FGF 209 AA; | ; I. 22284 MW; | | 25C43E | 27925C43E5167823 | CRC64; | | | |
| | 40.40 | | 00 48. | | 1106. | Score 1106. DB 4: | Length 209; | :60 | | |
| Best Local | Best Local Similarity | ilarity | 99.58; | • | ed. No. 8.2 | Pred. No. 8.2e-94; | Tridela | Ö | Gaps | 0 |
| Matches | s 208; | Conservative | acive | () M | SMACCI | 17 | a topic | 3 | 2 | ; |
| δλ | ı M | SDETGFEH | SGLWVSVI | AGLLLGA | COAHPI | PDSSPLLQ | MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYYTDDAQQTEAH | TYTODA | | 09 |
| 셤 | Ţ Ţ | SDETGFEH | SGLWVSVI | AGLLLGA | COAHPI | Posspiro | MDSDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH | LYTDDA | | 0.9 |
| ò | E1 19 | IREDGTVG | GAADQSPI | ESTLOLKA | LKPGVI | OILGVKTS | LEIREDGTVGGAADQSPRSLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPRA | ALYGSL | HEDPEA | 120 |
| g | 61 LE | IREDGTVG | GAADQSP1 | ESTLQLKA | LKPGVI | QILGVKTS | | ALYGSL | | 120 |

Ear

10;

Gaps

33;

DB 13; Length 227;

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71 GAADQSPESILIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLED 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 LAGLILGACQAH--PIPD-SSPLLQFG-GQ-VRQRYLYTDDAQQ--TEAHLEIREDGTVG
                                                                                                                                                                                                                                                                                                                                                                                                                              19.5%; Score 216.5; DB 13; Length 30.9%; Pred. No. 6.6e-12; tive 33; Mismatches 84; Indels
  SEQUENCE FROM N.A.
MEDLINE=20564778; PubMed=11110663;
Ladher R.K., Anakwe K.U., Gurney A.L., Schoenwolf G.C.,
Francis-West P.H.;
"Identification of Synergistic Signals Initiating Inner I
                                                                                                                                                                                                                                                                  Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILIHBGF.
ProDom; PD000831; ILI HBGF; 1.
SMART; SM00442; FGF; I.
PROSITE; PS00247; HBGF FGF; 1.
SRQUENCE 227 AA; 24568 MW; 875D76FBFD09F8E2 CRC64;
                                                                                                       Development.";
Science 290:1965-1968(2000).
EMBL; AF315555; AAG39478.1; -.
HSSP; P09038; IBFG.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR00248; IL1_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00167; FGF; 1. PRINTS; PRODES; LILHBGF. PRODOMS; PRODOSS; LILHBGF. SMART; SMOG442; FGF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     L Similarity 30.9% 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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SEQUENCE 218 AA; 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
hes 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Itoh N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 GYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGLLAPQPPDVGS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CSFRELLLEDGYMVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPFAPPEPPGI 180
       CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 GLWVSVLAGL-LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 GLMVCLILPVFLLGVCEAYPISDSSPLLQFGGQVRQRYLYTDDDQDTEAHLEIREDGTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Futtus norvegicus FGF21.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB078901; BAB84299.1; --
GO; GO:0008089 ; F:growth factor activity; IEA.
InterPro; IPR008996; Cyrok II.1_like.
InterPro; IPR008996; II.1_HBGF.
PEam; PF00167; FGF; 1.
PRINTS; PR00167; FGF; 1.
PRINTS; PR00181; III.HBGF; 1.
SYART; SM00442; FGF; 1.
SEQUENCE 208 AA; 22857 MW; D232445902CDB8EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 803.5; DB 11; ......
Pred. No. 5.6e-66;
......+rheg 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 19.
                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.2%; Scor. No. 5...
78.3%; Pred. No. 5...
've 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 AA
                                                                                                                       LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                181 LAPOPPDVGSSDPLSMVGPSOGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 SDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 SDPLSMVEPLQGRSPSYAS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Itoh N.;
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                                                                                                                                                                                                                                                         Q8VIB0
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Q9DDN0
AC Q9DDN
DT 01-M
DT 01-M
DT 01-C
DB Fibx
CGN FGF-C
DB FIBX
CGN FIBX

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1:
131 GYNVYQSEAHGLPLHLPGNKSPH----RDPAPRGPARFLPLPGLPPA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.6%; Score 206.5; DB 11; Length 218; 30.7%; Pred. No. 5.2e-11; Live 37; Mismatches 92; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Rattus norvegicus FGF15.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB078900; BAB84298.1;
GO; GO:0008083; F:growth factor activity; IEA.
INTERPRO; IPR008996; Cytok_ILI_like.
InterPro; IPR008996; ILI_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 AA; 25207 MW; ED898684B5307C58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 15.
                                                                                                                                                                                                                                                         193 AFEPE----VYSSPLETDSMDPFGITSKLSPVKSPSF 225
                                                                                                                                                                                                 174 --LPEPPGILAPQPPDVGSSDPLSMVGP-SQGRSPSY 207
                                                                                                                                                                                                                                                                                                                                                                                                      218 AA
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 LGVKTSRFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYOSEAH-GLPLHLPGN--- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | : | : | | | | : | | | | : | | 1.8 YGVKSGLFVAMSSRGRLYGTRAFRDE-CKFKETLLPINYNAYESSIXKGFYMALSKHGRL 186
                                                                  GYNVYQSEAHGLPLHLPGNKS-PHRDPAPRGPARFLPL--PGLPPALPEPPGILAPQPPD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 SSPLLOFGGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESILGLKALKPGVIQI 93
70
             13 LWVSVLAGLILGACQAHPIPDSSPLLQFG-GQV-RQRYLYTDDAQQTEAHLEIREDGTVG
                                                   71 GAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPRACSFRELLLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                             Ralliere C., Rescan P.-Y.;

Ralliere C., Rescan P.-Y.;

"Identification of a fgf6 gene in zebrafish.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RADIS, AFS16334; AA015997.1; -.

GO; GO:0008083; F:growth factor activity; IEA.

InterPro; IPR001064; Cytok IL1_like.

InterPro; IPR002348; IL1_HBGF.

Pfam; PF00167; FGF; 1.

RATIS; RR00262; IL1_HBGF; 1.

SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match
Local Similarity 28.4%; Pred. No. 2.8e-08;
hes 56; Conservative 26; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00225; CRYSTALLIN BETAGANMA; 1.
PROSITE; PS00247; HBGF FGF; 1.
SEQUENCE 205 AA; 23244 MW; 2BDB1D93D6533696 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 EHSGLW---VSVLAGLLLGACQAHPIPD-----VSVLAGLLLGACQAHPIPD------
                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 6.
                                                                                                                                                                                                                                               205 AA
                                                                                                                                                                      | || || : ||| || 195 SDSMDPRANTEDVDHLVKSPSF 216
                                                                                                                                                         188 VGSSDPLSMVGPSQG--RSPSY 207
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 KRGHRASPAMTVTHFLP 203
                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Ralliere C., Resca
                                                                                                      131
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                                                                                                                                                                                                                                               QBAXA1
QBAXA1;
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Matches
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Q8R5L5
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208 AA.

PRT;

PRELIMINARY;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rescan P.Y.;
"Identification of a fibroblast growth factor 6 (FGF6) in a non-
mammalian vertebrate: Continuous expression of FGF6 accompanies muscle
                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota; Metazoda; Chordeta; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 208;
                                                                                                                                                                                                                                                       "Rattus norvegicus FGF6 mRNA."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; ABO79674; BABB4704.1; -... GO; GO:0008081; F:growth factor activity; IEA. InterPro; IPR001064; Cryokallin. InterPro; IPR001064; Cryokallin. InterPro; IPR001064; Cryokallin. FFam: PF00167; FGF; 1... HBGF. PFam: PF00167; FGF; 1... PRINTS; FR00262; ILIHBGF; 1... ProDom; PD000811; ILIHBGF; 1... SMART; SM00442; FGF; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
PROSITE; PS00247; HBGF FGF; 1.
SEQUENCE 208 AA; 22789 MW; 4BEEA0301BB78986 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 LCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 6-related protein.
                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 15.4%; Score 171.5; DB 1 Local Similarity 36.4%; Pred. No. 8.2e-08; Nes 36; Conservative 21; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1443:305-314 (1998).

BNISL; Y1680; CAA76422.1; -.

HSSP; P31371; 1G82.

GO; GO: 0008083; F: growth factor activity; IEA.

InterPro; IPR001064; Crystallin.

InterPro; IPR008996; Cytok ILI_like.

InterPro; IPR002348; ILI_HBGF.

PFam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 AA.
Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=99096461; PubMed=9878802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                  Fibroblast growth factor.
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                                                                                                              Rattus norvegicus (Rat)
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                     NCBI_TaxID=10116;
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NCBI_TaxID=8316;
                                             NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09YH31
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Q9YH31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 FLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 YLAMNKKGRIYASEHYNAE-CEFVERIHELGYNTYASR-----LYRTGPGGRRQPGA 149
                                                                                                                                                        78 LGIKRVRRLYCNAG--IGFHLQVLPDGRINGVHNENQYSLIEISTVERGVVSLYGVRSEL 135
                                                                                                                                         44 ---VRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
                                                                                                                18 HWILTAIVLIGFIVGIVSSYPIPSRINATLIEKRWETLFSRSILGISGEKSDLNWESDYL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 HSGLWVSVLAGLLLGACQAHPIPD------SSPLLQFGGQ------
                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                           Query March 15.4%; Score 171; DB 13; Length 206; Best Local Similarity 26.9%; Pred. No. 9e-08; Matches 43; Conservative 28; Mismatches 57; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.4%; Score 171; DB 11; Length 245; 35.0%; Pred. No. 1.1e-07; tive 20; Mismatches 48; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                "Rattus norvegicus FGF3 mRNA.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO79262; BAB84564.1; -
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok Iii_like.
InterPro; IPR008996; Cytok Iii_like.
InterPro; IPR00269; Iii_HBGF.
ProDom; PF00167; FGF; I.
PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; III_HBGF; I.
SWART; SW00442; FGF; I.
PROSITE; PS00247; HBGF FGF; I.
SRQUENCE 245 AA; 27150 MW; C9305D307E7D0648 CRC64;
 PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
PROSITE; PS00247; HBGF_FGF; 1.
SEQUENCE 206 AA; 23375 MW; BB883328F17EB6E4 CRC64;
                                                                                                                                                                                          101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYOSEAH 140
                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                              245 AA
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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01-MAR-2003 (
01-OCT-2003 (
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Q8C399;
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                                                                                                                                                                                                                                                       RESULT 8
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ID Q8
AC Q8
DT 01
DT 01
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42 GOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESILIQLKALKPGVIQILGVKTSRF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 GIKRQRRIYCNVG--IGFHLQVPPDGRISGTHEENPYSLLEISTVERGVVSLFGVKSALF 125
                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK086530; BAC39686.1; -.
EMBL; AK086530; BAC39686.1; -.
EMBL; AK086530; CAYORL ELL!
InterPro; IPR001064; Crystallin.
InterPro; IPR001248; ILI_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Gaps
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative fibroblast growth factor-4.
Bukaryota, Metageons (Bastern newt) (Triturus viridescens).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Caudata; Salamandridae;
Notophthalmus.
Fibroblast growth factor 6 (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.3%; Score 170.5; DB 11; Length 195; 36.4%; Pred. No. 9:3e-08; tive 21; Mismatches 39; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Putative Newt Fibroblast Growth Factor-4.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U76998; AAC98812.1; --
HSSP; P09038; 1BFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEGM; PP00167; FGF; 1.

PRINTS; PR00262; ILLHBGF.

PRODOM; PD000831; ILL HBGF; 1.

SWART; SM00442; FGF; ILL

PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.

PROSITE; PS00247; HBGF FGF; I.

SEQUENCE 196 AA; 22033 MW; AC4688CD989C6EAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER 1 1 1 2 SEQUENCE 195 AA; 21318 MW; BABA90EF368994FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 LCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0008083; F:growth factor activity; IEA InterPro; IPR001064; Crystallin. InterPro; IPR008996; Cytok IL1_like. InterPro; IPR002348; IL1_HBGF.
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PRINTS; PR00262; ILIHBGF.
PRODOM; PD000831; ILI HBGF; 1.
PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 IQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 KRLRRLYCNVGIGFHLQVLPDGRIHGMHSESRXSLLEISPVERGVVCMFGVQSGLFLAMN 130
                                                                                         60 ------HIBIREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV 90
                                                           ----- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Gaps
                       Gaps
                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.1%; Score 168; DB 11; Length 212; Best Local Similarity 33.5%; Pred. No. 1.8e-07; Matches 54; Conservative 19; Mismatches 62; Indels 2
Query Match 15.1%; Score 168; DB 13; Length 196; Best Local Similarity 28.9%; Pred. No. 1.6e-07; Matches 44; Conservative 27; Mismatches 45; Indels 36
                                              ----AQQTEA-
                                                                                                                                                                                                                                                                                                                                                                          Itch N.;
"Mus musculus mRNA for FGF-20(FGF20).";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB049218; BAB16406.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00262; IL1HBGF.

ProDom; PD000831; IL1 HBGF; 1.

SMART; SM00442; FGF; 1.

SROASTIE; PS00247; HBGF FGF; 1.

SEQUENCE 212 AA; 23659 MW; 174DBCE8915B69EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SPHRDPAPRGPAR-----FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 GRRYFVALNKDGTPRDGARSKRRQKFTHFLPRPVDPERVPE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q90XQ5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 4 (Fragment).
                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 20.
                                              17 VLAGLILGACQAHPIPD-SSPLLQFGGQVRQRYLYTDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1891346; Fgf20.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok_III_like.
InterPro; IPR0012348; ILI_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                         106 PDGALYGSLHFDPEACSFRELLLEDGYNVYQS 137
                                                                                                                                                     124 AA.
                                                                                                                                                                                                                       212 AA.
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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CSTRAIN=CSTBL/60; TISSUE=Heart;

MEDLINE=22354683; PubMed=12466851;

A The FANTOW Consortium,

The FANTOW Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A "Analysis of the mouse transcriptome based on functional annotation of

10 And "A STATE CONTROL CONTROL"

MED MAIL-Length CONTROL

MED; MAIL-Sength CONTROL

MED; MAIL-Sength FST20.

MED; MAIL-Sength FST20.

MED; MAIL-Sength factor activity; IEA.

MICHEPRO; IPR008996; Cytok IL1_like.

InterPro; IPR008996; Cytok IL1_like.

RILL-REPRO; IPR008996; Cytok IL1_like.

PRODO; PR000691; II.1 HBGF.

PRODO; PR000691; II.1 HBGF.

PRODO; PR000691; MAFF: 1.

ROMART; SM00442; FGF; 1.

SMART; SM0442; FGF; 1.

SMART; SM0442; FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21439472; PubMed=11555861;
Christensen R.N., Weinstein M., Tassava R.A.;
"Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
and semi-quantitative RT-PCR expression studies.";
J. Exp. Zool. 290:529-540(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
15.0%; Score 167.5; DB 13; Length
Best Local Similarity 35.1%; Pred. No. 9.9e-08;
Matches 39; Conservative 23; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 124 AA; 14161 MW; 919CE10E9F66CEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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EMBL, AR360984; AAL16957.1; ...

GO; GO:0008083; Fgrowth factor activity; IEA.

InterPro; IPR001064; Crystallin.

InterPro; IPR0010896; Cytok ILI_like.

R interPro; IPR002348; ILI_HBGF.

R Fam; PF00107; FGF; 1.

R PRINTS; PR00262; ILIHBGF.

R PRINTS; PR00262; ILIHBGF.

R PROM; PD000831; ILI_HBGF; 1.

R SMART; SM00442; FGF; 1.

R ROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.

PROSITE; PS002247; HBGF_FGF; 1.
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(Axolot1).
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   Ambystoma mexicanum
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                                                                                                                      NCBL_TaxID=8296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 VIYSSMLYRQQBSGRAWFLGLNKEGQVMKGNRVKKTKPA----AHFLPKP-LEVAMYREP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 IQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
                                                                                                         108 VSIRGVDSGLYLGMNDKGELYGSEKLTSE-CIFREQFEENWYNTYSSNIYKHGDTGRRYF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 GACQAHPIPDSSPLLQFGGQVRQRXLYTDDAQ------QTEAHLEIREDGTVGGAA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 GLCNGNLVDIFSKVRIFG--LKKRRLRRQDPQLKGIVTRLYCRQGYYLQMHPDGALDGTK 95
                                            90
                                           32 PDSSPLLOFGGOVRORYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV
                                                                                                                                                                                                                                                                                  Partus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80; Indels 38; Gaps
                     24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.5%; Score 161; DB 11; Length 247; 29.8%; Pred. No. 9.4e-07; tive 28; Mismatches 80; Indels 38
 14.8%; Score 165; DB 11; Length 211; 34.4%; Pred. No. 3.3e-07; ive 16; Mismatches 65; Indels 2
                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB079500; BAB84580.1; -.
GO, GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR002348; ILI_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                           PEAM; PP00167; FGF; 1.
PRINTS; PR00262; ILIHBGF.
ProDom; PD000831; ILI HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
SEQUENCE 247 AA; 27720 MW; 427C3C760894996E CRC64;
                                                                                                                                146 LPGNKSPHRDPAPRGPAR-----FLPLPGLPPALPE 176
                                                                                                                                                   167 VALNK----DGTPRDGARSKRHQKFTHFLPRPVDPERVPE 202
                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                   Tron N.;
"Rattus norvegicus FGF14 mRNA.";
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                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
Fibroblast growth factor14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 29.8%
Matches 62; Conservative
                        55; Conservative
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                                                                                                                                                                                                           PRELIMINARY;
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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01-MAR-2003
01-MAR-2003
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                        Matches
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SEQUENCE FROM N.A.

STRAIN=C57BL/60; TISSUE=Pituitary;

MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium,

At the RIKEN Genome Exploration Research Group Phase I & II Team;

At the RIKEN Genome Exploration Research Group Phase I & II Team;

At the RIKEN Genome Exploration Research Group Phase I & II Team;

Thanlysis of the mouse transcriptome based on functional annotation of a value 420:563-573(2002).

By the All AROSTOGIC; BAZ27049:1; ...

REGIO, 00008083; F:growth factor activity; IEA.

InterPro; IPR00248; III_HSGF.

REFTO; IPR00248; III_HSGF.

PRINTS; PR00167; FGF; 1.

PRODOM; PD000831; III_HSGF; 1.

RINTS; PR00167; FGF; 1.

SWART; SM0442; FGF; 1.

SWART; SM0442; FGF; 1.

SGUENCE 247 AA; 27720 WW; 427C3C760894996E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 VIYSSMLYRQQESGRAWFLGLNKEGQVMKGNRVKKTKPA----AHFLPKP-LEVAMYREP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | : : | | : | | : | | 38 GLCNGNIVDIFSKVRIFG--LKKRRLRRQDPQLKGIVTRLYCRQGYYLQMHPDGALDGTK 95
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MEDIJINE-21439472; PubMed=11555861;
MEDIJINE-21439472; PubMed=11555861;
MEDIJINE-21439472; PubMed=11555861;
MEDIJINE-21439472; PubMed=11555861;
"Pibroblast growth factors in regenerating limbs of Ambystoma: Cloning and semi-quantitative RT-PCR expression studies.";
J. EXP. Zool. 290:529-540(2001).
BMB1, AF360988; AAL16961.1.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR001064; Crystallin.
InterPro; IPR002348; ILI_like.
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Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Fibroblast growth factor 4 (Fragment).
Ambystoma maculatum (Spotted salamander).
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.8%; Pred. No. 9.4e-07;
Matches 62; Conservative 28; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 GILAPOPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 SL----HDVGETVPKAGVTPSKSTSAS
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01-DEC-2001 (TrEMBLrel. 19, Created)
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01-OCT-2003 (TrEMBLrel. 25, I
Fibroblast growth factor 14.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                  NCBI_TaxID=10090;
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SEQUENCE FROM N.A.
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                                                Q9DFC9;
                                   Q9DFC9
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             RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 VSİRGVDSGLYLGMNGKGELYGSEKLTSE-CIFREQFEENWYNTYSSNIYKHGDTGRRYF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 PGSVELAHIHGILRRRQLYC----RTGFHLQILPDGSVQGTRQDHSLFGILBFISVAVGL 107
                                                                                                                                                             60 HLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV 90
                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "FGE-20," a novel neurotrophic factor, preferentially expressed in the substantia nigra pars compacta of rat brain.";
Blochem, Bioghys. Res. Commun. 277:355-360(2000).
BMB.; AB020021; BAB13763.1; -.
PIR; JC7511; JC7511.
HSSP; P31371; JG82.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008956; Cytok_ILL_like.
                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Gaps
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohmachi S., Watanabe Y., Mikami T., Kusu N., Ibi T., Akaike A.,
                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 14.4%; Score 160; DB 11; Length 212; Local Similarity 33.8%; Pred. No. 9.6e-07; and 54; Conservative 17; Mismatches 65; Indels 24
                                                                                                            ch 14.4%; Score 160; DB 13; Length 111; 1 Similarity 37.4%; Pred. No. 4.2e-07; 34; Conservative 21; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan; PF00167; FGF; 1. PRINTS; PR00262; IL1HBGF.
PRINTS; PR000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
PROSTITE; PS00247; HBGF FGF; 1.
SEQUENCE 212 AA; 23537 MW; 4F858BEFE772B977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 LPGNKSPHRDPAPRGPAR-----FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 111
111 AA; 12607 MW; 4A3A52ED39001057 CRC64;
                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
PRINTS; PR00262; ILIHBGF.
ProDom; PD000831; ILI HBGF; 1.
SWART; SMO4422; FGF; 1.
PROSITE; PS00247; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
NON TER 11 111
SEQUENCE 111 AA; 12607 MW; 4A3A52ED390010
                                                                                                                                                                                                                                72 ECKFKEPLLANNYNAYESRQYPGMYIALSKN 102
                                                                                                                                                                                                                 120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN 149
                                                                                                                                                                                                                                                                                                       212 AA.
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01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=20490008; PubMed=11032730;
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                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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01-MAR-2001
01-MAR-2001
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FGF-20.
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                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 IKRLRRLYCNVG--IGFHLQVLPGGKITGVHNENRYSLLEISBVERGVVTLFGVRSGLFV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDIJNE=20433237; PubMed=10976049;
Grandel H., Draper B.W., Schulte-Merker S.;
"dackel acts in the ectoderm of the zebrafish pectoral fin bud maintain AER signaling.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 SGLWVSVLAGLLLGACQAHPIPD------SSPLLQFGGQVRQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Development 127:4169-4178(2000).
| EMBL; AF283555; AAG13950.1; -...
| EMBL; AF2875; 1692.0.1 | Egf4. | Egf6. | E
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor homologous factor 4 isoform 1A
                                                                                           01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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191 AA
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 NRVSTSMTMTHFLP 189
                                                                                                                                                                                                                                                                  Fibroblast growth factor 4.
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     PRELIMINARY;
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Best Local Similarity
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us-10-060-765-4.rspt

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85 DDSSNSTLFNLIPVGLRVVAIQGVKTGLYIALNNEGFLYTSELFTPE-CKFKESVFENYY 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 NVYQS------EAHGLPLH----LPGNKSPHRDPAPRGPARFLPLPGLPPALPEPP 178
                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                           24 GACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQ------QTEAHLEIREDGTVGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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Yoshioka H., Ishimaru Y., Sugiyama N., Tsunekawa N., Noce T.,
Kasahara M., Morohashi K.;
"Mesonephric FGF9 is the initiation signal for Gonadal Organogenesis in chick.";
MEDLINE=20112823; PubMed=10644718;
Munoz-Sanjuan I., Snallwood P.M., Nathans J.;
"Isoform Diversity among Fibroblast Growth Factor Homologous Factors
Is Generated by Alternative Promoter Usage and Differential
                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                 14.3%; Score 159; DB 13; Length 237; 29.3%; Pred. No. 1.4e-06; ive 30; Mismatches 79; IndelB 3
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GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR08996; Cytok III_like.
InterPro; IPR08996; Cytok III_like.
InterPro; IPR08996; Cytok III_like.
Propon; PR00262; III_HBGF.
PRINTS; PR00262; III_HBGF.
Propon; PR00831; III_HBGF.
SWART; SW00442; FGF; I.
SWART; SW00247; FGF; I.
SROSITE; PS00247; HGF FOF; I.
SEQUENCE 208 AA; 23382 MW; DC73CDB7329D36CA CRC64;
                                                                                                                                                                                                                                                                                   237 AA; 26816 MW; F13076736548BB22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                            GO; GO:000803; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok IL1_like.
PinterPro; IPR00348; IL1_HBGF.
PRINTS; PR00262; IL1HBGF.
PRINTS; PR00262; IL1HBGF.
PRODER: SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
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                                                               Splicing.";
7. Biol. Chem. 275:2589-2597(2000).
EMBL; AF199605; AAF31392.1; -.
HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25, Fibroblast groth factor 9.
                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                   Local Similarity
Les 61, Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                   Query Match
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Q7ZZN4
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14.2%; Score 157.5; DB 13; Length 208;

Query Match

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61 SSPAASLGSQGSGLEQSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEANMLSV 120
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                                                                                                                                              141 ----GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLP----PAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 RIEKIGREMYVALNK---RGKAKRGCSPRVKPOHISTHFLPRFKQSEQPELSFTVTVPEK 236
                                                                         37 LGQAEAGGLPRGPAVTDLDHLKGILRRRQLYC----RTGFHLEIFPNGTIQGTRQDHSRF 92
                                                    23 LGACQAHPIPDS---SPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPE
                                                                                                                        79 SLLOLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 SSPLLQFGGQ----VRQRYLYTDDAQQTEA-----HLEIREDGTVGGAADQSPESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yang J.C.;
"Identification of fibroblast growth factor-5 as an overexpressed
autigen in wiltiple human adenocarcinomas.";
Cancer Res. 61:5511-5516(2001).
                                                                                                                                                                                               139 AH-----GLPLHLPGNKSPHRDPAPRGPAR------FLPLPGLPPALPE 176
                                                                                                                                                                                                                               152 LYKHVDIGRRYYVALNK----DGTPREGTRIKRHOKFIHFLPRPVDPEKVPE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-21347229; PubMed=11454700;
Hanada K.-I., Perry-Lalley D.M., Ohnmacht G.A., Bettinotti M.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanada K.-I., Yang J.C.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABSJ3149; ANNO4097.1.
GO; GO:00080081; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR003948; IL1_HBGF.
InterPro; IPR00248; IL1_HBGF.
ProDom; PD000831; IL1_HBGF.
PROSITE; SG00247; HBGF FGF; I.
SMART; SM00442; FGF; I.
SMART; SM00442; FGF; I.
SEQUENCE 268 AA; 29550 MW; 28B7268B2678IBCF CRC64;
Pred. No. 1.6e-06;
; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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27.6%; Pred. No. 2.2e-06;
tive 28; Mismatches 68
                                                                                                                                                                                                                                                                                                                     PRT;
ilarity 32.0%; Pro Conservative 21;
                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25, Fibroblast growth factor-5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 KKPPSPIKPKIP 248
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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Similarity
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Best Local
Matches 5
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Q8NF90
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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                                                                     SEQUENCE FROM N.A.
                       NCBI TaxID=9823;
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         OC REAL BY SERVICE OC CONTRACT OF SERVICE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 -SPESILLQIKALKPGVIQILGVKTSRFLCQRPDGALYGSIHFDPEACSFREILLEDGYNV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 DSSYTLENLIPVGLRVVALQGVQTKLYLAMNSEGYLYTSEHFTPE-CKFKESIFENYYVT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 GACQAHPIPDSSPLLQFGGQVRQRY-----LYTDDAQQTEAHLBIREDGTVGGAADQ
                                                                                                                                                                                                                                                     Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain,
MEDIZBE20112823; PubMed=10644718;
MEDIZBE20112823; PubMed=10644718;
MEDIZBE20112823; PubMed=10644718;
MINDOZ-Sanjuan I., Smallwood P.M., Nathans J.;
Isoform Diversity among Fibroblast Growth Factor Homologous Factors Is Generated by Alternative Promoter Usage and Differential Splicing.";
J. Biol. Chem. 275:2589-2597(2000).
EMBL; AF19875; AAD21576.1;
EMBL; AF196611; AAF31398.1;
HSSP; P31371; 1G82.
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=99065510; PubMed=9847253;
Munoz-Sanjuan I., Simandl B.K., Fallon J.F., Nathans J.;
Munor-Sanjuan II., Simandl B.K., Fallon J.F., Nathans J.;
Expression of chicken fibroblast growth factor homologous factor
(FHF)-1 and of differentially spliced isoforms of FHF-2 during
development and involvement of FHF-2 in chicken limb development.";
Development 126:409-421 (1999).
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                                                                                                                   Last sequence update)
Last annotation update)
isoform 1S (Fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.0%; Score 155.5; DB 13; Length
29.4%; Pred. No. 3e-06;
tive 26; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PROD262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; RGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
SRQUENCE 245 AA; 27605 MW; DAODAFEDBALB8F28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95L12;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0008083; F:growth factor activity; IEA.
Interpro; IPR008996; Cytok_IL1_like.
Interpro; IPR002348; IL1_HBGF.
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                                                            245 AA
                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last and Fibroblast growth factor 13 isoform. homologous factor 2 isoform 1T+1S').
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                                                            PRELIMINARY;
                                                                                                                                                                                                                    FGF13 OR FHF-2.
Sallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00167; FGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
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Q95L12
                                                              Q9W6A2
                  RESULT 22
                                         D9W6A2
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91 IQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV 90
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MEDLINE-99373151; PubMed=10441498;

MEDLINE-99373151; PubMed=10441498;

R Koga C., Adati N., Nakata K., Mikoshiba K., Furuhata Y., Sato S.,

R Koga C., Adati N., Nakata T., Shiokawa K., Yokoyama K.K.;

The H., Sakaki Y., Kurokawa T., Shiokawa K., Yokoyama K.K.;

Transcretzization of a novel member of the FGF family, KFGF-20, in the FMDL BAD1261; BAD34 BAD3414.1;

Biochem Biophys. Res. Commun. 261:756-765(1999).

R FIR: JC7082; JC7082.

R RSSP, P31371; JG82.

R RSSP, P31371; JG82.

R RSSP, P31371; JG82.

R RSSP, P31371; JG82.

R InterPro; IPR008995; Cytok III_like.

R InterPro; IPR00151; FGF; II.

R Ffam; PF00167; FGF; II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 208;
Paradis V., Silversides D.W.;
Paradis V., Silversides D.W.;
"Sus scrofa fgf9 cDNA.";
"Sus scrofa fgf9 cDNA.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY033825; AAK61609.2; -.
GO, GO,0008083; F:growth factor activity; IEA.
InterPro; IPR003396; Cytok III_like.
InterPro; IPR002348; III_HBGF.
Prints; PR00467; FGF; I.
ProDom; PD000831; III_HBGF.
SMART; SM00442; FGF; I.
PROSITE; PS00247; HBGF_FGF; I.
SEQUENCE 208 AA; 23454 MW; OSFD0E2048CCCSES CRC64;
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SEQUENCE 208 AA; 23438 MM; 268881D36E757D4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 LPGNKSPHRDPAPRGPAR-----FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 VALNK----DGTPREGTRIKRHOKFIHFLPRPVDPDKVPE 199
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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11arity 31.5%; Pred. No. 4.1e-06;
Conservative 22; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 13.9%; Score 155; DB 6; Local Similarity 32.5%; Pred. No. 2.7e-06; nes 52; Conservative 19; Mismatches 65
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ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
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PRELIMINARY;
MCBI_TaxID=10090, 10116;
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Q8VCY9
DD Q8VCX9
DD O1-MA
DT 01-MA
DT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 EACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSPHRDPAPRGPARF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160
                                                                                                                                                       98 ISVAIĞLVSIRĞVDTĞLYLĞMNDKĞELFĞSEKLTSE-CIFREQFEENWYNTYSSN---- 151
                                                                                                            84 KALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLP 143
                                             OAHPIPDSSP--LLQFGGQVRQRYLYTDDAQQTBAHLBIREDGTVGGA-ADQSPESLLQL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 YLQMHPDGALDGTKDDSTUSTLFNLIPVGLRVVAIQGVKTGLYIAMNGBGYLYPSELFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 HLEIREDGTVGGAADQSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP
                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor-like factor-4D (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                    152 LYKHGDSGRRYFVALNKDGTPRDGTRAKRHQKFTHFLPRPVDPEKVPE 199
                                                                                                                                                                                                   144 IHLPGNK-----SPHRDPAPRGPAR------FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Liu C., Dib-Hajj S.D., Waxman S.G.;

Fint Collast growth factor homologous factor-4D.";

Fint Collast growth factor homologous factor-4D.";

Submitted (FEB-2001) to the EMBL/Genbank/DDBJ databases.

EMBL, AF948523; AAL93904 11;

EMBL, AF948523; AAL93904 11;

EMBL, Figrowth factor activity; IEA.

InterPro; IPR00836; Cytok III, like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 LPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS 206
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 13.7%; Score 153; DB 11;
1 Similarity 32.7%; Pred. No. 4.2e-06;
53; Conservative 21; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00167; FGF; 1.
PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00247; HBGF_FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 06, 01-OCT-2003 (TrEMBLrel. 25, Fibroblast growth factor 14 PGF14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Best Local Similarity
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089096
089096
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DT 01-NO
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DT FFIbro
CN FFIbro
CN Mus m
OC Rattu
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119 EACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSPHRDPAPRGPARF 164
SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon; MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 HIBIREDGTVGGAADQSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES=Mouse, and Rat; TISSUE=Brain;
MEDLINE=98567141; PubMed=9602045;
WEDLINE=98567141; PubMed=9602045;
"Strancture and expression of a novel isoform of mouse FGF homologous factor (FHP)-4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
110090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.7%; Score 153; DB 11; Length 2 Best Local Similarity 32.7%; Pred. No. 5.2e-06; Matches 53; Conservative 21; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 LPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 LPKP-LEVAMYREPSL----HDVGETVPKAGVTPSKSTSAS 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERNTS; PR00167; FGF; 1.
PRINTS; PR00262; ILIHBGF.
PRODOM; PD000831; ILI HBGF; 1.
SWART; SW00442; FGF; 1.
SEQUENCE 252 AA; 28364 MW; 281781EEBA63AB44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 13.
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MGD; MG1.001/19; Fgf13.
InterPro; IPR008996; Cytok_IL1_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:109189; Fgf14.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok II.1_like.
InterPro; IPR002348; II.1_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1398:38-41(1998).
BMBL; AK035974; BAC29265.1; -.
EMBL; AK079100; BAC3740.1; -.
EMBL; AB008908; BAA31544.1; -.
EMBL; AB008907; BAA31544.1; -.
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169 GLPPALP 175
                                      191 VDPSKLP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                            RESULT 29
Q86YN7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 SFRELLLEDGYNVYQSEAHGLPLHLPGNK----SPHRDPAPRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 IFPNGTVHGTRHDHSRFGILEFISLAVGLISIRGVDSGLYLGMNERGELYGSKKLTRE-C 133
                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                    76 SPESILQIKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVY 135
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                                                                                                                                                                                                                                                                                                                                                                                                25 ACQAHPIPDSSPLLQFGGQVRQRY-----LYTDDAQQTEAHLEIREDGTVGGAADQ- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QSEAHGLPLHL-----PGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 SSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNKPA----AHFLPKP-LKVAMYKEPSL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                                                                                        37 SCDKNKLNVFSRVKLFGSKKRRRRRPEPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.6%; Score 151.5; DB 11; Length 207; 32.6%; Pred. No. 5.6e-06; Live 20; Mismatches 75; Indel8 31; Gaps
                                                                                                                                                                                                                                    Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                    29;
                                                                                                                                                                                    13.7%; Score 152.5; DB 11; Length 245; 29.6%; Pred. No. 5.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Heart;
Sontag D.P., Cattini P.A.;
Sontag D.P., Cattini P.A.;
"Cloning and biological function of FGF-16 in the heart.";
"Cloning and biological tention of FGF-16 in the heart.";
submitted (AuG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF292104; AAG29501.1; -.
HSSP; P31371; 1G82.
                                                                                                                                                                                                                                    72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300247; HBGF FGF; 1.
207 AA; 23739 MW; E28004DED598A2C6 CRC64;
                                 Pfam; PF00167; FGF; 1.

PRINTS; PR00262; ILIHBGF.

Prodom; PD000831; ILI HBGF; 1.

SMART; SM00442; FGF; 1.

PROSITE; PS00247; HBGF FGF; 1.

SEQUENCE 245 AA; 27587 MW; 5B96D41AC3A3DF78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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GO; GO:0006083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR002348; III_HBGF.
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nes 61; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 AA.
                                                                                                                                                                                                                                    25; Mismatches
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PRINTS; PR00262; IL1HBGF.

ProDom; PD000831; IL1 HBGF; 1.

SMART; SM00442; FGF; 1.

PROSITE; PS00247; HBGF FGF; 1.

SEQUENCE 207 AA; 23739 MW;
              InterPro; IPR002348; ILL HBGF.
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                                                                                                                                                                                                                                         53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                              Query Match
Best Local S:
Matches 53,
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Matches
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87 YLQMHPDGALDGTKDDSTNSTLFNLIPVGLRVVALQGVKTGLYIAMNGEGYLYPSELFTP 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 HLEIREDGTVGGAADQSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
13.6%; Score 151; DB 4; Length 252;
Best Local Similarity 32.7%; Pred. No. 8e-06;
Matches 53; Conservative 20; Mismatches 63; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20112803; PubMed=10644718; Mathans J.; Munoz-Sanjuan I., Smallwood P.M., Nathans J.; Isocorm Diversity among Fibroblast Growth Factor Homologous Factors Is Generated by Alternative Promoter Usage and Differential
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                              Bonner T.I.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY188178; AA031806.1; -
CO; GO:0080818; F:growth factor activity; IEA.
InterPero; IPR0018996; Cytok III_like.
InterPero; IPR0018996; III_HBGF.
InterPero; IPR001879; III_HBGF.
ProDom; PD000811; III_HBGF.
ProDom; PD000831; III_HBGF; I.
SWART; SM00442; FGF; I.
PROSITE; PS00247; HBGF FGF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor homologous factor 4 isoform 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 LPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 LPKP-LEVAMYREPSL----HDVGETVPKPGVTPSKSTSAS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28462 MW; 305B0B9A3F56D577 CRC64;
                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 AA.
Z
252
                                                                                01-JUN-2003 (TrEMBLrel. 24, Last sequen 01-OCT-2003 (TrEMBLrel. 25, Last annota Fibroblast growth factor 14 isoform 1B. Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Splicing.";
J. Biol. Chem. 275:2589-2597(2000).
EMBL; AF199606; AAF31393.1; -.
                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
PRT;
                                                          L-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken)
      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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156 PAPR---GPARFLPL 167
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                                                                                                                                                                                                                                                                                                                                095K97
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Q9ERW3
                                                                                                                                                                                                                                    RESULT 32
Q95K97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQS---EAHGLPLH--LPGNKSPHRD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 HIBIREDGTVGGAADQSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 EACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSPHRDPAPRGPARF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 GDVRWRKLFS----FTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bagai S., Rubio B., Cheng J.F., Sweet R., Thomas R., Fuchs E., Grady R., Mitchell M., Bassuk J.A.;
Grady R., Mitchell M., Bassuk J.A.;
"Fibroblast Growth Factor-10 Is a Mitogen for Urothelial Cells.";
"Fibroblast Growth Factor J. - Cool."

EMBL; AF508782; AAM46226.1;
"O, Go.,0008083; Figrowth factor activity; IEA.
InterPro, IPR0003948; ILL_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch al Similarity 32.1%; Pred. No. 8e-06; 52; Conservative 23; Mismatches 61; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
13.5%; Score 150; DB 4; Length 170;
Best Local Similarity 30.4%; Pred. No. 6e-06;
Matches 41; Conservative 31; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 LPLPGLPPALPEPPGILAPOPPDVGSSDPLSMVGPSOGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 LPKP-LEVAMYREPSL----HDIGETVPKAGVTPSKSTSAS 237
                                                GO, GO:0008083; F:growth factor activity; IEA.
InterPro; IPR08895; Cytok ILL_like.
InterPro; IPR08896; Cytok ILL_like.
InterPro; IPR008948; ILL_HBGF.
Pfan; PR00157; PGF; I.
PRINTS; PR00262; ILLHBGF.
ProDon; P000831; ILL HBGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
SEQUENCE 253 AA; 28640 MW; 5ABFD9F9D6E74305 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 AA; 19195 MW; 4EA43515F758327A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 10 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 AA.
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PRODOM: PDO00931; ILLHBGF: 1.
SMART; SMO442; FGF; 1.
PROSITE; PSO0247; HBGF_FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 52; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Bladder;
PubMed=11923311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8NFI9
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42 GOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQS-PESILQLKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Medulla oblongata; Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                          Mácaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSNEE-Doreal root ganglion; Xiao H., Huan Z., Zhang X.; Xiao H., Huan Q., Zhang F., Guo C., Chen Z., Han Z., Zhang X.; "Rattus norvegicus fibroblast growth factor 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
13.5%; Score 150; DB 6; Length 208;
Best Local Similarity 30.4%; Pred. No. 7.8e-06;
Matches 41; Conservative 31; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              libraries.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB063051; BAB60779.1; -.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok ILL_like.
InterPro; IPR002348; ILL_HBGF.
PFam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00247; HBGF_FGF; 1.
Hypothetical protein.
SEQUENCE 208 AA; 23466 MW; 0766A787609B3661 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.1-WAR-2001 (TrEMBLrel. 16, Created)
1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 13.
                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 AA
                                                                                                                                                  208 AA
                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; IL1 HBGF; 1.
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152 OKTRRKNTSÁHFLPM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00442; FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9541;
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63 IREDGTVGGAA-DQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPRAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 IFPNGTVHGTRHDHSRFGILEFISLAVGLISİRGYDSGLYLGMNERGELYGSKKLIRE-C 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 SFRELLLEDGYNVYQSEAHGL----PLHLPGNKSPHRDPAPRGPAR-----FLPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 AIQGVQTKLYLANMSBGYLYTSEHFTPE-CKFKESIFENYYVTYSSMIYRQQQSGRGWYL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SDETGFEHSGIMVSVLAGLLLGACÇAHPIPDSSPLLOFGGOVRORYLYTDDAQOTEAHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 ADSPĠFINERL-----ĠQIEĠKLĠRGSPIDFAHL---KĠILRRRQLYC----RIGFHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%; Score 147.5; DB 11; Length 207; 32.4%; Pred. No. 1.3e-05; Indels 33; ive 19; Mismatches 75; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Itoh N.;

"Mus musculus mRNA for FGF-16 (FGF16).";

Submitted (SFP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB049219; BAB16405.1; -.

HSSP; P31371; 1G82.
                                                                                             145 HL-----PGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                  126 GINKEGEIMKGNHVKKNKPA---AHFLEKP-LKVAMYKEPSL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 AA; 23751 MW; 68BD03EBDAA1D84E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Keratinocyte growth factor 2.
                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Fibroblast growth factor 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1931627; Fgf16.
GO; GO:0008083; F:growth factor activity; IEA
InterPro; IPR008996; Cytok III_like.
InterPro; IPR002348; III_HEGF.
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ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
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61; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00167; FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=10090;
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Best Local S:
Matches 61:
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Q9ESL8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-CKFKESVFENYYVTYSSMIYRQQSGRGWYLGINKEGEIMKGNHVKKNKPA----AHF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 EACSFRELLLEDGYNVY-----QSEAHGLPLHL-----PGNKSPHRDPAPRGPARF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 HLQLQADGTIDGTKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLAMNSEGYLYTSEHFTP 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 HLEIREDGTVGGAADQ-SPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukarycia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-20112833; PubMed=10644718;
Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
Is Generated by Alternative Promoter Usage and Differential
Splicing.,
J. Blol. Chem. 275:2589-2597 (2000).
BENBL; AF199610; AAF31397.1;
HSSP; P31371; 1GB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    13.3%; Score 148.5; DB 11; Length 192; 33.8%; Pred. No. 9.7e-06; Live 17; Mismatches 52; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBirel. 15, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
Fibroblast growth factor homologous factor 2 isoform 10+1Y'
                            Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF271786; AAG15492.1; -.
HSSP; P31371; 1G82.
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199 AA; 22316 MW; FCEC93ABFCEDE22C CRC64;
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00247; HBGF FGF; 1.
SEQUENCE 192 AA; 21604 MW; 7736A3671677B263 CRC64;
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InterPro; IPR008996; Cytok_ILI_like.
InterPro; IPR002348; ILI_HBGF.
                                                                                                                   GO, GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR002348; III_HBGF.
Pfam; PF00167; FGF; 1.
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Pfam; PR00167; FGF; 1.
PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
                                                                                                                                                                                                                                                  PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || | | | : | : | : 142 LPKP-LKVAMYKEPSL 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Conservative
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PROSITE; PS00247; HBGF
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
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042407;
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Q9N1B9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 FLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQS---EAHGLPLH--LPGNKSPHRD 155
                                                                                                                                                                                                                                                                                                                                                                                                                     14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauxia; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
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A SEQUENCE FROM N.A.

A Langy Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, AF411527; AAL05875.1; -.

R GO; GO: 0008083; F:growth factor activity; IEA.

InterPro; IPR002348; IL1_HBGF.

R PRINTS; PR00247; FGF; IL1_HBGF.

R PRINTS; PR00263; IL1_HBGF.

R PRODOM; PD000831; IL1_HBGF; 1.

R SWART; SM00442; FGF; 1.

R PROSITE; PS00247; HBGF FGF; 1.

R PROSITE; PS00243; HBGF FGF; 1.
                                                                                                                                                                                                                                                                                                                                                            Query Match
13.2%; Score 147; DB 4; Length 208;
Best Local Similarity 29.6%; Pred. No. 1.5e-05;
Matches 40; Conservative 32; Mismatches 49; Indels
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Last annotation update)
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EMBL; AF540440; AA033291.1; -.

GO; GO:0008083; F:growth factor activity; IEA.

InterPro; IPR008996; Cytok ILI_like.

Pfam; PF00167; FGF: 1.
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"FHF-2 in the turkey (Meleagris gallopavo).";
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
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Best Local Similarity
Matches 45; Conserv
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42 GOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQS-PESLLQLKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Obuchi H., Nakagawa T., Yamamoto A., Araga A., Ohta T., Ishimaru Y., Yoshioka H., Kuwana T., Yohno T., Yamasaki M., Itoh N., Noji S., "The mesenchymal factor, FGF10, initiates and maintains the outgrowth of the chick limb bud through interaction with FGF8, an apical ectobermal factor.";
                                                                                                                                                                                                                                                                                                                                Fibroblast growth factor 10.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.9%; Score 144; DB 13; Length 212; 28.9%; Pred. No. 2.8e-05; tive 30; Mismatches 52; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 AA; 23631 MW; AB4C0B32C72A0D90 CRC64;
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Last annotation update)
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Last annotation update)
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InterPro; IPR008956; Cytok III. like.
InterPro; IPR002348; ILI. HBGF.
Pfam; PF00167; PGF; 1.
PRINTS; PR00262; ILI.HBGF.
PRINTS; PR000625; ILI.HBGF; 1.
SMART; SM00442; FGF; 1.
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01-0cT-2000 (TrEMBLrel. 15, Last seq
01-0cT-2003 (TrEMBLrel. 25, Last ann
Fibroblast growth factor 10.
                                                                                                                                                                                                                                                     01-JAN 1998 (TEMBLrel. 05, Created)
01-JUN-1998 (TEMBLrel. 06, Last seq
01-OCT-2003 (TEMBLrel. 25, Last ann
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MEDLINE=97330690; PubMed=9187149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Development 124:2235-2244(1997).
EMBL; D86333; BAA24945.1; -.
HSSP; P31371; 1G82.
                             156 PAPR---GPARFLPL 167
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165 LPLPGLPPALPEPPGI
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Matches 39; Conservative
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12.7%; Score 141.5; DB 5; Length 268;
Best Local Similarity 29.3%; Pred. No. 6.5e-05;
Matches 44; Conservative 23; Mismatches 50; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Ciona intestinalis.
Bukaryota, Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
                 A Chem C. Spencer T.E., Bazer F.W.;

Thirtoplast growth factor-10: A stromal mediator of epithelial function in the ovine uterus.";

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1 Similarity 31.1%; Pred. No. 3.2e-05;
42; Conservative 30; Mismatches 48; Indels 15;
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MEDLINE=22259793; PubMed=12373588;
Satou V., Imai K.S., Satoh N.;

"Fgf genes in the basal chordate Ciona intestinalis.";
Dev. Genes Evol. 212:432-438 (2002).

EMBL, AB086094; BAC22066.1; ---

EMBL, RA088098; P:growth factor activity; IEA.

InterPro; IPR008996; Cytok IL1 like.

InterPro; IRR002348; IL1 HBGF.
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MEDLINE=20411101; PubMed=10952944;
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Best Local Similarity
Matches 42; Conserv
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Q816J7
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 2, 2004, 15:51:17 ; Search time 20.0292 Seconds
 (without alignments)
 543.341 Million cell updates/sec Run on:

US-10-060-765-4 1113 1 MDSDETGFEHSGLWVSVLAG......SSDPLSMVGPSQGRSPSYAS 209

Title: Perfect score: Sequence:

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | • | Description | | O9jjni mus muscuiu | | _ | | Oggzv9 nomo saplen | BUM | mus . | pour , | | nomo sap | | _ | rattus | | | xenop | pomod. | | | рошо | | | _ | meso | mus | mus | _ | DEOR | mus m | homod | | P70492 rattus norv |
|-----------|------------|-------------|-------|--------------------|------------|------------|----------|--------------------|-------|------------|------------|------------|------------|------------|------------|----------|------------|------------|------------|------------|------------|------------|------------|------------|-------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--------------------|
| SUMMAKIES | | TD | | | FGFJ HUMAN | FGFN MOUSE | FGFN RAT | FGFN HUMAN | | FGF3 MOUSE | FGF3 HUMAN | FGF4_BOVIN | FGF6 HUMAN | FGFA_XENLA | FGF6 MOUSE | FGF5 RAT | FGF4_CHICK | FGFS MOUSE | FGFB XENLA | FGF4 HUMAN | FGFK HUMAN | FGF3 BRARE | FGFE HUMAN | FGF9 HUMAN | | FGF9 MOUSE | FGF1_MESAU | FGF1 MOUSE | FGF4 MOUSE | FGFE MOUSE | FGF5 HUMAN | FGFD MOUSE | FGFG HUMAN | FGFA HUMAN | FGFA_RAT |
| | | Length DB | 209 1 | | | | | | | | | | | | | | 194 1 | | 192 1 | 206 1 | 211 1 | 256 1 | 247 1 | 208 1 | 208 1 | 208 1 | 155 1 | | | | | 245 1 | | 208 1 | |
| | * Query | _ | 100.0 | 71.3 | 23.8 | 22.4 | | ٥. | 9.8 | | | | 5.9 | 5.6 | 5.3 | | 4.8 | 4.7 | 4.7 | 4.7 | 4.5 | 4 | 4.3 | - | ۲. | 14.1 | 0. | 13.9 | 8. | | .7 | ٠, | ι. | Ŋ | ī. |
| | | Score | 1113 | 793.5 | 265 | 249.5 | 235.5 | 222.5 | 206.5 | 179 | 177.5 | 177 | 176.5 | 174 | 170.5 | 167 | 165 | 164 | 163.5 | 163.5 | 161 | 160.5 | 159 | 157 | 157 | LO | 155.5 | u | L U | | 153 | - 41 | ď | 15 | 150 |
| | Result | No. | | 7 | m | 4 | ហ | 9 | 7 | 00 | 0 | 10 | 11 | 12 | 13 | 4. | 15 | 91 | 17 | 18 | 19 | 250 | 22 | 22 | 23 | 24 | 25 | 26 | 27 | 800 | 29 | 30 | 3 6 | 3.5 | 33 |

| 035565 mus musculu P05230 homo sapien 054769 rattus norv p36386 xenopus lae p01968 bos taurus p20002 sus scrofa 091875 xenopus lae p48801 gallus gall 092913 homo sapien 094808 ovis aries p79150 canis famil |
|---|
| FGFA MOUSE FGFI_HUMAN FGFG_TAAT FGFG_SAT FGFI_BOVIN FGFI_BOYIN FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG FGFG_TGFG |
| нанананана |
| 209 237 237 155 152 2209 2209 170 194 |
| 1133.23 1122.3 122.7 122.7 122.7 |
| 148 146.5 146.5 146.5 146.5 147.5 141.5 141.1 141.1 |
| 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 |

ALIGNMENTS

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Query Match
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XX KEDLINE-21085660; PubMed=11217851;
XX Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
XX Kawai J., Shinaqawa A., Shibata K., Yoshino H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konoo H., Adachi J., Fukuda S.,
A Arakawa T., Jawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
XX Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
XX Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
XX Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
XX Anthl P., Lewis S., Matsuo Y., Niksido I., Fesole G., Quackenbush J.,
XX Chriml L.M., Staubli F., Suzuki R., Tomita M., Magnet L., Washio T.,
XX Sakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barsh G.,
XX Sakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barsh G.,
XX Bakai K., Okido T., Fletcher C., Fujita M., Gariboldi M.,
XX Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
XX Sakai H., Salto K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
XX Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
                                                                                                                                                                        ö
                                                                                                                                                                                                                                               LEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEA 120
                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                               121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPPGI 180
                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                              1 MDSDETGFEHSGLMVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=2046177; PubMed=10858549; Nishimura T., Nakatake Y., Konishi M., Itoh N.; Itoh N.; Identification of a novel FGF, FGF-21, preferentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                         ô
                                                                                                                                              100.0%; Score 1113; DB 1; Length 209; 100.0%; Pred. No. 7.7e-75;
                                                                                     POTENTIAL.
FIBROBLAST GROWTH FACTOR-21.
RISSING (IN REF. 2).
27925C52A0023823 CRC64;
                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-21 precursor (FGF-21)
                                                                                                                                                                                                                                                                                                                                                                                                                                       210 AA
                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1492:203-206(2000).
                                                                                                                                                                                                                                                                                                                                                                 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
  Pfam; PFO0167; FGF; 1.
PRINTS; PR00262; ILIHBGF.
PYODOM; PD000831; ILI HBGF; 1.
PROSITE; PS00247; HBGF; 1.
PROSITE; PS00247; HBGF. FFF; FALSE_NEG.
Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                             23 23 M
209 AA; 22300 MW;
                                                                                                                                                                          Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                        FGFL MOUSE
Q9JJN1;
                                                                                                                                                                                                                                                                                                                                                     181
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                                                                                                             CONFLICT
                                                                                                                            SEQUENCE
                                                                                                                                                    Query Match
                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 GYNVYOSEAHGLPIHLPGNKSPHRDPAPRGPARFLPLPLPGLPPALPEPPGILAPQPPDVGS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 GAADQSPESILIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 GAAHRSPESILELKALKPGVIQILGVKASRFLCQQPDGALYGSPHFDFBACSFRELLLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLWVS-VLAGLLLGACQAHPIPDSSPLLQFGGQVRQRXIYTDDAQQTEAHLEIREDGTVG
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Nishimura T., Utsunomiya Y., Hoshikawa M., Ohuchi H., Itoh N.;
"Structure and expression of a novel human FGF, FGF-19, expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                      -i- SUBCELLUIAR LOCATION: Secreted (Potential).
-i- TISSUE SPECIFICITY: Most abundantly expressed in the liver, also expressed in the thymus at lower levels.
-i- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Fibroblast growth factor-19 precursor (FGF-19) (UNQ334/PRO533).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1, Length 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 AA; 23237 MW; AE02AABA6477E6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 793.5; DB 1
; Pred. No. 1.8e-51;
10; Mismatches 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; PD000831; IL1 HBGF; 1.
SMART; SM0442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
PROSITE; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P03968; 1BAR.
MGD; MGI:1861377; FGf21.
InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 SDPLSMVEPLOGRSPSYAS 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB025718; BAA99416.1; -. EMBL; AK007574; BAB25115.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00262; ILLHBGF
                                                                                                        Nature 409:685-690(2001)
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                                            Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          **MEDLINE=22388257; PubMed=12477932;

**MEDLINE=22388257; PubMed=12477932;

**A trausberg R.D., Celling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

**A trausberg R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

**A trausberg R.D., Grouse T., Max S.I., Wang J., Hsieh F.,

**A trausberg R.D., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A trausberg R.D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

**Broken M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

**Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

**Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

**Brownstein M.J., Usdin T.B., Poshiyuki S., Carninci P., Prange C.,

**Brownstein M.J., Usdin T.B., Poshiyuki S., Carninci P., Prange C.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hully S.J.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hully S.J.,

**A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**A Hilalon B., Ketteman M., Madan A., Rodrigues S., Sanchez A.C.,

**A Hilalon B., Katteman J.W., Green E.D., Dickson M.C.,

**Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

**Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

**A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

**T human and mouse CDNA sequences.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                embryogenesis.
--- SUBCELLIULAR LOCATION: Secreted.
--- TISSUB SPECIFICITY: Expressed only in fetal brain.
--- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                        PGR-19, a novel fibroblast growth factor with unique specificity for
                                                                                                                                                                                                                                                                                                                   MEDLINE=2288726; PubMed=12975309; MEDLINE=2288726; PubMed=12975309; MEDLINE=2288726; PubMed=12975309; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Clan J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Edhen J., Poster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wiesand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                SEQUENCE FROM N.A.
Xie M.-H., Holcomb I., Deuel B., Dowd P., Huang A., Vagts A.,
Foster J., Brush J., Gu Q., Liang J., Hillan K., Goddard A.,
Gurney A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. Ü.S.A. 99:16899-16903(2002).
-!- FUNCTION: May be involved in brain development during
                                                                                                                                                                                                                                                   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
the fetal brain.";
Biochim. Biophye. Acta 1444:148-151(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 603891; -.
GO; GO:0007399; P:neurogenesis; TAS.
InterPro; IPR008996; Cytok_IL1_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AB018122; BAA75500.1; --
EMBL, AF110400; AAD455973.1; --
EMBL, AX358302; AAD48669.1; --
EMBL, BC017664; AAH17664.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:3675; FGF19.
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                                                                                                                                                                                                                                          FGFR4.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                          128 LEDGYNVYQSEAHGLFLHLPGNKSPHRDPAPRGPARFLPLPGLPPALP----EPPGI--- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 RPDGYNVYRSEKHRLPVSLSSAKQ-RQLYKNRG---FLPLSHFLPMLPMLPWPEEPEDLRGH 182
                                                                                                                                                                                                                                                                                                                                                               68 TVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSIHFDPEACSFRELL 127
                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=20490027; PubMed=11032749;
Yamashita T., Yoshioka M., Itoh N.;
Yamashita T., Yoshioka M., Itoh N.;
"Identification of a novel fibroblast growth factor, FGF-23,
preferentially expressed in the ventrolateral thalamic nucleus of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -.- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                      11 SGLWVSVLAGLLIGACQAHPIPDSSPLLQF--GGQVRQRYLYTDDAQ-QTEAHLBIREDG
                                                                                                                                                                                                                                                                                                            14 AGLWLAV-AGRPLA----FSDAGPHVHYGWGDPIRLRHLYTGGPHGLSSCFLRIRADG
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 26:345-348(2000).
-!- SUBCELIULAR LOCATION: Secreted (Potential).
-!- TISSUE SPECIFICITY: Mainly expressed in the brain and thymus at low levels. In brain; preferentially expressed in the ventrolateral thalamic nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/C; TISSUE=Embryo; MEDLINE=20517346; PubMed=11062477; MEDLINE=20517346; PubMed=11062477; MATHIE K.E., Fvana W.E., O'Kiordan J.L.H., Speer M.C., Econs M.J., Mhite K.E., Fvana W.E., O'Kiordan J.L.H., Strom T.M.; Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.; "Autoseomal dominant hypophosphataemic rickets is associated with
                                                                                                                                                                                                           Length 216;
                                                                                                                                    POTENTIAL.
FIBROBLAST GROWTH FACTOR-19.
                                                                                                                                                                                                                                                 82; Indels
                                                                                                                                                CHAIN 23 216 FIBROBLAST GROWTH FACTOR-: SEQUENCE 216 AA; 24002 MW; EOBCBC9C220F9832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 277:494-498(2000)
                                                                                                                                                                                                               23.8%; Score 265; DB 1; 36.3%; Pred. No. 8.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-23 precursor (FGF-23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ----LAPOPPDVGSSDPLSMV-GPSQGRSPSY 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 LESDMFSSPLETDSMDPFGLVTGLEAVRSPSF 214
                                                                                                                                                                                                         Query Match
Best Local Similarity 36.3%; Pred. No. ....
Matches 77; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                  Pram; Pr00167; FGF; 1.
PRINTS; PR00262; ILHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM0442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
Growth factor; Signal.
InterPro; IPR002348; IL1_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutations in FGF23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGFN MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        brain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGF23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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FGFN HUMAN
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                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09GZV9;
                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGFN HUMAN
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFREL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 ILEDGYNVYQSEAHGLPLHLPGNK---SPHRDPAPRGPARFL-----PLPGLPPALPEP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLWVSVLAGLLLGACQ---AHPIPDSSPLL--QFGGQVRQRYLYTDDAQQTEAHLEIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 251;
                                                                                                                                                                                                                                                                                                                                                 1 24 POTENTIAL.
25 251 FIBROBLAST GROWTH FACTOR-23.
251 AA; 27757 MW; 110C1F2C735DC360 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
22.4%; Score 249.5; DB 1
Best Local Similarity 35.1%; Pred. No. 1.4e-11;
Matches 73; Conservative 27; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fibroblast growth factor-23 precursor (FGF-23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 PGILAPOPPDVGSSDPLSMVGPSQGRSP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 HTRSAEDPPE---RDPLNVLKPRPRATP 201
                                                                                                                                                                                                                           Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILLHBGF; 1.
ProDom, PD0000831; IL1 HBGF; 1.
SWART; SN00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMEL; AB078777; BAB84108.1; -.
Interpro; IPR008996; Cytok III_like.
Interpro; IPR002348; III_HBGF.
                                                                                                             PIR; UC7513; UC7513.
HSSP, P03968; IBAR.
MGD; MGI:1891427; F9f23.
InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR002348; ILI_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
                                                                       EMBL; AB037889; BAB13478.1; -. EMBL; AF263536; AAG09916.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Rattus norvegicus fgf23.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                 Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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FOFN RATH
TO FORN RATH
TO BUT 28-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 LLEDGYNVYQSBAHGLPLHLPGNK---SPHRDPAPRGPARFL-----PLPGLPPALPEP 177
                                                                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                                                                                                                         12 GLWVSVLAGLILGACQ---AHPIPDSSPLL--OFGGQVRQRYLYTDDAQQTEAHLBIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20490027; PubMed=11032749; Yamashita T., Yoshioka M., Itoh N.; Yamashita T., Yoshioka M., Itoh N.; *Identification of a novel fibroblast growth factor, FGF-23, preferentially expressed in the ventrolateral thalamic nucleus of the
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., VARIANTS ADHR GLN-176; GLN-179 AND TRP-179, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22887296; Pubmed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20517346; PubMed=11062477; White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J., White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J., Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.; Autosomal dominant hypophosphataemic rickets is associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21267444; PubMed=11344269; Shimada T., Hino R., Takeda S., Shimada T., Mizutani S., Muto T., Yoneya T., Hino R., Takedohi Y., Pujita T., Fukumoto S., Yamashita T.; "Cloning and characterization of FGF23 as a causative factor of
                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Tumor-derived
                                                                                                                                                                                                                                   Score 235.5; DB 1; Length 251; Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                        FIBROBLAST GROWTH FACTOR-23
                                                                                                                                                  CHAIN 25 251 FIBROBLAST GROWTH FACTOR-SEQUENCE 251 AA; 27911 MW; 35A229E1B3900593 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-MAR-2004 (Rel. 43, Last annotation update)
Fibroblast growth factor-23 precursor (FGF-23) (Tum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 98:6500-6505(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 277:494-498(2000).
                                                                                                                                                                                                                                                                                             86:
                                                                                                                                                                                                                        21.2%; Sco...
34.1%; Pred. No. 1...
've 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 PGILAPOPPDVGSSDPLSMVGPSQGRSP 205
                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 HTRSAEDPPE---RDPLNVLKPRPRATP
Pfam; PF00167; FGF; 1.
ProDom; PD000831; IL1_HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
Growth factor; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Genet. 26:345-348(2000).
                                                                                                                                                                                                                                                                 Best Local Similarity 34.18
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutations in FGF23."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT MET-239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGF23 OR HYPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 GGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 DGYNYYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPP------ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 NGYDVYHSPQYHFLVSL------GRAKRAFLPGMNP----PPYSQFLSRRNEI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LWVCALCSVCSMSVLRAY--PNASPLLGSSWGGLI---HLYTATARNS-YHLQIHKNGHV
                                                                                                                                                                                                                                    DISEASE: Defects in FGF23 are the cause of autosomal dominant hypophosphataemic rickets (ADHR) [MIN:193100]. ADHR is characterized by low serum phosphorus concentrations, rickets, osteomalacia, leg deformities, short stature, bone pain and dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Gaps
                                                                                                                                               "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the heparin-binding growth factors family.
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Foster J., Grinaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Vashagri S., Simmons L., Singh V., Stinson J., Vagts A., Vandlen R., Watanabe C., Waleand D., Woods K., Xie M.-H., Yansura D., Yie, Y. Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 20.0%; Score 222.5; DB 1; Length 251; Local Similarity 30.8%; Pred. No. 1.3e-09; and 68; Conservative 36; Mismatches 70; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.

FIBROBLAST GROWTH FACTOR-23.

R -> Q (in ADHR).

FILGE-WAR 010717.

R -> Q (in ADHR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6093BD0CC50C2489 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMRAT; SW00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
Growth factor; Signal; Disease mutation; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FIId=VAR_010719.
R -> W (in ADHR).
/FIId=VAR_010718.
                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Secreted (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 193100; -. Gextracellular space; NAS. GO; GO:0005615; C:extracellular space; NAS. GO; GO:0030154; P:cell differentiation; NAS. InterPro; IPR008996; Cyrck III_like. InterPro; IPR002348; ILI_HBGF.
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or send an email to license@isb-sib.ch).
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EMBL; AF263537; AAG09917.1; -.
EMBL; AB047858; BAB55889.1; -.
EMBL; AX358323; AAQ8669.1; -.
HSSP; P03968; 1ARC.
Genew; HGNC:3680; FGF23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00167; FGF; 1.
PRINTS, PR00262; ILIHBGF.
ProDom; PD000831; ILI HBGF; 1.
SMART; SMO0442; FGF; 1.
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RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., R. Kawai U., Shinagawa A., Shibata K., Yonno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Anakawa T., Hara M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Rajata T., Okazaki Y., Gojobori T., Bono H., Ksukawa T., Saito R., Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavan T., RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Rakaih P., Lewis S., Matsuo Y., Nikaido I., Magner I., Washio T., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Ramateri M. J. Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Raustoch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Roustoch S., Mill D., Hofmann M., Mazzarelli J., Mombaerts P., Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Shons P., Marchia K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Rhysaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Stableton B.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A proper M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Brapleton M.J., Usdin T.B., Tobhlyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Willialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Willialon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

A Willialon D.K., Muzny D.W., Schermen M., Madan A., Rodrigues S., Sanchez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Turchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McWhirter J.R., Goulding M., Weiner J.A., Chun J., Murre C.; "A novel fibroblast growth factor gene expressed in the developing nervous system is a downstream target of the chimeric homeodomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                       165 PLIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPAS 205
179 ---GILAPOP-----PDVGSSDPLSMVGPSQGRSPSYAS
                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibroblast growth factor-15 precursor (FGF-15)
                                                                                                                                                                                                                   218 AA
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                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oncoprotein E2A-Pbx1.";
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MEDLINE=88296404; PubMed=2841106;
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                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-86247582; PubMed-3013624;
Moore R., Casey G., Brookes S., Dixon M., Peters G., Dickson C.;
"Sequence, topography and protein coding potential of mouse int-2: a
putative oncogene activated by mouse mammary tumour virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: May play an important role in regulating cell division and patterning within specific regions of the embryonic brain, spinal cord and sensory organs.
                                                                                                            -!- TISSUE SPECIFICATY: Expressed in the developing brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1MT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
1RGF-3 (FRGF-3).
FGF3 OR FGF-3 OR INT-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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18.6%; Score 206.5; DB 1; Length 218;
Best Local Similarity 33.8%; Pred. No. 1.6e-08;
Matches 53; Conservative 29; Mismatches 70; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBROBLAST GROWTH FACTOR-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25236 MW; A96B0D771FE125A5 CRC64;
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MGD, MGI:1096383; Fgf15.
InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
PRINTS; PR00262; IL1HBGF.
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                                                                                                   SUBCELLULAR LOCATION: Secreted.
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01-NOV-1988 (Rel. 09, Last seqn
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; T.
PROSITE; PS00247; HBGF_FGF; 1.
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EMBL; AK017829; BAB30961.1; -.
EMBL; BC021328; AAH21328.1; -.
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SEQUENCE OF 1-73 FROM N.A.
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Growth factor; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 218 AA;
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FGF3 MOUSE
TO 701-NOV
DT 01-NOV
DT 28-FEB
DE INT-2
DE (FGF-3)
CO ENGRIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 GGQVRQRYLXTDDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 FLCQRPDGALYGSLHPDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 YLAMNKRGRLYASDHYNAE-CEFVERIHELGYNTYASR----LYRTGSSGPGAQRQPGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 RGP-----ARFLPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 GGAPRRKKIYC----ATKXHLQLHPSGRVNGSLENSAVSILEITAVEVGVVAIKGLFSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                     family.";
J. Cell Sci. Suppl. 13:87-96(1990).
-!- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
-!- INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
FGF3 OR INT2.
                                                                                                                                                                                   MEDLINE=91193291; PubMed=1964688; Dixon M., Deed R., McAllan D., Dickson C., Acland P., Smith R., Dixon M., Peters G.; Malther W., Fuller-Pace F., Kiefer P., Peters G.; "Characterization of int-2: a member of the fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGF3 OR INTZ.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Smith R., Peters G., Dickson C., "Multiple RNAs expressed from the int-2 gene in mouse embryonal carcinoma cell lines encode a protein with homology to fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch
1 Similarity 28.8%; Pred. No. 1.9e-06;
51; Conservative 30; Mismatches 78; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INT-2 PROTO-ONCOGENE PROTEIN.
N-LINKED (GLCNAC. .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 AA; 27214 MW; 70D94FD6A7837C79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y00848; CAA68767.1; -. PIR; A23930; TVMST2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                            EMBO J. 7:1013-1022(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245
65
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is n no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 FLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAP-- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 YLAMNKRGRLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGAR---RQPSAER 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 GGAPRRKLYC----ATKYHLQLHPSGRVNGSLENSAYSILEITAVBVGIVAIRGLFSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Gaps
                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 -----RGPAR------FLP------DGLPPALPEPPG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 IMYVSVNGKGRPRRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPG 203
                                                                                                                                                              MEDLINE-89239468; PubMed-2470007;
Brooks S., Smith R., Casey G., Dickson C., Peters G.;
Sequence organization of the human int-2 gene and its expression
teracocarcinoma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERINTS; PRODO262; LLLIHBGF.
PRODOM; PRO00831; ILLIHBGF; 1.
SMART; SMO442; FGF; 1.
PROSITE: PS00247; HBGF FGF; 1.
PROSITE: PS00247; Growth factor; Mitogen; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.9%; Score 177.5; DB 1; Length 2
29.7%; Pred. No. 2.4e-06;
tive 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INT-2 PROTO-ONCOGENE PROTEIN.
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 164950; -
GO; GO: 0005576; C: extracellular; TAS.
GO; GO: 0005763; F: growth factor activity; TAS.
GO; GO: 0007267; P: cell-cell signaling; TAS.
GO; GO: 0007345; P: embryogenesis and morphogenesis; TAS.
GO; GO: 0007185; P: histogenesis and organogenesis; TAS.
GO; GO: 00007165; P: signal transduction; TAS.
InterPro; IPR008996; Cytok ILL like.
InterPro; IPR02248; ILL HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bb bb N-LINKED (GLCKAC. . .) (PK 239 AA; 26886 MW; 8DBEF17D2B2E3C63 CRC64;
                                                                                                                                                                                                                                                                                                     Oncogene 4:429-436(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X14445; CAA32615.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P31371; 1G82.
HGNC:3681; FGF3.
                                                                                                                                                                                                                                                                              teratocarcinoma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S04742; S04742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                SEQUENCE FROM N.A.
                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
FGF4 BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew;
                          SOLUTION SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 VGGAADQSPESLLOLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAGSFRELLL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 WVSVLAGILLGACQAHPIPDSSPLLQFGGQV-----RQRYLYTDDAQQTEAHLEIREDGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 WESLVARSLIAGLPVAAQPKEAAVQSGAGDYLLGIKRLKRLYCNVG--IGFHLQVLPDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
MEDLINE=91360279; PubMed=1886714;
COULIET F., Batoz M., Marics I., de Lapeyriere O., Birnbaum D.;
Coulier F., Batoz M., Marics I., de Lapeyriere O., Birnbaum D.;
"Putative structure of the FGF6 gene product and role of the signal "Putative".
                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Gaps
                                                                                                                                                                                                                                                                                             An unexpected transforming gene in calf-thymus carrier DNA: bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo argiens (Human).
Homo bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
MCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fibroblast growth factor-6 precursor (FGF-6) (HBGF-6) (HST-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 206;
                                                                                                                                                                                                        MEDLINE=96032369; PubMed=7557455;
Yu J.C., Deseabra A.J., Wang L.M., Fleming T.P., Chedid M.,
Miki T., Heidaran M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 206 FIBROBLAST GROWTH FACTOR-4.
206 AA; 22041 MW; F9B7A86066E56613 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 EDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.9%; Score 177; DB 1; 32.1%; Pred. No. 2.2e-06; iive 23; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00247; HBGF FGF; 1.
Proto-oncogene; Growth factor; Mitogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR0089996; Cytok IL1_like.
InterPro; IPR002348; IL1_HBGF.
Pfam: PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0262; IL1HBGF.
ProDom; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U15969; AAA91622.1; -.
HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 32.1%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   Gene 162:333-334(1995).
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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82 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLEISTVERGVVSLFGVRSALFV 139
                                                103 CQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                       | || : | | || : || 10 amnskgrlyatpsfQ-eeckfretllpnnynayesdly 176
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                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00167; FGF; 1.
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                                                                                                                                                                                                       FGFA XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                         MEDIINE=89201880; PubMed=2649847;
Marics I., Adelaide J., Raybaud F., Mattei M.-G., Coulier F.,
Planche J., de Lapeyriere O., Birnbaum D.;
"Characterization of the HST-related FGF.6 gene, a new member of the
fibroblast growth factor gene family.";
Oncogene 4:335-340(1989).
                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CAN TRANSFORM NIH 3T3 CELLS. EXHIBITS STRONG MITOGENIC AND ANGIOGENIC PROPERTIES.
                                            SECURNCE OF 11-208 FROM N.A.
MEDLINE=92195660; PubMed=1549352;
MIda S., Yoshida T., Nalto K., Sakamoto H., Katoh O., Hirohashi S.,
Sudimura T., Terada M.;
"Human hst-2 (FGF-6) oncogene: cDNA cloning and characterization.";
Oncogene 7:303-309(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
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N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LWVSVLAGLLLGACQAHP-----IPDS---SPLLQ-----FGGQV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00247; HBGF_FGF; 1.
Proto-oncogene; Growth factor; Mitogen; Angiogenesis; Signal; Glycoprotein.

1 37 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%; Score 176.5; DB 1; Length 208; 29.1%; Pred. No. 2.4e-06; ative 27; Mismatches 52; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Leukemia cell lines with platelet/
megakaryocytic differentiation potential.
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208 FIBROBLAST GROWTH FACTOR-6
45 N-LINKED (GLCNAC. . .) (PO
157 POTENTIAL.
100 V -> G (IN REF. 3).
22904 MW; 79EF44685B324322 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 134921; -
GO; GO:0005576; C:extracellular; TAS.
GO; GO:0008083; F:growth factor activity; TAS.
GO; GO:0008283; F:cell proliferation; TAS.
GO; GO:0007267; F:cell-cell signaling; TAS.
GO; GO:0007165; P:cell-cell signaling; TAS.
InterPro; IPR002996; Cytok ILI_like.
InterPro; IPR002348; ILI_HEGF.
FFam; FFOOL67; FGF; I.
FFANTS; FRO0265; ILIHEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (or send an email to license@isb-sib.ch)
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EMBL; X57075; CAA40359.1; ALT_INIT.
EMBL; X63454; CAA40360.1; ALT_INIT.
EMBL; X63454; CAA45054.1; -.
EMBL; X14071; CAB37648.2; -.
EMBL; X14072; CAB37648.2; JOINED.
EMBL; X14073; CAB37648.2; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD000831; IL1 HBGF; 1.
SM00442; FGF; 1.
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SEOUENCE OF 81-208 FROM N.A.
             Oncogene 6:1437-1444(1991).
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38 20
45 ,
90 1:
100 1:
208 AA;
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HSSP; P09038; 1BFG.
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MIM; 13.
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             SOLUTION DE LA PRESENTATION DE L
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor 4-I precursor (FGF-4-I) (HBGF-4-I) (Embryonic fibroblast growth factor I) (XEFGF-I).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92115916; PubMed=1618138;
Isaacs H.V., Tannahill D., Slack J.M.W.;
Isaacs H.V., Tannahill D., Slack J.M.W.;
Isaacs H.V., Tannahill D., Slack J.M.W.;
"Expression of a novel FGF in the Xenopus embryo. A new candidate inducting factor for mesoderm formation and anteroposterior specification.";
Development 114:711-720(1992).
-!- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STACE AND IN THE FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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CHAIN 23 187 FIBROBLAST GROWTH FACTOR-4-I.
SEQUENCE 187 AA; 21223 MW; AARG3D65E82AD1BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Indels
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InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR002348; IL1_HBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0262; ILLHBGF.
PRODON; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; I.
PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Signal.
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102 LCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: CAN TRANSFORM NIH 3T3 CELLS. EXHIBITS STRONG MITOGENIC PUNCTION: CAN TRANSFORM NIH 3T3 CELLS. EXHIBITS STRONG MITOGENIC PROPERTIES (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Embryos, adult muscles and adult testis.
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                          MEDLINE=90295275; PubMed=2193291;
MEDLINE=90295275; PubMed=2193291;
de Lapeyriere O., Rosnet O., Benharroch D., Raybaud F.,
de Lapeyriere O., Rosnet O., Banharroch D., Raybaud F.,
denkins N.-Goulier F., Birnbaum D.;
                                                                                                                                                                                                                                                                                                                                                          "Structure, chromosome mapping and expression of the murine Fgf-6
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                         Ollendorf V., Rosnet O., Marics I., Birnbaum D., Delapeyriere O., "Isolation and sequence of the murine Fgf6 cDNA.";
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N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch
1 Similarity 36.4%; Pred. No. 6.7e-06;
36; Conservative 21; Mismatches 39; Indels 3;
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Proto-oncogene; Growth factor; Mitogen; Anglogenesis; Signal;
                                                                       01-MAY-1991 (Rel. 18, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fibroblast growth factor-6 precursor (FGF-6) (HBGF-6) (HST-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 37 POTENTIAL.
38 208 FIBROBLAST GROWTH FACTOR-6
45 F. N-LINKED (GLCNAC. . .) (PC
90 157 POTENTIAL.
208 AA; 22798 MW; BBF7B9301BB79A1B CRC64;
                                                208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M2415; AAA62260.1; ---
EMBL; M2416; AAA62261.1; ---
EMBL; S14192; CAA35925.1; ---
FIR; S14192; S14192.
HSSP; P09038; 1BFG.
MGD; MG195520; F9f6.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR008998; IL1 HBGF.
                                                                                                                                                                                                                       TISSUE=Embryo;
MEDLINE=93120244; PubMed=1477139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0262; ILLHBGF.
PROD001; PRO00831; ILL HBGF; 1.
SMART; SMO0442; FGF; 1.
                                                                                                                                                                                                                                                                     Biochimie 74:1035-1038(1992).
                                                                                                                                                                                                                                                                                                SEQUENCE OF 11-208 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        Oncogene 5:823-831(1990)
                                                   STANDARD;
                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein.
                                                                                                                              FGF6 OR FGF-6.
                                                 FGF6 MOUSE P21658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                            RESULT 13
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42 GQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRF 101

Matches

δ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ASPGSQGSGSEHSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEASVLSILEIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 SSPLLQFGGQVRQRYLYTDDAQQTEA-----HLEIREDGTVGGAADQSPESLLQLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEAM; PF00167; FGF; 1.
PRINTS; PR00262; ILIHBGF.
PRODOM; PD000831; ILI HBGF; 1.
SMART; SM0047; HBGF T.
PROSTITS; PS00247; HBGF FGF; 1.
PROSTITS; PS00247; HBGF RGF; 1.
Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Short; Synonyms=FGF-58; Isold=PA8807-2; Sequence=VSP_001522, VSP_001523; Isold=PA8807-2; Sequence=VSP_001522, VSP_001523; -:- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hattori Y., Yamasaki M., Itoh N.; "The rat FGF-5 mRNA variant generated by alternative splicing encodes "The rat FGF-5 mRNA variant generated by alternative splicing
                                                                                                                                                                                                                                                                                                                           Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
LINKED (GLCNAC. .) (POTENTIAL)
ILEI -> QIYR (in isoform Short).
/FIId=VSP_001522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.0%; Score 167; DB 1; Length 266; 30.3%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (In isoform Short). /FTIG=VSP_001523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBROBLAST GROWTH FACTOR-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95B0A0CA7C0A200C CRC64;
                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Mismatches
                                                                                                                                         266 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Long;
IsoId=P48807-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a novel truncated form of FGF-5.";
Biochim, Biophys. Acta 1306:31-33(1996)
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D64085; BAA10966.1; -.
EMBL; D64086; BAA10967.1; -.
PTR; S68144; S68144.
PTR; S68145; S68145.
HSSP; P09038; 1BFG.
InterPro; IPR008996; Cytok_IL1_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Wistar;
MEDLINE=96201703; PubMed=8611621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 AA; 29264 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
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                    97 KTSRFLCQRPDGALYGSLHFDPBACSFRELLLEDGYNVYQSBAH-GLPLHLPGN---KSP 152
                                                                                       120 RSGLFVAMNSKGKLYGSTHVNDE-CKFKEILLDNNYNAYESRIYPGMYIALSKNGRTKKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECURNCE FROM N.A. (ISOFORM LONG).
MEDLINE=90201563; PubMed=2318343;
Hebert J.M., Basilitoc C., Goldfarb M., Haub O., Martin G.R.;
Habert J.M., Basilitoc C., Goldfarb M., Haub O., Martin G.R.;
"Isolation of cDNAs encoding four mouse FGF family members and characterization of their expression patterns during embryogenesis.";
Dev. Biol. 138:454-463 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Short; Synonyms=FGF-58;
IsoId=P15656-2; Sequence=VSP_001520, VSP_001521;
SIMILARITY: Belongs to the heparin-binding growth factors family.
LIQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99003286; PubMed=9786939; Ozawa K., Suruki S., Asada M., Tomooka Y., Li A.J., Yoneda A., Romi A., Imamura T.; Apaliced fibroblast growth factor (FGF)-5 mRNA is abundant in brain and translates into a partial agonist/antagonist
                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene in the
                                                                                                                                                                                                                                                            FIGES MOUSE STANDARD; PRT; 264 AA. PIGES MOUSE STANDARD; PRT; 264 AA. PIGES OB MOUSE. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haub O., Drucker B., Goldfarb M.;
"Expression of the murine fibroblast growth factor 5 adult central nervous system.";
proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Long;
IsoId=P15656-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGF-5 neurotrophic activity.";
J. Biol. Chem. 273:29262-29271(1998).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6;
MEDLINE=91045929; PubMed=1700424;
                                                                                                                                             153 HRDPAPRGPARFLP 166
                                                                                                                                                                                  179 NKVSPTMTVTHFLP 192
                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M37821; AAB020
EMBL; AB016516; BAA:
PIR; A36207; A36207
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
       37
                                        65
                                                                                                                                                                                                                                        RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DSSP 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AALLPALLIGLIWPGAVRGRPPPGRLPPGPRORRWDAALFARSVARLPAERRDAARDGDY 64
                          ALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH---- 140
                                                                                              141 -GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLP-----PALPEPP 178
                                                                                                                                182 IGREMYVALNK---RGKAKRGCSPRVKPQHVSTHFLPRFKQSEQPELSFTVTVPEKKKPP 238
                                                       Nature 371:609-612 (1994).

-I- FUNCTION: MAY BE THE ENDOGENOUS RIDGE SIGNAL FOR LIMB DEVELOPMENT.

-I- FUNCTION: MAY BE THE ENDOGENOUS RIDGE SIGNAL FOR LIMB DEVELOPMENT.

BETWEEN SONIC HEDGEHOG (SHH) AND FGF4.

-I- TISSUE SPECIFICITY: POSTERIOR RIDGE.

-I- INDUCTION: By retinoic acid.

-I- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95021713; PubMed-7935794;
Niswander L., Jeffrey S., Martin G.R., Tickle C.;
"A positive feedback loop coordinates growth and patterning in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.8%; Score 165; DB 1; Length 194; 27.3%; Pred. No. 1.6e-05; tive 29; Mismatches 68; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
FIBROBLAST GROWTH FACTOR-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 AA; 21642 MW; 5D44245BE97E664A CRC64;
                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-4 precursor (FGF-4) (HBGF-4).
                                                                                                                                                                                                                                                                                                   194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 SGLWVSVLAGLLL-GACQAHPIP------
                                                                                                                                                                                               ---RPWKPKV----PLS---PSR-RSPS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRSP; S78500; 100.

HRSP; P09038; IBFF.

InterPro; IPR002948; ILI_HBGF.

Ffam; PF00167; FGF; I.I.

PRINTS; PR00262; ILIHBGF.

PRINTS; PR002631; ILIHBGF; I.

PRODOM; P0000831; ILI_HBGF; I.
                                                                                                                                                                         179 GILAPQPPDVGSSDPLSMVGPSQGRSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SMOO442; FGF; I.
PROSITE; PSO0247; HBGF FGF; 1.
Growth factor; Mitogen; Signal SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U14654; AAA58706.1; -. PIR; S78506; I50710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53; Conservative
                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                           gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vertebrate limb.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=9031;
                                                                                                                                                                                                                                                                                                     FGF4 CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                    P48804;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                 ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF-FGF; 1.
Growth factor; Mitogen; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGF4 OR HST OR HSTF1 OR KS3.
                                                EMBL; X62594; CAA44480.1; -. PIR; S54407; S54407.
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                    PRINTS; PR00262; ILIHBGF.
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                    Query Match
Best Local Simil
Matches 36; C
                                                                                                                                                                                                                                                                                                                                                                                                                          FGF4 HUMAN
P08620;
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rotein
                                                                                                                                                                                                                                                                                                                                                                                                                FGF4_HUMAN
                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
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                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                     85 ALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFREILLEDGYNVYQSEAH---- 140
                                                                                                                                                                                                                                                                                                                                                                    141 -GLPLHLPGNKSPHRDPAPRG------PARFLP-----LPGLPPALPEPPGILAP 183
                                                                                                                                                                                                                                                                                                                                                                                                                           182 TGREWYVALNK---RGKAKRGCSPRVKPQHVSTHFLPRFKQSEQPELSFTVTVPEKKKPP 238
                                                                                                                                                                                                                                                                                                                     63 ASPGSQGSGSEHSSFQWSPSGRRTGSLXCRVQIGFHLQIYPDGKVNGSHEASVLSILEIF 122
                                                                                                                                                                                                                                                                                                    34 SSPILQFGGQVRQRYLYIDDAQQTEA-----HLEIREDGTVGGAADQSPESILQLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Development 114:711-720(1992).

-i- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted (Probable).
                     MGD; MGI:95519; Fgf5.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR00248; IL1 HBGF.
InterPro; IR00248; IL1 HBGF.
INTER: PR00262; IL1HBGF.
ProDom; PD000831; IL1 HBGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92315916; PubMed=1618138;
Isaacs H.V., Tannahill D., Slack J.M.W.;
"Expression of a novel FGF in the Xenopus embryo. A new candidate inducing factor for mesoderm formation and anteroposterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-4-II precursor (FGF-4-II) (HBGF-4-II)
Fibroblast growth factor I) (XEFGF-II).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Amphibia: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                         POLY-SER.
LINKED (GLCNAC. .) (POTENTIAL)
ILEI -> QIYG (in isoform Short).
/FTId=VSP_001520.
                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                    Length 264;
                                                                                                                                                                                                                                                                               78; Indels
                                                                                                                                                                                                    122 264 Missing (in isoform Short).
/FIId-VSP_001521.
264 AA; 29103 MW; F6A9C8153EE923D1 CRC64;
                                                                                                                                           FIBROBLAST GROWTH FACTOR-5.
                                                                                                                                                                                                                                                       14.7%; Score 164; DB 1;
28.6%; Pred. No. 2.6e-05;
tive 25; Mismatches 78,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 QPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 VKPKVPLSQP-----RRSPS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                     58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                         59
108
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                         Similarity
               HSSP; P09038; 1BFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                18
53
108
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGFB_XENLA
                                                                                                                                                             DOMAIN
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P48806;
                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 17
FGFB_XENLA
                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth factor that is a member of the FGF family."; cell 50:729-737(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: CAN TRANSFORM NIH 3T3 CELLS PROM A HUMAN STOMACH TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transforming protein) (HST-1) (HST) (Transforming protein KS3) (HBGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA sequence of human transforming gene hst and identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOTEL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-88041096; PubMed=2959959;
Yoshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.R.,
Terada M., Sugimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN----KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Heparin secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delli Bovi P., Curatola A.M., Kern F.G., Greco A., Ittmann M.,
Basilico C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic sequence of hst, a transforming gene encoding a protonomologous to fibroblast growth factors and the int-2-encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 192;
                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
FIBROBLAST GROWTH FACTOR-4-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-87204251; Pubwed=2953031;
Taira M., Yoshida T., Miyagawa K., Sakamoto H., Terada M.,
Sugimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the coding sequence required for transforming activity.";
proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           23 192 FIBROBLAST GROWTH FACTOR-
192 AA; 21903 MW; 2B01B0BBB824E3B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roc. Natl. Acad. Sci. U.S.A. 84:7305-7309(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.7%; Score 163.5; DB
ilarity 32.4%; Pred. No. 2e-05;
Conservative 26; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibroblast growth factor-4 precursor (FGF-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 AA
                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                          HSSP, P31371; 1682.
InterPro; IPR008996; Cytok ILL like.
InterPro; IPR002348; ILL HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=87301716; Pubmed=2957062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 IQILGYKTSRFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 PGAAQLAHLHGILRRRQLYC----RTGFHLQILPDGSVQGTRQDHSLFGILEFISVAVGL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 VSİRGVDSGLYLGMNDKGELYGSEKLTSE-CIPREQFEENWYNTYSSNIYKHGDTGRRYF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
             -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 AA; 23498 MW; AB04608C16060CC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FFB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 LPGNKSPHRDPAPRGPAR-----FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 VALNK----DGTPRDGARSKRHQKFTHFLPRPVDPERVPE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%; Score 161; DB 1; ilarity 33.1%; Pred. No. 3.4e-05; Conservative 19; Mismatches 64
SUBCELLULAR LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 AA.
                                                                                                                                                                                                                                                                                                                                          MIM, 605588; -
G0; 60:0005576; C:extracellular; TAS.
G0; G0:0005625; C:soluble fraction; TAS.
G0; G0:0007267; P:cell-cell signaling; TAS.
G0; G0:0007165; P:signal transduction; TAS.
InterPro; IPR008996; Cytok ILL like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                             EMBL; AB044277; BAB03530.1; -. EMBL; AB030648; BAB03530.1; -. PIR; JC7353; JC7353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS00247; HBGF_FGF; 1.
Growth factor.
SEQUENCE 211 AA; 23498 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                     HSSP; P31371; 1G82.
Genew; HGNC:3677; FGF20.
MIM; 605558; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00167; FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGF3 OR FGF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGF3 BRARE
P48802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGF3_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   심
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 HLEIREDGTVGGAADQSPESILLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] — SEQUENCE FROM N.A. MEDLINE=20374469; PubMed=10913340; MEDLINE=20374469; PubMed=10913340; Kirikoshi H., Sagara N., Saitoh T., Tanaka K., Sekihara H., Shiokawa K., Katoh M.; "Molecular cloning and characterization of human FGF-20 on chromosome
                                              -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                         GO: 00:005576; C:extracellular; TAS.
GO: 00:0005576; C:extracellular; TAS.
GO: GO:0000838; F:growth factor activity; TAS.
GO; GO:0000284; P:cell-cell signaling; TAS.
GO; GO:00008284; P:positive regulation of cell proliferation; TAS.
GO; GO:0001165; P:signal transduction; TAS.
InterPro; IPR002996; Cytok IL1 like.
InterPro; IPR002948; IL1 HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HST) AND FROM KARPOSI'S SARCOMA (KS3). IT HAS A MITOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.7%; Score 163.5; DB 1; Length 206; 36.9%; Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00247; HBGF FGF; 1.
PROSIDE; PS00247; HBGF FGF; 1.
PROSIDE; PS00247; HBGF FGF; 1.
PROSIDE; SIGNAL; 3D-structure.
STGNAT.
1 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Itch N.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
FIBROBLAST GROWTH FACTOR-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 AA; 22047 MW; C7FD54A0272A1569 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 274:337-343(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
Fibroblast growth factor-20 (FGF-20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PD000831; IL1 HBGF; 1.
SM00442; FGF; 1.
                                                                                                                                                                                                                                                                 EMBL; JO2986; AAB59555.1; -.
EMBL; MI7446; AAA59473.1; -.
PIR; A28417; TVHUUHS.
PDB; IIJT; 15-AUG-01.
Genew; HGNC:3682; FGF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00262; ILLHBGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8p21.3-p22
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SEQUENCE Query Match Local

Matches

RESULT 19

à

ProDom;

SMART;

9

Gaps

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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQ-SPESLLQLKALKPGVIQILGVKTS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chumakov I., Blumenfeld M., Guerassimenko O., Cavarec L., Palicio M., Abderrahim H., Bougueleret L., Barry C., Tanaka H., La Rosa P., Puech A., Tahri N., Cohen-Akenine A., Delabrosse S., Lissarrague S., Picard F.-P., Maurice K., Essioux L., Millasseau P., Grel P., Debailleul V., Simon A.-M., Caterina D., Dufaure I., Malekzadeh K., Balova M., Luan J.-J., Bouillot M., Sambucy J.-L., Primas G., Saumier M., Boubkiri N., Martin-Saumier S., Nasroune M., Peixoto H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smallwood P.M., Munoz-Sanjuan I., Tong P., Macke J.P., Hendry S.H., Glibert D.J., Copeland N.G., Jenkins N.A., Nathans J.; "Fibroblast growth factor (FGF) homologous factors: new members of the FGF family implicated in nervous system development."; Proc. Natl. Acad. Sci. U.S.A. 93:9850-9857(1996).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fibroblast growth factor-14 (FGF-14) (Fibroblast growth factor homologous factor 4) (FHF-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.1%; Pred. No. 4.5e-05;
Matches 47; Conservative 22; Mismatches 47; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 GPARFLPLAGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 RYLAMNEKGRLYASEVFNRE-CEFLERIHELGYNTYASRHHA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. FIBROBLAST GROWTH FACTOR-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEBAIC72A170BBDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 AA
                                                                                                                                                                                                                                      EMBL, Z48714, CAA88596.1; -.
PIR, JC4627, JC4627.
HSSP, P09038, LBFG.
ZFIN, ZDB-GENE-980526-178, Fgf3.
InterPro, IPR008996; Cytok IL1_like.
InterPro, IPR002348; IL1_HBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28923 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILLHBGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256
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256 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=9606;
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ID FGFE HUMAN
AC Q92915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 VIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKKTKPA----AHFLPKP-LEVAMYREP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
Delaye A., Pinchot V., Bastucci M., Guillou S., Chevillon M., Sainz-Fueres R., Meguenni S., Aurich-Costa J., Chevillo., Gimalac A., Van Duijn C., Gauvreau D., Ouelette G., Fortier I., Realson J., Sherbatich T., Riazanskay N., Rogew E., Baeymaekers P., Aerssens J., Konings F., Luyten W., Macciardi F., Sham P.C., Straub R.E., Weinberger D.R., Cohen N., Cohen D.; Fortier I., Sham B.C., Straub R.E., Heinberger D.R., Cohen N., Cohen D.; Fenck D. Proc. Natl. Acad. Sci. U.S.A. 99:13675-13680(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 GLCNGNLVDIFSKVRIFG--LKKRRLRRQDPQLKGIVTRLYCRQGYYLQMHPDGALDGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 DOSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 DDSTNSTLENLIPVGERVVAIQGVKTGLYIAMNGBGYLYPSBLFTPE-CKFKESVFENYY
                                                                                                                                                                                                                          -i- TISSUE SPECIFICITY: Nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1994 (Rel. 30, Last sequence update)
10-OCT-1994 (Rel. 42, Last amotation update)
Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
FGF-9) (HBGF-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 AA; 27702 MW; 427C3373198B967E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 159; DB 1;
llarity 29.8%; Pred. No. 5.6e-05;
Conservative 27; Mismatches 81;
                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0008083; F:growth factor activity; TV
GO; GO:0007257; P:cell-cell signaling; TAS.
GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 GILAPOPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 SL----HDVGETVPKPGVTPSKSTSAS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR008996; Cytok_IL1_like.
Interpro; IPR002348; IL1_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00262; ILIHBGF.
ProDom; PD000831; ILI HBGF; 1.
SMART; SM00442; FGF; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:3671; FGF14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00167; FGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P31371; 1G82
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P31371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOCRAPHY (2.60 ANGSTROMS).

MEDLINE=21127675; PubMed=11223514;

MEDLINE=21127675; PubMed=11223514;

Hecht H.J., Adar R., Hofmann B., Bogin O., Weich H., Yayon A.;

Hecht H.J., Adar R., Hofmann B., Bogin O., Weich H., Yayon A.;

Hoth Crystallogr. D. 100 and heparin-binding interfaces.";

Acta Crystallogr. D. 57:378-384(2001).

-! FUNCTION: May have a role in glial cell growth and differentiation of during development, gliosis during repair and regeneration of brain tissue after damage, differentiation and survival of neuronal cells, and growth stimulation of glial tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FTM: N-glycosylated.
-!- DISEASE: The continuous overexpression of GAFS may lead to malignant cell growth caused by an autocrine loop.
--- SIMILARITY: Belongs to the heparin-binding growth factors family.
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
-!- DATABASE: NAME-R&D Systems' cytokine source book: FGF9;
--- WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=199".
                                                                                                                                                                                                             "Molecular cloning of a novel cytokine cDNA encoding the ninth member of the fibroblast growth factor family, which has a unique secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCNIT: Monomer.
-i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Glial cells.
-i- PTM: Three molecular species were found (30 kDa, 29 kDa and 25
-i- PTM: Three molecular species were found (30 kDa, 29 kDa and 25
kDa), cleaved at Leu-4, Val-13 and Ser-34 respectively. The smaller ones might be products of proteolytic digestion.
Furthermore, there may be a functional signal sequence in the 30 kDa species which is uncleavable in the secretion step.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Novel secretory heparin-binding factors from human glioma cells (glia-activating factors) involved in glial cell growth.

Purification and biological properties.";
J. Biol. Chem. 268:2857-2864(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                        IISSUB=Glial tumor;
MEDLINE=93155105; PubMed=8428960;
Naruo K.-I., Seko C., Kuroshima K.-I., Matsutani E., Saвada R.,
Kondo T., Kurokawa T.;
                                                                                                                                                                     Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 600921; -. Gextracellular space; TAS. GO:0008615; C:extracellular space; TAS. GO:0008083; F:growth factor activity; TAS. GO:0007267; P:cell-cell signaling; TAS. GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                       Mol. Cell. Biol. 13:4251-4259(1993).
                                                                                                                                    TISSUE=Foreskin;
MEDLINE=93309459; PubMed=8321227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AL13978, CAC17692.1, -.
PIR, A48137, A48137.
PDB, 1G82, 00-MAR-01.
PDB, 11HK, 02-MAY-01.
Genew, HGNC:3687, FGF9.
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 4-26 AND 34-54.
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                      Kurokawa T.;
                                                                                                                                                                                                                                                                       property.
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63 IREDGTVGGA-ADOSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SDETGREHSGLWVSVLAGILLGACQAHPIPDSSPILLOFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 SDHLGQSEAG-----GLPRG------PAVTDLDHLKGILRRRQLYC----RTGFHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Gaps
R InterPro; IPR008996; Cytok III. like.

R pfam; PF00167; FGF; 1.

R PRINTS; PR00262; ILLHBGF.

R PRINTS; PR00262; ILLHBGF.

R PROSTE; PS00247; HBGF; 1.

R PROSTE; PS00247; HBGF; 1.

R Growth factor; Differentiation; Mitogen; Heparin-binding; Glycoprotein; 3D-structure.

T CHAIN 4 208 GLIA-ACTIVATING FACTOR.

T CHAIN 79 79 N-LINNED (GLCNAC...).

CARBOHYD 79 79 N-LINNED (GLCNAC...).

T CONFLICT 24 26 VLP -> SLL (IN REF. 2).

T CONFLICT 54 61

F HELLX 54 61

STRAND 65 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.1%; Score 157; DB 1; Length 208; 31.2%; Pred. No. 6:5e-05; Live 20; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23440 MW; F32A0E7106EF59C9 CRC64;
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01-OCT-1994 (Rel. 30, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 PGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 PVDPDKVPE 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                    FGF9 RAT P36364;
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ID FGF9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 IREDGIVGGA-ADOSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 İFPNGİLIQĞIRKDHSRFGILEFISIAVĞLVSİRĞVDSGLYLGMNEKĞELYĞSEKLTQE-C 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 SFRELLLEDGYNVYQSEAH----GLPLHLPGNKSPHRDPAPRGPAR-----FLPL 167
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                                                                                                                                                                         34 SPHLGOSEAG-----GLPRG-----PAVTDLDHLKGILRRRQLYC----RTGFHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                          "Molecular cloning of a novel cytokine cDNA encoding the ninth member of the fibroblast growth factor family, which has a unique secretion
                                                                                                                                                                                                                                                          - |- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                     Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
01-NOV-1997 (Rel. 35, Last annotation update)
Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
(FGF-9) (HBGF-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 3 BY SIMILARITY.
4 208 GLIA-ACTIVATING FACTOR.
79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
208 AA; 23413 MW; 4A3CE894DFF643EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
14.1%; Score 157; DB 1; Length 208;
Best Local Similarity 31.2%; Pred. No. 6.5e-05;
Matches 59; Conservative 20; Mismatches 72; Indels
                                                                                                                    Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
Kurokawa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00262; ILIHBGF.
Probom; PR00131; ILIHBGF; 1.
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Differentiation; Mitogen; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P31371; 1G82.
InterPro; IPR008996; Cytok_IL1_like.
InterPro; IPR002348; IL1_HBGF.
                                                                                                               MEDLINE=93309459; PubMed=8321227;
                                                                                                                                                                                                                                                                                                                                                                     EMBL; D14839; BAA03573.1; -.
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PVDPDKVPE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 PGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00167; FGF; 1
                                                                                              SEQUENCE FROM N.A.
                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein.
                               FGF9 OR FGF-9
                                                                                                         rissue=Brain;
                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P31371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95385801; PubMed=7656983; See M., Neguchi K.; "Retinoic acid induces gene expression of fibroblast growth factor-9 during induction of neuronal differentiation of mouse embryonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDIATE=56129259; PubMed=8619928;
MEDIATE=56129259; PubMed=8619928;
MEDIATE=56129259; PubMed=8619928;
"Identification of fibroblast growth factor 9 (FGF9) as a high affinity, heparin dependent ligand for FGF receptors 3 and 2 but not for FGF receptors 1 and 4";
Growth Factors 12:223-233(1995).
                                             01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glia activating factor precursor (GAF) (Fibroblast growth factor-9)
(FGF-9) (HBGF-9).
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        Santos-Ocampo S., Colvin J.S., Chellaiah A.T., Ornitz D.M.; Bapression and biological activity of mouse fibroblast growth
208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:104723; Fgf9.
InterPro; IPR008996; Cyrok_III_like.
InterPro; IPR002348; ILI_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF144626; AAD49222.1; --
EMBL; AF144624; AAD49222.1; JOINED.
EMBL; AF144625; AAD49222.1; JOINED.
HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 271:1726-1731(1996)
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96139512; PubMed=8576175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U33535; AAC52529.1; -. EMBL, D38258; BAA07410.1; -. EMBL, S82023; AAB36429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EBS Lett. 370:231-235(1995)
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carcinoma P19 cells."
                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                               FGF9 OR FGF-9.
     PGF9 MOUSE
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48;
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Matches
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                                                                                                                                                                              23 IGACQAHPIPDS---SPLLQFGGOVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPE 78
                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=9020291; PubMed=1693366; Mansson P.E., Zhou H., Harris S.E.; Hall U.A., Harris M.A., Malark M., Mansson P.E., Zhou H., Harris S.E.; Hall U.A., Harris M.A., Malark M., Mansson P.E., Zhou H., Harris S.E.; Hall U.A., Harris M.A., Malark M., Mansson P.E., Zhou H., Harris S.E.; J. Cell. Biochem. 43:17-26(1990).

-! FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Monomer.
-!- MISCELLANEOUS: This protein binds heparin, although less strongly than does bFGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILACED MEST.
PIRI, A60721; A60721.
HISSP: P05209, IRML.
HISSP: P05209, IRML.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR002348; III_HEGF.
PRINTS; PR00252; IIIHEGF.
PRINTS; PR00262; IIIHEGF.
PRODOM; PR000831, III_HEGF.
PRODOM; PR000831, III_HEGF.
                                                                                                                                                                                                             37 IGOSEAGGLPRGPAVTDLDHLKGILRRRQLYC----RIGFHLEIFPNGTIQGTRKDHSRF
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                       139 AH-----GLPLHLPGNKSPHRDPAPRGPAR------FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                        27;
                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 155.5; DB 1; Length 155; Pred. No. 6.1e-05;
                                                                                                                    ch 14.1%; Score 156.5; DB 1; Length 208; I Similarity 32.0%; Pred. No. 7.1e-05; 55; Conservative 21; Mismatches 69; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEPARIN-BINDING GROWTH FACTOR
    PROSITE; PS00247; HBGF_FGF; 1.
Growth factor; Differentiation; Mitogen; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41E5EC760E412CC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Anglogenesis; Heparin-binding.
                                               BY SIMILARITY.
GLIA-ACTIVATING FACTOR.
N-LINKED (GLCNAC. . .) (PC.
; E8DE1EEDFB70979E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEPARIN (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                155 AA.
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                                                                                            208 AA; 23440 MW;
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155
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116
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208
79
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                                                                                                                          Query Match
Best Local Similarity
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                                     Glycoprotein
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CARBOHYD
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                                                                                            SEQUENCE
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Query Match Best Local Similarity

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                                                                                                               100 RFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPR 159
                                                                                                                                                      78 OYLAMDIDGLLYGS-QIPNEECLFLERLEENHYNIYISKKHAEKNWFVGLKK--NGSCKR 134
                                   41 GGQVRQRYLIYIDDAQQTBAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGVKTS 99
                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of the 1B promoter of fibroblast growth factor 1 and its expression in the adult and developing mouse brain.";
J. Biol. Chem. 271:30263-30271(1996)
-!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90201563; PubMed=2318343;
Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;
"Isolation of cDNAs encoding four mouse FGF family members and
characterization of their expression patterns during embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                            21 GNYKKPKLLYCSNGGH---FLRILPDGTVDGTRDRSDQHIQLQLSAESAGEVYIKGTETG
                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (ARGF).
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   martus "Otyvejitus" (Nordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Wuridae; Murinae; Mus
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89240051, PubMed=2470029;
Goodrich S., Yan G.C., Bahrenburg K., Mansson P.E.;
"The nucleotide sequence of rat heparin binding growth factor 1
  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97094746; PubMed=8939980;
Alam K.Y., Frostholm A., Hackshaw K.V., Evans J.E., Rotter A.,
Chiu I.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJNE-97128312; PubMed-8972905;
Madiai F., Hackshaw K.V., Chiu I.M.;
"Cloning and characterization of the mouse Fgf-1 gene.";
    62; Indels
                                                                                                                                                                                                                                                                                                                                             155 AA.
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mucleic Acids Res. 17:2867-2867(1989).
                                                                                                                                                                                                                                                                                                                                             PRT;
      12;
                                                                                                                                                                                                    160 GPAR-----FLPLP 168
                                                                                                                                                                                                                                           135 GPRTHYGOKAILFLPLP 151
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    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factor) (AFGF).
FGF1 OR FGF-1 OR FGFA.
Mus musculus (Mouse), and
                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 179:231-236(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=Mouse;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 KTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 IQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 LPLGNYKKPKLLYCSNGGH---FLRILPDGTVDGTRDRSDQHIQLQLSAESAGEVYLKGT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE-90201563; PubMed=2318343;
Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;
Hebert J.M., Constantion of Constantion of Constantion of Constantion of their expression patterns during embryogenesis.",
Cerracterization of their expression patterns during embryogenesis.",
Dev. Biol. 138:454-463(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The mouse homologue of hst/k-FGF: sequence, genome organization and location relative to int-2."; Nucleic Acids Res. 17:4037-4045(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pil403; Pi5657;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1989 (Rel. 11, Last sequence update)
Fibroblast growth factor-4 precursor (FGF-4) (K-fibroblast growth factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 155;
                                                                                                                                                                                                                                                                                                                                                                            HEPARIN-BINDING GROWTH FACTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity 34.3%; Score 154.5; DB 1; Length 1 Similarity 34.3%; Pred. No. 7.2e-05; 18; Conservative 13; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                             HEPARIN (POTENTIAL).
HEPARIN (POTENTIAL).
9 8880E4FF0FBA4161 CRC64;
                                                                                                                                                                                                                                                                                                            SMART; SW00442; FGF; I.
PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Angiogenesis; Heparin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 AA
                                                                      EMBL; X14232; CAA32448.1; --
EMBL; M30641; AAA37618.1; --
EMBL; M30645; AAC52969.1; --
EMBL; U36459; AAC52969.1; --
EMBL; U36457; AAC52969.1; JOINED.
EMBL; U36458; AAC52969.1; JOINED.
EMBL; U367610; AAC52907.1; --
PIR, D37360; D37360.
PIR; S04147; S04147.
HSSP; P05230; IRML.
MGD; MG195515; PGf1.
InterPro; IPR008996; Cytok_III_like.
InterPro; IPR008998; ILI_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89296455; PubMed=2740210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 APRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 CKRGPRTHYGQKAILFLPLP 151
                                                                                                                                                                                                                                                                                                ProDom; PD000831; IL1 HBGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               17418 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                             Pfam; PF00167; FGF; 1. PRINTS; PR00262; ILIHBGF.
                                                                                                                                                                                                                                                                                                                                                                                  155
28
116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                  113 1
155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dickson C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGF4 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S:
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 HIBIREDGTVGGAADQSPESILLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 HLQVLPDGRIGGVHADTRDSLLELSPVQRGVVSIFGVASRFFVAMSSRGKLFGVPFFTDE 150
FUNCTION: IS ESSENTIAL FOR SURVIVAL OF THE POSTIMPLANTATION MOUSE EMBRYO AND AT LATER EMBRYONIC STAGES, IS AN ESSENTIAL COMPONENT OF SIGNALLING NETWORK REQUIRED FOR GROWTH AND PATTERNING OF THE
                                                                       TISSUE SPECIFICITY: EXPRESSED IN THE BLASTOCYST INNER CELL MASS AND LATER IN DISTINCT EMBRYONIC TISSUES. SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-96382556; PubMed=8790420; Smallwood P.M., Munoz-Sanjuan I., Tong P., Macke J.P., Smallwood P.M., Munoz-Sanjuan I., Tong P., Jenkins N.A., Nathans J.; Hendry S.H., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.; Frinchlast growth factor (FGF) homologous factors: new members of the FGF family implicated in nervous system development."; proc. Natl. Acad. Sci. U.S.A. 93:9850-9857(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGFE_MOUSE STANDARD; PRT; 247 AA.
P10379; Q90HLB;
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-3003 (Rel. 42, Last annotation update)
Pibroblast growth factor-14 (FGF-14) (Fibroblast growth factor homologous factor 4) (FHF-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
FIBROBLAST GROWTH FACTOR-4.
A -> S (IN REF. 2).
; 62D456231047CA31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:95518; Fgf4.
GO; GO:0042475; P:odontogenesis (sensu Vertebrata); IDA.
                                                                                                                                                                                                                                                                                                                                                                                                 uni ociovatario; riculanto generali interpro; IPR008996; Cytok ILL like.
Interpro; IPR002484; ILL HBGF.
Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILLHBGF.
Probom; PD000811; ILLHBGF; 1.
SMART; SM0442; FGF; 1.
PR05ITE; PS00247; HBGF FGF; 1.
PR05ITE; PS00247; HBGF FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.8%; Score 153.5; DB 1
34.2%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21902 MW;
                                                                                                                                                                                                                                                                                             EMBL; X14849; CAA32967.1; -. EMBL; M30642; AAA37619.1; -. PIR; S04741; TVMSHS. HSSP; P09038; 1BFG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 34.2% hes 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 1
202 AA;
                                                                  DEVELOPING LIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGF14 OR FHF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 28
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SEQUENCE FROM N.A.

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activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 E-CKFKESVFENYYVIYSSMLYRQDESGRAWFLGLNKEGQVMKGNRVKKTKPA---AHF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 HLEIREDGTVGGAADQSPES-LLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 BACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSPHRDPAPRGPARF 164
                                                                                                                                    Isodd=P70379-1; Sequence=Displayed;
Name=2; Synonyms=FGF-14C;
Isold=P70379-2; Sequence=VSP 001530;
Isold=P70379-2; Sequence=VSP 001530;
--- TISSUE SPECIFICITY: Brain and Testis; widely distributed in the developing nervous system. In adult, high levels in the granular layer of the cerebellum, less in hippocampus and olfactory bulb.
--- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Gaps
            Yamamoto S., Mikami T., Konishi M., Itoh N.; "Stage-specific expression of a novel isoform of mouse FGF-14 (FRF-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                 Biochim, Biophys. Acta 1490:121-124(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-077-1989 (Rel. 12, Created)
16-007-2001 (Rel. 40, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5) (Smag-82)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.7%; Score 153; DB 1; Length 247; 32.7%; Pred. No. 0.00015; tive 21; Mismatches 62; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 LPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 247 AA; 27764 MW; 372C6FC0BDC72FDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missing (in isoform 2). /FTId=VSP_001530.
                                                                                     -!- SUBCELLUTAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00247; HBGF_FGF; 1.
Growth factor; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                HSSP, P31371; 1G82.
MGD; MGIL09189; F8f14.
InferPro; IPR006996; Cycok LLL_like.
InterPro; IPR002348; ILL_HBGF.
      MEDLINE=20246297; PubMed=10786625;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS, PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                       EMBL; AB029498; BAA89483.1; -.
                                                                                                                                                                                                                                                                                                                                          EMBL; U66204; AAB18920.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                        in spermatocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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P12034; 075846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
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1D FGF5 H

AC P1-0CT4

DT 16-0CT4

DT 16-0CT

DE FIbrob

GN FGF5.

OC Bukmarly

OC Mammarly

OX NCBI_T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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MEDLINE=20379035; PubMed=10823842;

MEDLINE=20379035; PubMed=10823842;

MEDLINE=20379035; PubMed=10823842;

de Vries C.J.W., van Achterberg T.A.E., Horrevoets A.J.G.,

ten Cate J.W., Pannekoek H.;

"Differential display identification of 40 genes with altered
expression in activated human smooth muscle cells. Local expression
in atherosclerotic lesions of smags, smooth muscle
activation-specific genes.";
J. Biol. Chem. 275:23399-23947(2000).

--- FUNCTION: THIS ONCGENE IS EXPRESSED IN NEONATAL BRAIN. FGF-5 CAN
TRANSFORM NIH 313 CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Short; Synonyms=FGF-58; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Sequence=VSP_001518, VSP_001519; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2; Isold=P12034-2
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Imamura T.;
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                                                                                                                                                                                                                 Haub O., Drucker B., Goldfarb M.;
"Expression of the murine fibroblast growth factor 5 gene in the adult central nervous system.";
Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "An alternatively-spliced FGF-5 mRNA is abundant in brain and
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SEQUENCE FROM N.A. (ISOFORM LONG).
Zhan X., Bates B., Hu X., Goldfarb M.;
Than X., Bates B., Hu X., Goldfarb M.;
"The human FGF-5 oncogene encodes a novel protein related to
"The buman FGF-8 oncogene.";
"Introblage growth factors.";
Mol. Cell. Biol. 8:3487-3495(1988).
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EMBL; M23536; AAB60699.1; ---
EMBL; M23534; AAB60699.1; JOINED.
EMBL; M23535; AAB60699.1; JOINED.
EMBL; M23534; AAB60698.1; ALT_SEQ.
EMBL; AR31517; BAA33738.1; ---
EMBL; AR171928; AAR89742.1; ---
PIR; A31194; TVHUES.
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[1] SEQUENCE FROM N.A. (ISOFORM LONG).
TISSUE=Brain stem;
MEDLINE=91045929; PubMed=1700424;
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ProDom; PD000831; ILL HBGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                      141 ----GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLPPALPEPPG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 RIEKTGREWYVALNK---RGKAKRGCSPRVKPQHISTHFLPRFKQSEQPELSFTVTVPEK 236
                                                                                                                                                                                                                                                                                                      34 SSPLLQFGGQ----VRQRYLYTDDAQQTEA-----HLBIREDGTVGGAADQSPBSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- TISSUE SPECIFICITY: Brain, eye and heart; in embryonic brain, present in all divisions of the central and peripheral nervous system and it is at least 5 times more abundant than other FHFB.
                                                                                                                                                                                                                                                                            Gaps
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smallwood P.M., Munoz-Sanjuan I., Tong P., Macke J.P., Hendry S.H., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.; "Fibroblast growth factor (FGF) homologous factors: new members of the FGF family implicated in nervous system development."; Proc. Natl. Acad. Sci. U.S.A. 93:9850-9857(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldfarb M.;
"Murine FGF-12 and FGF-13: expression in embryonic nervous system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              connective tissue and heart.";
Mech. Dev. 64:31-39(1997).
-!- FUNCTION: Probably involved in nervous system development and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                     POLY-SER.
POLY-SER.
N-LINKED (GLCNAC. . .) (POTENTIAL).
VLEI -> QVHR (in isoform Short).
/FIId=VSP 001519.
Missing (in isoform Short).
/FIId=VSP_001519.
                                                                                                                                                                                                                                                                            40;
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P70377; 035338;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUJ-1999 (Rel. 38, Last annotation update)
Fibroblast growth factor-13 (FGF-13) (Fibroblast growth factor-10 (FHF-2).
                                                                                                                                                                                                                                           13.7%; Score 153; DB 1; Length 268; 28.1%; Pred. No. 0.00017; Live 27; Mismatches 74; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hartung H., Feldman B., Lovec H., Coulier F., Birnbaum D.,
                                                        FIBROBLAST GROWTH FACTOR-5
                                                                                                                                                                                                                  08F4268B26781E9D CRC64;
                                                                                                                                                                                R -> I (IN REF. 1).
PSGR -> LGA (IN REF. 2)
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TISSUE-EYe;
MEDLINE-96382556; PubMed-8790420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | : | | | | 237 KNPPSP--IKSKIPLS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 ILAPOPPDVGSSDPLS 195
                                                                                                                                                                                                                     29526 MW;
                                                                                                                                                                                                                                                                Similarity 28.13 S5; Conservative
                                                                                                       110
                                                                                                                                                       268
                                                           268
52
62
                                                                                                                                                                                                                     268 AA;
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                                                           18
49
55
110
120
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83
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                                                                                                                                                                                      CONFLICT
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Best Local
                                                                                                            CARBOHYD
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                                              SIGNAL
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 SSMIYRQQSGRGWYLGLNKEGEIMKGNHVKKNKRÄA----ÄHFLPKP-LKVAMYKEPSL 209
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Biochem. Biophys. Res. Commun. 243:148-152(1998).
I-FUNCTION: Induces heparcocallular proliferation. Has no biological effect on the heart (By similarity).
I-SUBCELIULAR LOCATION: Secreted (By similarity).
SINILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 ACQAHPIPDSSPLLQFGGQVRQRY-----LYTDDAQQTEAHLEIREDGTVGGAADQ-
In adult, most abundant in hippocampus. SIMILARITY: Belongs to the heparin-binding growth factors family.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 13.7%; Score 152.5; DB 1; Length 245; 1 Similarity 29.6%; Pred. No. 0.00017; 53; Conservative 25; Mismatches 72; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 MISSING (IN REF. 2).
199 L -> Q (IN REF. 2).
27617 NW; 5B96D41C190975DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-16 (FGF-16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 AA
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MGD; MG1:109178; F8f13.

InterPro; IPR008996; Cytok III_like.

InterPro; IPR0012348; III_HBGF.

Pfam; FF00167; FGF, I.

PRINTS; PR00162; ILIHBGF.

Probom; PD000831; ILI_HBGF; I.

PROSITE; PS00247; HBGF; I.

Growth factor.
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MEDLINE=98139883; PubMed=9473496;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF020737; AAB71606.1; -.
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                                                                                                                                                                                                                                                                                                                                                               EMBL; U66202; AAB18918.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 AA;
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Rattus norvegicus (Rat).
   [2]
SEQUENCE FROM N.A.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 SFRELLLEDGYNVYQSEAHGLPLHLPGNK----SPHRDPAPRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 IREDGTYGGAA-DQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 IFPNGTVHGTRHDHSRFGILEFISLAVGLISIRGVDSGLYLGMNERGELYGSKKLTRE-C 133
                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                             28 ADSPGFLNERL-----GQIEGKLQRGSPTDFAHL---KGILRRRQLYC----RTGFHLE 74
                                                                                                                                                                                                                                                                                                                                                                                                                       3 SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                                                                                                                                      13.5%; Score 150.5; DB 1; Length 207; 32.6%; Pred. No. 0.00019; Indels 31; Gaps ative 20; Mismatches 75; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibroblast growth factor-10 precursor (FGF-10) (Keratinocyte growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Itoh N.;
"Structure and expression of human fibroblast growth factor-10.";
J. Biol. Chem. 272:23191-23194(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emoto H., Tagashira S., Mattei M.-G., Yamasaki M., Hashimoto G.,
Katsumata T., Negoro T., Nakatsuka M., Birnbaum D., Coulier F.,
                                                                                                                                                                                                                                                                                                                                 CARBOHYD 78 78 N-LINKED (GLCNAC. ..) (POTENTIAL.) SEQUENCE 207 Aa; 23759 MW; D8AD160BDABDB5F8 CRC64;
                                                                                                                                         Oct. 000005615; C:extracellular space; TAS.

GO; GO:0008083; F:growth factor activity; TAS.

GO; GO:0007267; P:cell-cell signaling; TAS.

GO; GO:0007397; P:intergenesis and organogenesis; TAS.

GO; GO:0008152; P:metabolism; TAS.

GO; GO:000266; P:response to temperature; TAS.

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR008996; Cytok III_like.

InterPro; IPR002348; III_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 AA
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                                                                                                                                                                                                                                                                      PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                              EMBL; AB009391; BAA24956.1; -. PIR; JCS941; JC5941.
HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                              PROSITE; PS00247; HBGF_FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                    Genew; HGNC:3672; FGF16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 GLPPALP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 VDPSKLP 197
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                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                            Pfam; PF00167; FGF;
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                                                                                                                                                                                                                                                                                                                           Growth factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 FLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQS---EAHGLPLH--LPGNKSPHRD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%; Score 150; DB 1; Length 208;
30.4%; Pred. No. 0.00021;
tive 31; Mismatches 49; Indels 14; Gaps
                                                                                                                                                                                                                                                          -!-SUBCELLULAR LOCATION: Secreted (Potential).
-!-SUBCELLULAR LOCATION: Secreted (Potential).
-!-SIMILARITY: Belongs to the heparin-binding growth factors family.
Jumente P.A., Gruber J.R., Liu B., Feng P., Florence C., Blunt A., Huddleston K.A., Teliska M., Alfonso P., Coleman T.A., Ornitz D.M., Dilon P.A., Duan R.D., Subilton P.A., Duan R.D., Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WO SIMILAR TO FGF-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SEK.
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; JB002097; BAA22331.1; -.
EMBL; U67919; AAB61991.1; -.
PDB; JNNO; 04-MAR-03.
Genew; HGNC:3666; FGF10.
MIM; 602115; --66; FGF10.
MIM; 602015615; C:extracellular space; TAS.
GO; GO:000804; P:growth factor activity; TAS.
GO; GO:0000074; P:regulation of cell cycle; TAS.
GO; GO:0000074; P:regulation of cell cycle; TAS.
InterPro; IRR002348; ILI_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBROBLAST GROWTH FACTOR-10. POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 208 FIBROBLAST GROWTH FACTOR-1
52 62 POLY-SER.
51 51 N-LINKED (GLCNAC. . .) (PC
196 196 N-LINKED (GLCNAC. . .) (PC
208 AA; 23436 MW; COA0705C108680B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILIHBGF.
PRODOM; PD000831; ILI HBGF; 1.
PROSTITS; SR00442; FGF; 1.
PROSTITS; PS00247; HBGF FGF; 1.
Growth factor; Glycoprotein; Signal; 3D-structure.
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15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-10 precursor (FGF-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 PAPR---GPARFLPL 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 41; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                               MOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-10 precursor (FGF-10) (Keratinocyte growth
                                                                                     MEDLINE=96279129; PubMed=8663172;
MEDLINE=96279129; All Anyake A., Tagashira S., Itoh N.;
"Structure and expression of the rat mRNA encoding a novel member of the fibroblast growth factor family.";
J. Biol. Chem. 271:15918-15921(1996).
- PINGTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUNI HEALING. ACTS AS A MITGESN IN THE LUNG. MAY ACT IN A MANNER
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.5%; Score 150; DB 1; Length 21: 30.4%; Pred. No. 0.00022; tive 31; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
FIBROBLAST GROWTH FACTOR-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (P. 93778EFA6FC0866A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR002348; ILI_HBGF.
Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILIHBGF.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS00247; HBGF FGF; 1.
Growth factor; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 PC
50 N.
203 N.
24029 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 OKTRRKNTSAHFLPM 211
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D79215; BAA11468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
50
203
215 AA;
                                                                                                                                                                                              SIMILAR TO FGF-7
                                                                  FROM N.A.
                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P31371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGFA MOUSE
035565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 GOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQS-PESLLQLKALKPGVIQILGVKTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 GDVRWRRLFS----FIKXFLTIEKNGKVSGTRNEDCPYSVLEITSVEIGVVAVKAINSNY
                                                                                                                                                                                           TISSUE=Lung;
Duan D.R., Plorence C.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUND
-!- FUNCTION: ACTS AS A MITOGEN IN THE LUNG. MAY ACT IN A MANNER
SIMILAR TO FGF-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%; Score 148; DB 1; Length 209;
30.4%; Pred. No. 0.0003;
tive 30; Mismatches 50; Indels 14; Gaps
                                                                                                                                                                                                                                                                                     -!- SUBCELLIULAR LOCATION: Secreted (Potential).
-!- TISSUB SPECIFICITY: Expressed abundantly in embryos and the lung, and at much lower levels in brain and heart.
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
Mammalia, Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                              Tagashira S., Harada H., Katsumata T., Itoh N., Nakatsuka M.; "Cloning of mouse FGF10 and up-regulation of its gene expression during wound healing."; Gene 197:399-404(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-SER.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
, 7FD22227BF4943CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIBROBLAST GROWTH FACTOR-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1099809; Fgf10.
MGD; MGI:1099809; Fgf10.
GO; GO:0001099; P:induction of an organ; IMP.
GO; GO:0009887; P:organogenesis; IMP.
InterPro; IPR008996; Cytok_IL1_like.
InterPro; IPR008996; II1_HBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO0247; HBGF_FGF; 1.
Growth factor; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                         MEDLINE=97473538; PubMed=9332392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 209 FII
52 63 POI
50 50 N-1
197 197 N-1
209 AA; 23597 MW;
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P05230; P07502;
13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00262; ILIHBGF.
ProDom; PD000831; ILI HBGF; 1.
SMART; SM00442; FGF; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 PAPR---GPARFLPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D89080; BAA22836.1; -. EMBL; U94517; AAD00761.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                             SEQUENCE FROM N.A.
                       NCBI_TaxID=10090;
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SEQUENCE
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MEDLINE=22388257; PubMed=12477932; Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Straubberg R.L., Feingold E.A., Grouse L.H., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Estapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., Mozkan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Bosak S.A., Mozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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growth factor) (AFGF) (Beta-endothelial cell growth factor) (ECGF-
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Mergia Z., Abraham J.A., Shipley G.D., Fiddes J.C.;
"Structural analysis of the gene for human acidic fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain stem;
MEDLINE=90265618; PubMed=1693186;
MEDLINE=90265618; PubMed=1693186;
Malternative splicing generates two forms of mRNA coding for human heparin-binding growth factor 1.";
Oncogene 5:755-762(1990).
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"An acidic fibroblast growth factor protein generated by alternate
                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92202857; Pubmed=1372643;
Li Y.L., Kha H., Golden J.A., Migchielsen A.A.J., Goetzl E.J.,
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J. Exp. Med. 175:1073-1080(1992).
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=86261805; PubMed=3523756;
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain stem;
MEDLINE-89343957; PubMed=2474753;
                                                                                                                                Homo sapiens (Human).
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                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                         FGF1 OR FGFA.
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SECUENCE OF 16-49.
MEDLINE=86275260; PubMed=3732516;
Gautschl P., Farter-Schroeder M., Boehlen P.;
Gautschl P., Farter-Schroeder M., Boehlen P.;
"Partial molecular characterization of endothelial cell mitogens from human brain: acidic and basic fibroblast growth factors.";
FEBS Lett. 204:203-207(1986).
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Harper J.W., Strydom D.J., Lobb R.R.;
"Human class 1 hepain-binding growth factor: structure and homology
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Theo X.M., Yooh T.K., Hiebert M., Frist W.H. (Heparin-binding growth factor (heparin-binding growth factor-1) and cytokine genes in human cardiac allografts and
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MEDLINE=86186784; PubMed=3964259;
Gimenez-Gallego G., Conn G., Hatcher V.B., Thomas K.A.;
Gimenez-Gallego G., Conn G., Hatcher V.B., Thomas K.A.;
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amino terminal sequences and specific mitogenic activities.";
Biochem. Biophys. Res. Commun. 135:541-548(1986).
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WEDDINES-94358885; PubMed=7521397;
Pineda-Lucena A., Jimenez M.A., Nieto J.L., Santoro J., Rico M., Ginenez-callego G.;
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MEDLINE=86295741; PubMed=3527167;
Gimenez-Gallego G., Conn G., Hatcher V.B., Thomas K.A.;
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Gautschi-Sova P., Mueller T., Boehlen P.;
"Amino acid sequence of human acidic fibroblast
Biochem. Biophys. Res. Commun. 140:874-880 (1986)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transplantation 56:1177-1182(1993).
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MEDLINE=90365758; PubMed=2393407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 RFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLFLHLPGNKSPHRDPAPR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 OYLAMDTÜĞLLİYĞS-QTPNEECLFLERLEBNHYNTYISKKHAEKUWFVGLKK--NGSCKR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGVKTS 99
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                                                                                                            -1- SUBUNIT: Monomer.
-1- MISCELLANEOUS: This protein binds heparin, although less strongly than does DFGF.
                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
MEDLINE=97107535; PubMed=8950275;
Pineda-Lucena A., Jimenez M.A., Lozano R.M., Nieto J.L., Santoro J.,
Rico M., Gimenez-Gallego G.;
                              "Three-dimensional structure of acidic fibroblast growth factor in solution: effects of binding to a heparin functional analog."; J. Mol. Biol. 264:162-178 [1996].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.2%; Score 146.5; DB 1
Best Local Similarity 34.3%; Pred. No. 0.00028;
Matches 47; Conservative 12; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMEL; M30490; AAA52446.1; JOINED.
EMEL; M30491; AAA52446.1; JOINED.
EMEL; M60516; AAA51672.1; --
EMEL; M60516; AAA51672.1; --
EMEL; M60516; AAA52638.1; --
EMEL; M23087; AAA52638.1; --
EMEL; M23087; AAA52638.1; --
EMEL; M23087; AAA52638.1; --
EMEL; S67291; AAB29057.2; --
EMEL; S6778; CAA46661.1; --
EMEL; X65778; CAA46661.1; --
EMEL; X65778; CAA46661.1; --
EMEL; A33665; A33665.
PDB; ZAKM; 22-APR-98.
PDB; ZAKM; 22-APR-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M13361; AAA79245.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 SFRELLLEDGYNVYQSEAHGLPLHLPGNK----SPHRDPAPRGPAR------FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 IREDGTYGGAA-DQSPESLLQLKALKPGYLQILGYKTSRFLCQRPDGALYGSLHPDPEAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 İFPNGİVHĞTRHDHSKRGILBFISLAVĞLISİRĞVDSGLYLGMNBRĞELFĞSKKLTRE-C 133
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                                                                                                                                                                                                                                       28 ADSPGFINERL-----GQIEGKLQRGSFIDFAHL---KGIIRRRQLYC----RTGFHLE
                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUB=Heart;
MEDLINE=98139883; PubMa=1473496;
MiDALE=98139883; PubMa=173496;
Miyake A., Konishi M., Martin F.H., Hernday N.A., Ozaki K.,
Yamamoto S., Mikami T., Arakawa T., Itoh N.;
"Structure and expression of a novel member, FGF-16, on the fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                                                                                                                                                                                   greatly after birth.
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 78 N-LINKED (GLCNAC. . .) (POTENTIAL)
207 Aa; 23753 MW; 1C7A11C8BA3164BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
13.2%; Score 146.5; DB 1; Length 207;
Best Local Similarity 32.1%; Pred. No. 0.00038;
Matches 60; Conservative 21; Mismatches 75; Indels 31.
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-16 (FGF-16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AB002561; BAA24947.1; -.
PIR; JC5940; JC5940.
HSSP, P31371; 1G82.
InterPro; IPR008996; Cytok III_like.
InterPro; IPR002348; III_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00247; HBGF_FGF; 1.
                                                                             Rattus norvegicus (Rat)
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                                                                                                                          NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Growth factor
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207 AA.

STANDARD;

FGFG RAT ID FGFG RAT AC O54769;

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NCBI_TaxID=9913;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no festrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GGAPRNRKLYC----ATKYHLQIHLNGKINGTLEKNSVFSILEITAVDVGIVAIKGLFSG 113
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                                                                                                                                                                                                                                                                    Tannahill D., Isaacs H.V., Close M.J., Peters G., Slack J.M.W.;
"Developmental expression of the Xenopus int-2 (FGF-3) gene:
activation by mesodermal and neural induction.";
Development 115:65-702(1992).
-i. FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT.
-i. SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                  Xenopus laevis (African clawed frog).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3) (INT-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.1%; Score 146; DB 1; Length 237; 35.6%; Pred. No. 0.00048; tive 19; Mismatches 40; Indel8
                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=94038898; PubMed=8223431;
Kiefer P., Mathieu M., Close J.M., Peters G., Dickson C.;
"FGF3 from Xenopus laevis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIBROBLAST GROWTH FACTOR-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 RFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 83 N-LINKED (GLCNAC. . .).
237 AA; 26984 MW; EDD31B0893567A2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Signal; Glycoprotein.
                          237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                             PRT;
                                                                                                                                                                                                                                                            MEDLINE=93048831; PubMed=1425349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00262; IIIHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z25539; CAA80987.1; -. EMBL; X65237; CAA46341.1; -. PIR; S39582; S39582. HSSP; P31371; 1G82.
                                                                                                                                                                                                                                         SEQUENCE OF 39-137 FROM N.A.
                                                                                                                                                                                                                    EMBO J. 12:4159-4168(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237
                             STANDARD;
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                                                                                                                                                     NCBI_TaxID=8355;
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                              FGF3 XENLA P36386;
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          RESULT 37
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STANDARD;

FGF1 BOVIN ID FGF1 BOVIN AC P03968;

RESULT 38

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Sharma H.S., Schaper W.;
"Isolation of heparin-binding growth factors from bovine, porcine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halley C., Courtois Y., Laurent M.; "Nucleotide sequence of bovine acidic fibroblast growth factor CDNA."; Nucleic Acids Res. 16:10913-10913 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2-155.

SEQUENCE OF 2-155.

BURGESS W.H., Mehlman T., Marehak D.R., Fraser B.A., Maciag T.;

Burgess W.H., Mehlman T., Marehak D.R., Fraser B.A., Maciag T.;

Structural evidence that endothelial cell growth factor beta is the precursor of both endothelial cell growth factor alpha and acidic fibroblast growth factor.";

Proc. Natl. Acad. Sci. U.S.A. 83:7216-7220(1986).
23-OCT-1986 (Rel. 02, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
48-perin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (Argustarropin) (Endothelial cell growth factor beta and alpha.chains) (Acidic eye-derived growth factor II) (EDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86070224; PubMed=4071057; Mios-Candelore M., MEDLINE=8607024; Rodkey J., Bennett C., Rios-Candelore M., Disalvo J., Thomas K.; Incorplast growth factor: complete amino acid "Brain-derived acidic fibroblast growth factor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laurent M.;
its
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Crabb J.W., Armes L.G., Carr S.A., Johnson C.M., Roberts G.D.,
Bordoli R.S., McKeeban W.L.;
"Complete primary structure of prostatropin, a prostate epithelial
cell growth factor.";
                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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MEDLINE=86261806; PubMed=3425435;
Abraham J.A., Mergia A., Whang J.L., Tumolo A., Friedman J.,
Hjerrild K.A., Gospodarowicz D., Fiddes J.C.;
"Nucleotide sequence of a bovine clone encoding the angiogenic protein, basic fibroblast growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89231704; PubMed-2714282;
Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethe N.,
Sharma H.S., Schaper W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Depugner of 2750; PubMed=4065099; MEDLINE=6655750; PubMed=4065099; Bochlen P., Esch F., Baird A., Gospodarowicz D.; Machide fibroblast growth factor (FGF) from bovine brain: amino-terminal sequence and comparison with basic FGF."; EMBO J. 4:1951-1956(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alterio J., Halley C., Brou C., Soussi T., Courtois Y., "Characterization of a bovine acidic FGF cDNA clone and expression in brain and retina."; FEBS Lett. 242:41-46(1988).
                                                                                                                                                                                                                                                            FGF1 OR FGF-1 OR FGFA OR HBGF-1 OR AFGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 16-44, AND COMPOSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Retina;
MEDLINE=89078619; PubMed=2849564;
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Science 230:1385-1388(1985).
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TISSUE=Retina;
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                                                                                                SUBUNIT: Monomer.
MISCELLANEOUS: This protein binds heparin, although less strongly
                                                                                                                                                              than does bFGF. SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00442; FGF; Ī.
PROSITE; PS00247; HBGF_FGF; 1.
Growth factor; Mitogen; Anglogenesis; Heparin-binding; Acetylation;
                                                     MEDLINE=91095983; PubMed=1702556;
Zhu X., Komiya H., Chirino A., Faham S., Fox G.M., Arakawa T.,
Thu B.T., Rees D.C.;
"Three-dimensional structures of acidic and basic fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                       ENDOTHELIAL CELL GROWTH FACTOR BETA. HEPARIN-BINDING GROWTH FACTOR 1. ENDOTHELIAL CELL GROWTH FACTOR ALPHA. ACETYLATION.
                        SEQUENCE OF 1-18 FROM N.A. Philippe J.M., Renaud F., Desset S., Laurent M.; Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         HEPARIN (POTENTIAL)
                                                                                                                                                                                                                                                EMBL; M13439; AAA30516.1; --
EMBL; X13221; CAA31610.1; --
EMBL; X14032; CAA31512.1; --
EMBL; M35608; AAA30517.1; --
EMBL; M6646; CAA47063.1; --
EMBL; M97661; AAA30564.1; --
EMBL; M97661; AAA30564.1; --
PIR; JH0613; GKBOA.
PDB; 1BAR; 31-OCT-93.
PDB; 1BARC; 31-OCT-93.
INTERPRO; IPR008996; Cytok III like.
InterPro; IPR008996; Cytok III like.
   canine hearts.";
Eur. J. Biochem. 181:67-73(1989)
                                                                                                                                                                                                                                                                                                                                              PEAM; PF00167; FGF; 1.
PRINTS; PR00262; ILLHBGF.
PRODOM; PD000831; ILL HBGF; 1.
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Eur. J. Blochem. 181:67-73(1989).

-!- FUNCTION: The heparin-binding growth factors are angiogenic agents

-!- FUNCTION: The heparin-binding growth factors are angiogenic agents

in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.
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MEDLINE=89221704; PubMed=2714282;
Quinkler W., Maaaberg M., Bernotat-Danielowski S., Luethe N.,
Sharma H.S., Schaper W.;
Isolation of heparin-binding growth factors from bovine, porcine and canine hearts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pictors.
01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor 1 precursor (HBGF-1) (ACIDIC fibroblast growth factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 LPLGNYKKPKLLYCSNGGY---FLRILPDGTVDGTKDRSDQHIQLQLCAESIGEVYİKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92062117; PubMed=1719973; Schaper W.; Schaidt M., Sharma H.S., Schott R.J., Schaper W.; Schnidt M., Sharma H.S., Schott R.J., Schaper W.; Amplification and sequencing of mRNA encoding acidic fibroblast growth factor (aFGF) from porcine heart."; Biochem. Biophys. Res. Commun. 180:853-859(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 155;
                                                                                                                                                                                                                                                                                                                                                                               17493 MW; F636641F189F9BFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       13.0%; Score 144.5; DB 1;
35.0%; Pred. No. 0.00039;
iive 12; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 APRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 SKLGPRTHFGQKAILFLPLP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        155 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment).
FGF1 OR FGF-1
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CARBOHYD
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@leb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 QYLAMDISGILIYGS-QIPSEECLFIERLEENHYNIYISKKHAEKNWFVGLKK--NGSCKR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGVKTS
  -!- MISCELLANEOUS: This protein binds heparin, although less strongly
                                           -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
(FGF-9) (HBGF-9) (XFGF-9).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEPARIN-BINDING GROWTH FACTOR 1.
ENDOTHELIAL CELL GROWTH FACTOR ALPHA.
HEPARIN (POTENTIAL).
HEPARIN (POTENTIAL).
C -> S (IN REF. 2).
R -> Y (IN REF. 2).
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MEDLINE=97006698; PubMed=8853991;
Song J., Slack J.M.W.;
"XFGF-9: a new fibroblast growth factor from Xenopus embryos.";
Dev. Dyn. 206:427-436(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.9%; Score 143.5; DB 1; Length 152; 33.6%; Pred. No. 0.00045; tive 12; Mismatches 64; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17103 MW; AE853B0A92F9ABF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                      HSSP; P05230; ZAXM.
InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR002348; ILI_HBGF.
Pfam, PF00167; FGF; 1.
PRINTS; PR00262; ILI_HBGF.
SWART; SW00442; FGF; T.
PROSTIE; PS0247; HBGF FGF; 1.
PROSTIE; PS0247; HBGF FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 GPAR-----PLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 GPRTHYGOKAILFLPLP 151
                                                                                                                                                                                                                                                                                EMBL; X60317; CAA42869.1; -. PIR; JH0476; JH0476. PIR; S03954; S03954.
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>152
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116
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091875;
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FGF9 XENLA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@ib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 YLGMNEKGELYGSEKLIQE-CVFREQFEENWYNIYSSNIYKHADIGRRYYVALNK---D 170
                                 patterning.
SUBCELULUAR LOCATION: Secreted.
SUBCELULUAR LOCATION: Secreted.
TISSUE SPECIFICITY: Maternal transcript is found mainly in the animal hemisphere. Zygotic transcript is found around the blastopore and in the late gastrula stage, in the dorsal part. In later stages it is found along the dorsal part and head region. DEVELOPMENTAL STAGE HT MATERNAL PROTEIN IS DETECTED UP TO THE BLASTULA STAGE BUT DECLINES BY THE BRAILY GLASTRULA. ZYGOTIC EXPRESSION STARTS AT AROUND EARLY GASTRULA; THE LEVEL OF EXPRESSION REACHED AT STAGE 15 PERRSISTS DURING NEURILIA AND TAILBUD STAGES, AND IS FURTHER INCREASED DURING THE TADPOLE STAGES.
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differentiation, has no specific role in anteroposterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002348; IL1_HBGF.
InterPro; IPR002348; IL1_HBGF.
InterPro; IPR00148; IL1_HBGF.
PRIM: PR00167; FGF; 1.
ProDom; PD000831; IL1 HBGF; 1.
SWART; SW00442; FGF; 1.
Growth factor; Differentiation; Mitogen; Heparin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 3 BY SIMILARITY.
4 209 GLIA-ACTIVATING FACTOR.
80 80 N-LINKED (GLCNAC. . .) (P)
209 AA; 23662 MW; 26CBB229797FCFBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 PAPRGPAR-----FLPLPGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 GISKDGIRIKRHQKFIHFLPRÞVDPEKVPE 200
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HSSP; P31371; 1G82.
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Job time : 21.0292 secs
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                                                                 2004, 16:00:38 ; Search time 29.6083 Seconds (without alignments) 678.999 Million cell updates/sec
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1113
1 MDSDETGFEHSGLWVSVLAG......SSDPLSMVGPSQGRSPSYAS 209
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                             OM protein - protein search, using sw model
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S04147
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| 194 | 220 | 104 | 17. | 194 | 194 | 189 | 155 | 155 | 155 | 164 | | 77. | 154 | 154 | 168 | 137 | 146 | ř | |
| 12.8 | 8 6 6 | | 7.51 | 12.6 | 12.5 | 12.4 | 12.1 | 11.8 | 11. | 4 | 1 - | T • T T | 11.0 | 11.0 | 11.0 | 10.9 | 1 | 10.3 | |
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ALIGNMENTS

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JC7513

Elibroblast growth factor-23 - mouse

Ejbroblast growth factor-23 - mouse)

C;Gees: Mus musculus (house mouse)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7513

R;Yamashita, T.; Yoshioka, M.; Itoh, N.

R;Yamashita, T.; Yoshioka, M.; 494-498, 2000

A;Hitle: Identification of a novel fibroblast growth factor, FGF-23, preferentially expr.

A;Reference number: JC7513; WUID:20490027; PMID:11032749
                                                                                                                                                                              A;Contents: Embryo
A;Accession: UC7513
A;Accession: UC7513
A;Accession: UC7513
A;Accession: UC7513
A;Coss-references: DDBJ:AB037889
A;Cross-references: DDBJ:AB037889
C;Comment: This factor, a secreted protein, acts on proximal cells and plays roles in th A;Gene: fgf-23
C;Keywords: nucleus
                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 LLEDGYNVYQSEAHGLPLHLPGNK---SPHRDPAPRGPARFL-----PLPGLPPALPEP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 GLWVSVLAGLLLGACQ---AHPIPDSSPLL--QFGGQVRQRYLYTDDAQQTEAHLEIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                       Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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35.1%; Pred. No. 8.4e-13;
tive 27; Mismatches 85;
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transforming protein (int-2) - mouse (;Species: Mus musculus (house mouse) (;Species: Mus musculus (house mouse) (;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999 (;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #sequence_revision 31-Dec-1989 #sequence_revision 31-Dec-1989 #sequence_revision; S.; Dixon, M.; Peters, G.; Dickson, C. R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dickson, C. REMBO J. S., 919-924, 1986 #sequence coding potential of mouse int-2: a putative of A;Reference number: A23930; MUID:86247582; PMID:3013624

RESULT 2

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Fibroblast growth factor 6 precursor - human N.Alternate names: fibroblast growth factor-related protein FGF.6; transforming protein C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Barbos 1994 #sequence revision 12.Apr-1996 #text_change 21-Jul-2000 C.Bate: 18-Feb-1994 #sequence revision 12.Apr-1996 #text_change 21-Jul-2000 R.Scoulier, F.; Batoz, M.; Marics, I.; de Lapeyriere, O.; Birnbaum, D. Oncogene 6, 1437-1444, 1991 A.; de Lapeyriere, O.; Birnbaum, D. A,fittle: Butative structure of the FGF6 gene product and role of the signal peptide. A,Reference number: S20102; MUID:91360279; PMID:1886714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        embryonic fibroblast growth factor - African clawed frog c;Species: Xenopus laevis (African clawed frog) C;Species: Xenopus laevis (African clawed frog) C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999 C;Accession: S2395 R;Isaacs, H.V.; Tannahill, D.; Slack, J.W.W. Development 114, 711-720, 1992 A;Title: Expression of a novel FGF in the Xenopus embryo. A new candidate inducing fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X63454
A;Note: it is uncertain whether Met-1 or Met-11 is the initiator
R;Narics, I:; Adelaide, J.; Raybaud, F.; Mattei, M.G.; Coulier, F.; Flanche, J.; de Lap;
Rocogene 4, 335-340, 1989
A;Title: Characterization of the HST-related FGF.6 gene, a new member of the fibroblast
A;Reference number: S04204; MUID:89201880; PMID:2649847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Status: not compared with conceptual translation
A, Status: not compared with conceptual translation
A, Molecule type: DNA
A, Rolecule type: DNA
A, Rolecule type: DNA
A, Rolecule type: SINA
A, Rolecule type: SINA
A, Rolecule type: SINA
A, Rolecule type: SINA
A, Rolecule type: SINA
A, Rolecule type: SINA
A, Sobilda, S.; Yoshida, T.; Naito, K.; Sakamoto, H.; Katoh, O.; Hirohashi, S.; Sato, Oncogene type: 303-309, 1992.
A, Fitle: Human hst-2 (FGF-6) oncogene: CDNA cloning and characterization.
A, Reference number: S23739; MUID: 92195660; PMID: 1549352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 81-99,'G',101-208 <MAR>
A;Cross-references: EMBL:X14071; NID:G31354; PIDN:CAB37648.2; PID:g4467836
: | | | | | | | 152 LWYVSVNGKGRPRRGFKIRRIQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:119908; OMIM:134921
A;Map position: 12p13-12p13
A;Introns: 115/3; 150/2
C;Superfamily: fibroblast growth factor
F;1-40/Domain: (or 11-40 or 34-40) signal sequence #status predicted
F;41-208/Product: fibroblast growth factor 6 #status predicted <MAT>
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1 Similarity 29.1%; Pred. No. 4.6e-07;
46; Conservative 27; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 AMSKGRLYATPSFQ-EECKFRETLLPNNYNAYESDLY 176
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Best Local Similarity
Matches 46; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-208 <IID>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S04204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S23739
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N,Alternate names: transforming protein int-2

C;Species: Homo sapiens (man)

C;Accession: 504742

R;Brookes, S.; Smith, R.; Casey, G.; Dickson, C.; Peters, G.

A, Pitle: Sequence organization of the human int-2 gene and its expression in teratocarci
A;Reference number: 504742; MUD:89239468; PMID:2470007
                                                A; Residues: 1-245 < MOO.

A; Residues: 1-245 < MOO.

A; Residues: 1-245 < MOO.

A; Residues: 1-245 < MOO.

A; Residues: 1-245 < MOO.

A; Residues: 1-245; Bixon, M.; Peters, G.; Dickson, C.

B; Acland, P.; Dixon, M.; Peters, G.; Dickson, C.

B; Acland, P.; Dixon, M.; Peters, G.; Dickson, C.

A; Acland, P.; Dixon, M.; Peters, G.; Dickson, C.

A; Reference number: 808157; MUID: 90158795; PMID: 2406607

A; Accession: 808157

A; Accession: 808157

A; Accession: Solution

A; Residues: Moo.

A; Residues: 'HSRAGIARGRVLPAPRIRETRAGAAAAAGGRDAGM', 3-17 < ACL>

A; Residues: 'HSRAGIARGRVLPAPRIRETRAGAAAAAAGGRDAGM', 3-17 < ACL>

A; Accession: Solutions: 'HSRAGIARGRVLPAPRIRETRAGAAAAAAGGRDAGM', 3-17 < ACL>

A; Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solutions: Accession: Solution: Accession: Solution: Accession: Solution: Accession: Solution: Accession: Solution: Accession: Solution: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accessi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 YLAMNKRGRLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGAR---RQPSAER 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 YLAMNKRGRLYASDHYNAE-CEFVERIHELGYNTYASR----LYRTGSSGPGAQRQPGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 GGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESILLQLKALKPGVIQILGVKTSR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 RGP-----ARFLPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
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A, Residues: 1-239 < BRO>
A, Residues: 1-239 < BRO>
A, Crosser-references: EMBL:X14445; NID:g33937; PIDN:CAA32615.1; PID:g312409
C, Genetics:
A, Gene: GDB:FGF3; INT2
A, Crosser-references: GDB:120103; OMIM:164950
A, Map position: 11q13.3-11q13.3
A, introns: 74/1; 108/3
C, Superfamily: fibroblast growth factor
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C;Keywords: growth factor
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-239/Product: transforming protein (int-2) #status predicted <WAT>
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Best Local Similarity 29.7%; Pred. No. 4.5e-07;
Matches 51; Conservative 23; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.1%; Score 179; DB 1; Best Local Similarity 28.8%; Pred. No. 3.5e-07; Matches 51; Conservative 30; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 7
A;Introns: 74/1; 108/3
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; transforming protein
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fibroblast growth factor 5 - rat (5.5pecies: Rattus norvegicus (Norway rat) (5.5pecies: Rattus norvegicus (Norway rat) (5.5pecies: Rattus norvegicus (Norway rat) (5.5pecies: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000 (5.5peciesion: 86814, M.; Itoh, N. R.; Hattori, Y.; Yamasaki, M.; Itoh, N. Biochim. Biophys. Acta 1306, 31-33, 1996 (5.5pecies) M.; Reference number: 868144; MuID:96201703; PMID:8611621 (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies) (6.2pecies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 -GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLP-----PALPEPP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGREWYVALNK---RGKAKRGCSPRVKPQHVSTHFLPRFKQSEQPELSFTVTVPEKKKPP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 SSPLLQFGGQVRQRYLYTDDAQQTEA-----HLEIREDGTVGGAADQSPESLLQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 ALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;cross references: EMBL:D64085; NID:g992952; PIDN:BAA10966.1; PID:g992953
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 19-208 <RES>
A;Cross-references: GB:M92416; NID:g193288; PIDN:AAA62261.1; PID:g666915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Cross-references: GB. M92415; NID: 9193286; PIDN: AAA62260.1; PID: 9193287
                                    A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Motos: 1208 «LAP>
A; Cross references: EMBL: X51552
A; Note: it is uncertain whether Met-1 or Met-11 is the initiator
R; Ollendorff, V; Rosnet, O.; Marics, I.; Birnbaum, D.; deLapeyriere,
Biochimie 74, 1035-1038, 1992
A; Title: Isolation and sequence of the murine Fgf6 cDNA.
A; Reference number: 149664; MUID: 93120244; PMID: 1477139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.0%; Score 167; DB 2; Length 266; 30.3%; Pred. No. 3.6e-06; Live 26; Mismatches 69; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 LCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-266 <HAT>
A; Reference number: S14192; MUID: 90295275; PMID: 2193291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.3%; Score 170.5; DB 2; Best Local Similarity 36.4%; Pred. No. 1.4e-06; Matches 36; Conservative 21; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: 149664
A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 GILAPQPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 116/1; 150/3
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-18 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: Fgf6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Cross-references: GB:U15969
A)Note: The authors translated the codon GGC for residue 114 as Ser
C;Comment: This protein is a member of fibroblast growth factor family. The hstgene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibroblast growth factor 6 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 17-Mar-2000
C;Accession: S14192; I49665; I49664
R;de Lapeyriere, O.; Rosnet, O.; Benharroch, D.; Raybaud, F.; Marchetto, S.; Planche,
R;de Lapeyriere, O.; Rosnet, O.; Benharroch, D.; Raybaud, F.; Marchetto, S.; Planche,
A;Title: Structure, chromosome mapping and expression of the murine Fgf-6 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Yu, J.C.; DeSeabra, A.J.J.; Wang, L.M.; Fleming, T.P.; Chedid, M.; Miki, T.; H
Gene 162, 333-334, 1995
A;Title: An unexpected transforming gene in calf-thymus carrier DNA: Bovine hst.
A;Reference number: JC4268; MUID:96032369; PMID:7557455
                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 WESLVARSLIAGLPVAAQPKEAAVQSGAGDYLLGIKRLRRLYCNVG--IGFHLQVLPDGR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 DSDYLL---GIKRQRRLYCAVG--IGFHIQVLPDGRINGMHSENRYSLLELSPVEVGVVS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 ILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-GLPLHLPGN-- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
                                                                                                                                                                                                                                                                                                                                                                                                  33 DSSPLLOFGGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: transforming protein hst
C;Species: Bos primiganius taurus (cattle)
C;Date: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
C;Accession: JC4268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 WVSVLAGLLLGACQAHPIPDSSPLLQFGGQV----RQRYLYTDDAQQTEAHLEIREDGT
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Gaps
                                                                                   A,Molecule type: mRNA

*Residues: 1-187 <ISSA ;

A;Cross-references: EMEL:X62593; NID:g64692; PIDN:CAA44479.1; PID:g64693

C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                10;
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                                                                                                                                                                                                                                                           Length 187;
                                                                                                                                                                                                                                                                                                                                57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 EDGYNVYOSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reference number: $23595; MUID:92315916; PMID:1618138
                                                                                                                                                                                                                                                       Query Match 15.6%; Score 174; DB 2; Best Local Similarity 34.8%; Pred. No. 6.5e-07; Matches 48; Conservative 23; Mismatches 57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Introns: 113/3; 145/2
C,Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 -KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 TKKGNRVSPIMTLTHFLP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eibroblast growth factor 4 - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: JC4268
A; Molecule type: mRNA
A; Residues: 1-206 <YUJ>
                                                   A; Accession: S23595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
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7

Gaps

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Nighternate names: heparin secretory transforming protein 1; Kaposi sarcoma oncogene; C Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: J. Mar. 1989
C;Accession: A28417; A29876; A29649
R;Yoshida, T.; Miyagawa, K.; Odagiri, H.; Sakamoto, H.; Little, P.F.R.; Terada, M.; Sug
R;Yoshida, T.; Miyagawa, K.; Odagiri, H.; Sakamoto, H.; Little, P.F.R.; Terada, M.; Sug
A;Title: Genomic sequence of hst. a transforming gene encoding a protein homologous to
A;Reference number: A28417; MUID:88041096; PMID:2959959
A;Accession: A28417
A;Molecule type: DNA
A;Residues: 1-206 <705>
A;Cross-references: DDBJ:002986; NID:g184430; PIDN:AAB59555:1; PID:g386788
B;Taira, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987
A;Title: cDNA sequence of human transforming gene hst and identification of the coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             embryonic fibroblast growth factor II - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 06-Sep-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C;Accession: S54407
R;Isaacs, H.V.; Tannahill, D.; Slack, J.M.W.
By-elopment 114, 711-70, 1992
A;Title: Expression of a novel FGF in the Xenopus embryo. A new candidate inducing fact
A;Reference number: S23595; MUID:92315916; PMID:1618138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 HLEIREDGTVGGAADQSPESILLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 ASPGSQGSGEHSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEASVLSILEIF 122
                                                                                                                                                                                                                                                                                                                                                   85 ALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH---- 140
                                                                                                                                                                                                                                                                                                                                                                                        182 TGREWYVALNK----RGKAKRGCSPRVKPOHVSTHFLPRFKQSEQPELSFTVTVPEKKKPP 238
                                                                                                                                                                                                                                   34 SSPLLQFGGQVRQRYLYTDDAQQTEA-----HLEIREDGTVGGAADQSPESLLQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLPPALPEPPGILAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X62594; NID:9840919; PIDN:CAA44480.1; PID:9840920
C;Superfamily: fibroblast growth factor
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                        A;Cross-references: GB:M30643; NID:g193294; PIDN:AAA96698.1; PID:g309238
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 192;
                                                                                                                Length 264;
                                                                                                                Query Match
14.7%; Score 164; DB 2; Length 26.
Best Local Similarity 28.6%; Pred. No. 6.1e-06;
Matches 58; Conservative 25; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 163.5; DB 2 32.4%; Pred. No. 4.6e-06; tive 26; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 QPPDVGSSDPLSMVGPSQGRSPS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 VKPKVPLSQP-----RRSPS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibroblast growth factor 4 - human
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Conservative 2
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ses 36; Conserv
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-192 <ISA>
A;Residues: 1-264 <HEB>
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Best Local S:
Matches 36
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A,Residues: 1-194 <NIS.
A,Residues: 1-194 <NIS.
A,Cross-references: BMBL:U14654; NID:g609347; PIDN:AA58706.1; PID:g609348
R,Niswander, L.; Jeffrey, S.; Martin, G.R.; Tickle, C.
R,Niswander, L.; Jeffrey, S.; Martin, G.R.; Tickle, C.
A) Sture 31, 609-612, 199-614
A,Title: A positive feedback loop coordinates growth and patterning in the vertebrate li
A,Reference number: 150710; MUID:95021713; PMID:7935794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Title: Isolation of CDNAs encoding four mouse FGF family members and characterization A,Reference number: A37360; MUID:90201563; PMID:2318343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fibroblast growth factor 5 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 17-Mar-2000
C;Accession: A36207; B37360
R;Haub, O.; Drucker, B.; Goldfarb, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 8022-8026, 1990
Proc. Natl. Acad. Sci. U.S.A. 87, 8022-8026, 1990
A;Title: Expression of the murine fibroblast growth factor 5 gene in the adult central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross_references: GB:M37821; GB:M37822; GB:M37823; NID:g193280; PIDN:AAB02660.1; PID:R;Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 KTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-GLPLHLPGN---KSP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                            fibroblast growth factor 4 - chicken
C;Species: Gallus gallus (chicken)
C;Dates: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: S78506; S50858; I50710
R;Niswander, L.
submitted to the EMBL Data Library, September 1994
A;Reference number: S78506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AALILPALLIJGILWPGAVRGRPPPGRLPPGPRQRRWDAALFARSVARLPAERRDAARDGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 LLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESILQLKALKPGVIQILGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
MyResidues: 1-136,'Q',137-194,'I' <NIW>
A;Cross-references: EMBL:U14654; NID:g609347; PIDN:AAA58706.1; PID:g609348
C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; transforming protein
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A, Status: preliminary; not compared with conceptual translation
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Pred. No. 3.5e-06;
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   ---RPWKPKV----PLS---PSR-RSPS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 SGLWVSVLAGLLL-GACQAHPIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 HRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::
NKVSPTMTVTHFLP 192
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R;Ohmachi, S.; Watanabe, Y.; Mikami, T.; Kusu, N.; Ibi, T.; Akaike, A.; Itoh, N. Biochem. Biophys. Res. Commun. 277, 355-360, 2000
A;Title: F0F-20, a novel neurotrophic factor, preferentially expressed in the substantia A;Reference number: JC7511; MUID:20490008; PMID:11032730
A;Contents: Brain.
                                                                                                                                                                                                                                                                                                                                                                        A)Cross-references: EMBL:248714; NID:g971333; PIDN:CAA88596.1; PID:g971334
A)Experimental source: embryo
A)Note: The authors translated the codon TGG for residue 178 as His
C;Comment: This factor belongs to the fibroblast growth factor family which have the function is a cell signalling molecule and plays the roles during the early stages of devel
                                                                                                                                                                                                                             structure and genomic organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comment: This factor is secreted, and plays an important role as a neurotrophic factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 PGSVELAHLHGILRRRQLYC----RTGFHLQILPDGSVQGTRQDHSLFGILEFISVAVGL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 VSIRGVDSGLYLGMNGKGELYGSEKLTSE-CIFREQFEENWYNTYSSNIYKHGDTGRRYF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 RFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPR 159
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                                                    fibroblast growth factor 3 - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 10-May.1996 #sequence_revision 19-Jul-1996 #text_change 16-Jul-1999
C;Accession: JC4627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibroblast growth factor-20 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQ-SPESLLQLKALKPGVIQILGVKTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 GPARFLPLPGLPPALPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                   Rikiefer, P.; Straehle, U.; Dickson, C.
Gene 168, 211-215, 1996
A;Title: The zebrafish Fgf-3 gene: CDNA sequence, transcript
A;Reference number: JC4627; MUID:96194899; PMID:8654946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 14.4%; Score 160.5; DB 2; Similarity 28.1%; Pred. No. 1.1e-05; 47; Conservative 22; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: fgf-20
C;Keywords: brain; growth factor; neurotrophic factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: embryo; fibroblast; growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Introns: 93/2; 127/3
C,Superfamily: fibroblast growth factor
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A;Residues: 1-212 <OHM>
A;Cross-references: DDBJ:AB020021
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-256 <KIE>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                           A; Accession: JC4627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: Fgf-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibroblast growth factor-20 - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: OB-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 01-Dec-2000
C;Accession: JC7353
R;Kirikoshi, H.; Sagara, N.; Saitoh, T.; Tanaka, K.; Sekihara, H.; Shiokawa, K.; Katoh, A;Cohen Biophys. Res. Commun. 274, 337-343, 2000
A;Title: Molecular cloning and characterization of human FGF-20 on chromosome 8p21.3-p22
A;Reference number: JC7353
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M
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                                              A; Molecule type: mRNA
A; Regidues: 1-206 <TAI>
A; Cross-references: GB:J02986; GB:MI6338; NID:g184430; PIDN:AAB59555.1; PID:g386788
B; Delli Bovi, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Ittmann, M.; Basilico, C.
Cell 50, 729-737, 1987
A; Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth
A; Reference number: A29649; MUID:87301716; PMID:2957062
                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GB:M17446; NID:g186785; PIDN:AAA59473.1; PID:g307092
C,Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ñ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 HIBIREDGTVGGAADQSPESILIQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 PGAAQLAHLHGILRRRQLYC----RTGFHLQILPDGSVQGTRQDHSLFGILBFISVAVGL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 IQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 PDSSPLLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQLKALKPGV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Map position: 11q13.3-11q13.3
A;Introns: 114/1; 148/3
C;Superfamily: fiberblast growth factor
C;Keywords: growth factor; Kaposi sarcoma; transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 VALNK----DGTPRDGARSKRHOKFTHFLPRPVDPERVPE 202
number: A29876; MUID:87204251; PMID:2953031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.7%; Score 163.5; DB 1; 36.9%; Pred. No. 5e-06; tive 19; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 14.5%; Score 161; DB 2; Similarity 33.1%; Pred. No. 8.2e-06; 53; Conservative 19; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GDB:120066; OMIM:164980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Map position: 8p21.3-8p22;Superfamily: fibroblast growth factor;Keywords: angiogenesis; carcinogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 41; Conserva
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Best Local Similarity
Matches 53; Conservi
                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-206 <BOV>
                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Gene: GDB: FGF4; HSTF1
                                                                                                                                                                                                                                                                  A; Accession: A29649
                        Accession: A29876
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Nyllerrate names: heparin-binding growth factor 1
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A60721
R;Hall, J.A.; Harris, M.A.; Malark, M.; Mansson, P.E.; Zhou, H.; Harris, S.E.
J. Cell. Biochem. 43, 17-26, 1990
A;Ritle: Characterization of the hamster DDT-1 cell arGF/HGBF-I gene and cDNA and its A;Reference number: A60721; MUID:90270291; PMID:1693366
A;Actus: not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
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N'Alternate names: heparin-binding growth factor 1
C;Species Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 16-Jul-1999
C;Accession: S04147
C;Accession: S04147
Nucleic Acids Res. 17, 2867, 1989
A;Title: The nucleotide sequence of rat heparin binding growth factor 1 (HBGF-1).
A;Reference number: S04147; MUID:89240051; PMID:2470029
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                                                                                                                                                                                                                                                                          100 RFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 IFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYLGMNEKGELYGSEKLTQE-C 134
                                                                                                                                                                                                                         SFRELLLEDGYNVYQSEAH----GLPLHLPGNKSPHRDPAPRGPAR-----FLPL 167
                                                                        63 IREDGTVGGA-ADOSPESLLOLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
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--PAVTDLDHLKGILRRQLYC----RTGFHLE 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 GGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGVKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GNYKKPKLLYCSNGGH---FLRILPDGTVDGTRDRSDQHIQLQLSAESAGEVYIKGTETG
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A;Residues: 1-155 <GOO>
A;Ross-references: EMBL:X14232; NID:G56351; PIDN:CAA32448.1; PID:G56352
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; heparin binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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1 Similarity 35.0%; Pred. No. 1.6e-05;
48; Conservative 12; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acidic fibroblast growth factor - golden hamster
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C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; heparin binding
    ----GLPRG----
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                                                                                                                                                                                                                                                                                                                                                                                      168 PGLPPALPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVDPDKVPE 199
    34 SDHLGQSEAG--
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Best Local Similarity
Matches 48; Conserva
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A; Molecule type: mRNA
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Best Local S
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Mol. Cell. Biol. 13, 4251-4259, 1993
Mol. Cell. Biol. 13, 4251-4259, 1993
A;Title: Molecular cloning of a novel cytokine cDNA encoding the ninth member of the fib
A;Reference number: A48137; MUID:93309459; PMID:8321227
A;Accession: A48137
A;Status: preliminary
A;Molecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S66486
R;Seo, M.; Noguchi, K.
FEBS Lett. 370, 231-235, 1995
A;Title: Retinoic acid induces gene expression of fibroblast growth factor-9 during indu A;Reference number: S66486; MUID:95385801; PMID:7656983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 IREDGTVGGA-ADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: EMBL:D18258; NID:g1107458; PIDN:BAA07410.1; PID:g1107459
C.Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate_names: glia-activating factor
C;Species: lamo sapiens (man)
C;Date: 21-Jan.1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A48137
                                                                                                                                                                                                                                                                     fibroblast growth factor 9 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLOFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SDETGFEHSGLWVSVLAGLLLGACOAHPIPDSSPLLOFGGOVRORYLYTDDAQQTEAHLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A,Experimental source: foreskin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.1%; Score 157; DB 2; Length 208; 31.2%; Pred. No. 1.7e-05; Live 20; Mismatches 72; Indels
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C;Superfamily: fibroblast growth factor
            LPGNKSPHRDPAPRGPAR----
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Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-208 <SEO>
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession. JG7082.
C;Adcession. JG7082.
R;Koga, C.; Adati, N.; Nakata, K.; Mikoshiba, K.; Furuhata, Y.; Sato, S.; Tei, H.; Sakak
Biochem. Biophys. Res. Commun. 261, 756-765, 1999
A;Title: Characterization of a novel member of the FGF family, XFGF-20, in Xenopus laevi
A;Reference number: JG7082; MUID:99373151; PMID:10441498
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JC5941
R;Myake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mikami, Bicchem. Biophys. Res. Commun. 243, 148-152, 1998
A;Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth fa
                       A;Cross-references: GB:X14849; GB:M28516; NID:952791; FIDN:CAA32967.1; FID:952792
R;Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Bev. Biol. 138, 454-463, 1990
A;Title: Isolation of cDNAs encoding four mouse FGF family members and characterization A;Reference number: A37360; MUID:90201563; PMID:2318343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: DDBJ:AB012615; NID:g5762261; PIDN:BAA83474.1; PID:g5762262
C;Superfamily: fibroblast growth factor
C;Keywords: differentiation; fibroblast; growth factor; heparin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 HIETREDGTVGGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 KALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibroblast somatotropin-20 - African clawed frog
NiAlternate names: fibroblast growth factor-20
C;Species: Xenopus laevis (African clawed frog)
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 HLQVLPDGRIGGVHADTRDSLLELSPVQRGVVSIFGVASRFFVAMSSRGKLFGVPFFTDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 QAHPIPDSSP--LLQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGA-ADQSPESLLQL
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                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-166,'S',168-202 <HEB>
A;Cross-references: GB:M30642; NID:g193290; PIDN:AAA37619.1; PID:g309237
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN----KSPHRDPAPRGPARFLP 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%; Score 153.5; DB 1; 34.2%; Pred. No. 3.1e-05; iive 21; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 153; DB 2;
31.5%; Pred. No. 3.5e-05;
trive 22; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: hst
C,Superfamily: fibroblast growth factor
C,Keywords: growth factor; transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibroblast growth factor 16 - human
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Matches 38; Conserv
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Best Local Similarity
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A; Residues: 1-208 < KOG>
          A; Residues: 1-202 <BRO>
                                                                                                                                                                                               A; Accession: A37360
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C; Species: Mus musculus (house mouse)
C; Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 17-Mar-2000
C; Accession: 804741; A37360
R; Brookes, S.; Smith, R.; Thurlow, J.; Dickson, C.; Peters, G.
Avucleic Asida Ress 17, 437-4045, 1989
A; Title: The mouse homologue of hst /k-FGF; sequence, genome organization and location re
A; Reference number: 804741; MUID:89296455; PMID:2740210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:U36456
C;Comment: This protein is an inducer of neovascularization in angiogenic disease includ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NiAlternate names: aFGF, FGF-1
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C;Accession: D37360, UCS231
R;Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
A;Title: Isolation of cDNAs encoding four mouse FGF family members and characterization A;Reference number: A37360; MUID:90201563; PMID:2218343
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                                                                                                 97 KTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDP 156
                                                                                                                                         97 KTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLFGNKSPHRDP 156
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18 LPLGNYKKPKLLYCSNGGH---FLRILPDGTVDGTRDRSDQHIQLQLSABSAGEVYIKGT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 LPLGNYKKPKLLYCSNGGH---FLRILPDGTVDGTRDRSDQHIQLQLSAESAGEVYIKGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 LOFGGOVRORYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-155 cHEB>
A;Cross-references: GB:M30641; NID:g193284; PIDN:AAA37618.1; PID:g309236
R;Madial, F.; Hackshaw, K.V.; Chiu, I.M.
Gene 119, 2311-236, 1996
A;Title: Cloning and characterization of the mouse Fgf-1 gene.
A;Reference number: JG5231; MUID:97128312; PMID:8972905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 13.9%; Score 154.5; DB 2; Similarity 34.3%; Pred. No. 1.9e-05; 48; Conservative 13; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Introns: 57/1; 91/3
C; Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                            acidic fibroblast growth factor - mouse
                                                                                                                                                                                                                                 157 APRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 APRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 CKRGPRTHYGQKAILFLPLP 151
                                                                                                                                                                                                                                                                                          132 CKRGPRTHYGOKAILFLPLP 151
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Best Local Similarity
Matches 48; Conserv
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A;Molecule type: mRNA
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A,Status: translation not shown
A,Molecule type: mRNA
A,Residues: 1-58 <PAY>
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A, Status: translation not shown
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                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-155 < MER>
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A; Residues: 1-58 < PA2>
                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
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A33665
Acidic fibroblast growth factor 1 precursor [validated] - human
N;Alternate names: beta-ECCF; endothelial cell growth factor beta; heparin-binding growt
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: Ail194
R;Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.
Mol. Cell. Biol. 8, 3487-3495, 1988
A;Title: The human FGF-5 oncogene encodes a novel protein related to fibroblast growth A;Reference number: Ail194; MUID:89096942; PMID:3211147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Cross-references: GB:M23536; GB:M21617; NID:g182539; PIDN:AAB60699.1; PID:g182542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: JC5941
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-207 <MIY>
A,Coss-references: DDBJ:AB009391; NID:g2911169; PIDN:BAA24956.1; PID:g2911170
C,Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 HIETREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --PARF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                75 IPPNGTVHGTRHDHSRFGILEFISLAVGLISIRGVDSGLYLGMNERGELYGSKKLTRE-C 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 SFRELLLEDGYNVYQSEAHGLPLHLPGNK----SPHRDPAPRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                   IREDGIVGGAA-DQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                  28 ADSPGFINERL-----GOIEGKLORGSPTDFAHL---KGILKRROLYC----RTGFHLE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibroblast growth factor 5 - human
N;Alternate names: transforming protein FGF5
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                  SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAHLE
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                   Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.3%; Score 148.5; DB 1; Length 267; nilarity 31.2%; Pred. No. 0.00011; Conservative 20; Mismatches 61; Indels 27.
                                                                                                                                                                                            Query Match 13.5%; Score 150.5; DB 2; Length 207; Best Local Similarity 32.6%; Pred. No. 5.5e-05; Matches 61; Conservative 20; Mismatches 75; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 ACSFRELLLEDGYNVYQSEAH-----GLPLHLPGNKSPHRDPAPRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 LP-----LPGLPPALPEPPGILAPQPPDVGSSDPLS 195
A, Reference number: JC5940; MUID:98139883; PMID:9473496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Supertamily: IlDroblast growth factor;
C;Keywords: growth factor; transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:119907; OMIM:165190
A;Map position: 4q21-4q21
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLPPALP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 VDPSKLP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-267 <ZHA>
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Best Local Similarity
Matches 49; Conserv
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C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000 C; Accession: A33665; A32316; E1217; A43804; A24662; JH0707; S35535; S35536; I39413; A2: R; Mergia, A.; Tischer, E.; Graves, D.; Tumolo, A.; Miller, J.; Gospodarowicz, D.; Abrahɛ Biochem. Biochys. Res. Commun. 164, 1121-1129, 1989 A; Title: Structural analysis of the gene for human acidic fibroblast growth factor. A; Reference number: A33665; MUID:90073637; PMID:2590193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-155 < WAL2.
A; Residues: 1-155 < WAL2.
A; Cross-references: EMBL: MZ3086
B; Chiu, I.M.; Wang, W.P.; Lehtoma, K.
Chocyaene 5, 755-762, 1990
A; Title: Alternative splicing generates two forms of mRNA coding for human heparin-bind: A; Reference number: A43804; MUID:90265618; PMID:1693186
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A; Residues: 1-155 < YUY>
A; Cross-references: GB:X65778; NID:g396163; PIDN:CAA46661.1; PID:g396164
A; Cross-references: GB:X65778; NID:g396163; PIDN:CAA46661.1; PID:g396164
K; Payson, R.A.; Canatan, H.; Chotani, M.A.; Wang, W.P.; Harris, S.E.; Myers, R.L.; Chiu, Nucleic Acids Res. 21, 489-495, 1993
Nucleic Acids Res. 21, 489-495, 1993
A; Title: Cloning of two novel forms of human acidic fibroblast growth factor (aFGF) mRN/
A; Reference number: S35535; MUID:93181239; PMID:7680120
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A; Cross-references: GB:M23087; NID:g183875; PIDN:AAA52638.1; PID:g386768
A; Cross-references: GB:M23087; NID:g183875; PIDN:AAA52638.1; PID:g386768
R; Wang, W.P.; Quick, D.; Balcerzak, S.P.; Needleman, S.W.; Chiu, I.M.
Rocogene 6, 1521-1529, 1991
A; Title: Cloning and sequence analysis of the human acidic fibroblast growth factor generate number: S18217; MUID:92019819; PMID:177925
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A, Residues: 1-152 < CHT.

A, Fresidues: 1-152 < CHT.

A, Cross-references: BMBL: X51943; NID: 932435; PIDN: CAA36206.1; PID: 932436

A, Cross-references: BMBL: X51943; NID: 932435; PIDN: CAA36206.1; PID: 932436

R, Jaye, M.; Howk, R.; Burgess, W.; Ricca, G.A.; Chiu, I.M.; Ravera, M.W.; O'Brien, S.J...
Science 233, S41-1545, 1986

A; Title: Human endothelial cell growth factor: cloning, nucleotide sequence, and chromo: A, Reference number: A24662; MUID: 86261805; PMID: 3523756
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                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M30491
R;Wang, W.P.; Lebtoma, K.; Varban, M.L.; Krishnan, I.; Chiu, I.M.
Nol. Cell. Biol. 9, 2387-2395, 1999
A;Title: Cloning of the gene coding for human class 1 heparin-binding growth factor and
A;Reference number: A32316; MUID:89343957; PMID:2474753
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R,Crumley, G.; Dionne, C.A.; Jaye, M.
Biochem. Biophys. Res. Commun. 171, 7-13, 1990
A,Fitle: The gene for human acidic fibroblast growth factor A,Reference number: 139412; MUID:90365758; PMID:2393407
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A; Residues: 1-40 <RES>
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8;

Gaps

31;

Indels

Length 207;

74

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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: JC5940 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C;Accession: JC5940 R;Miyake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mikami, R;Miyake, A.; Konishi, M.S.; Comunn. 243, 148-152, 1998 A;Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth fac A;Reference number: JC5940; MUID:9913983; PMID:9473496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IREDGIVGGAA-DQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 SFRELLLEDGYNVYQSEAHGLPLHLPGNK----SPHRDPAPRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Residues: 1-207 AMIX>
A.Cross-references: DDBJ:AB002561; NID:g2911149; PIDN:BAA24947.1; PID:g2911150
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SDETGFEHSGLWVSVLAGLLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTBAHLE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transforming protein int-2 - African clawed frog
NiAlternate names: 168-3 protein; fibroblast growth factor 3
C:Species: Xenopus laevis (African clawed frog)
C:Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 GGQVRQRYLYIDDAQQTEAHLEIREDGTVGGAADQ-SPESLLQLKALKPGVIQILGVKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 ADSPGFLNERL-----GQIEGKLORGSPTDFAHL---KGILRRROLYC----RTGFHLE
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A; Residues: 1-237 <KIE>
A; Cross-references: EMBL: 225539; NID: 9396830; PIDN: CAA80987.1; PID: 9396831
A; Cross-references: H.V.; Close, M.J.; Peters, G.; Slack, J.M.W.
Development 115, 695-702, 1992
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C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: $39582; $25713 —
R;Kiefer, P.; Mathieu, M.; Close, M.J.; Peters, G.; Dickson, EMBO J. 12, 4159-4168, 1993
A;Title: FGF3 from Kenopus laevis.
A;Reference number: $39582; MUID:94038898; PMID:8223431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 RFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH 140
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Pred. No. 0.00015;
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C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.1%;
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A; Residues: 39-137 <TAN>
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Best Local Similarity
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                                                                                                                                                                                             A;Accession: JC5940
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S39582
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                                                                                                                      A,Molecule type: protein
A,Residues: 16-155 <HRR>
R;Gimenez-Gallego, G.; Conn, G.; Hatcher, V.B.; Thomas, K.A.
Biochem. Biophys. Res. Commun. 138, 611-617, 1986
A;Title: The complete amino acid sequence of human brain-derived acidic fibroblast growt
A;Reference number: A24820; MUID:86295741; PMID:3527167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endothelial cell mitogens from human brai
                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 16-155 <GIM>
R; Gimenes-Callego, G.; Conn, G.; Hatcher, V.B.; Thomas, K.A.
B; Cochem. Biophys. Res. Commun. 135, 541-548, 1986
A; Title: Human brain-derived acidic and basic fibroblast growth factors: amino terminal
A; Reference number: A90122; MUID:86186784; PMID:3964259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: brain
R;Chavan, A.J.; Haley, B.E.; Volkin, D.B.; Marfia, K.E.; Verticelli, A.M.; Bruner, M.W.
Biochemistry 33, 7193-7202, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A;Residues: 16-30, 'X', 32-38;73-75, 'X', 77-97, 'X', 99-101;128-131, 'X', 133-140, 'X', 142-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Interaction of nucleotides with acidic fibroblast growth factor (FGF-1). A; Reference number: A53639; MUID:94271773; PMID:7516183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: protein
A,Residues: 16-30, X',32-49 <GAU>
R,Gautschi-Sova, P.; Muller, T.; Bohlen, P.
R,Gautschi-Sova, P.; Muller, T.; Bohlen, P.
B,Ttibe: Anino acid sequence of human acidic fibroblast growth factor.
A,Reference number: A26386; MUID:87048871; PMID:3778488
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A;Residues: 16-47 <GI2>
A;Residues: 16-47 <GI2>
A;Ryperimental source: brain
R;Gautschi, P.; Frater-Schroder, M.; Bohlen, P.
FEBS Lett. 204, 203-207, 1986
A;Title: Partial molecular characterization of endotheli
A;Reference number: A91364; MUID:86275260; PMID:3732516
A;Accession: A24301
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   R;Harper, J.W.; Strydom, D.J.; Lobb, R.R.
Biochemistry 25, 4097-4103, 1986
A;Reference number: A23553; MUID:86296647; PMID:2427112
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34.3%; Pred. No. 8.2e-05;
tive 12; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:FGF1; FGFA
A;Cross-references: GDB:119909; OMIM:131220
A;Map position: 5431.3-5433.2
A;Introns: 57/1; 91/3
C;Superfamily: fibroblast growth factor
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fibroblaвt growth factor 16 - rat
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Best Local Similarity
Matches 47; Conserv
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Gaps

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Length 237; 40; Indels

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 16-30, X', 32-40 < KUO>
A; Residues: 16-30, X', 32-40 < KUO>
A; Residues: 16-30, X', 32-40 < KUO>
A; Residues: 16-30, X', 32-40 < KUO>
B; Mill, C.E.; Belford, D.A.; Godovac-Zimmermann, J.; Hendry, I.A.
B; Hill, C.E.; Belford, D.A.; Godovac-Zimmermann, J.; Hendry, I.A.
B; Fill: Class I heparin binding growth factor promotes the differentiation but not the A; Reference number: A61198; MUID:92164087; PMID:1724209
A; Recession: A61198
A; Rocession: A61198
A; Residues: 11-26;28-50;53-110, H',112, NHY';134-155 < HIL>
B; Philippe, J.M.; Renaud, F.; Desset, S.; Laurent, M.; Mallet, J.; Courtois, Y.; Edwarde Biochem Elophyse Res. Commun. 188, 843-850, 1992
A; Title: Cloning of two different 5' untranslated exons of bovine acidic fibroblast grow A; Reference number: 146024; MUID:93075172; PMID:1280126
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A)Residues: 16-24;121-127;134-143 <SAS>
A)Experimental source: heart
C)Comment: The acidic and basic fibroblast growth factors are the major endothelial-cell
ell types in vitro (although bFGF is 30-100 times more potent than aFGF in stimulating t
C)Comment: This protein binds heparin, although less strongly than does bFGF.
C)Comment: There are some sequence similarities between residues 117-126 (a region flank
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R;Sasaki, H.; Hoshi, H.; Hong, Y.M.; Suzuki, T.; Kato, T.; Sasaki, H.; Saito, M.; Youki, J. Biol. Chem. 264, 17606-17612, 1989
A; Fitle: Purification of acidic fibroblast growth factor from bovine heart and its local A; Reference number: A34477; MUID:90008933; PMID:2677012
A; Accession: A34477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Note: this form was designated alpha endothelial cell growth factor
R.Strydom, D.J.; Harper, J.W.; Lobb, R.R.
Biochemistry 25, 945-951, 1986
A.Title: Amino acid sequence of bovine brain derived class 1 heparin-binding growth fact
A.Reference number: A24539; MUID:86187766; PMID:2421762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AjMolecule type: protein
AjResidues: 16-155 <STR>
RjThomas, K.A.; Gimenez-Gallego, G.; Rios-Candelore, M.; DiSalvo, J.
J. Protein Chem. 6, 163-171, 1987
AjTitle: Primary structure and mitogenic and angiogenic activities of brain-derived acid
AjReference number: A60884
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A,Residues: 16-155 <THO>
R;Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 265, 16455-16463, 1990
A;Title: Acidic fibroblast growth factor receptor purified from bovine liver is a novel
A;Reference number: A37892; MUID:90375514; PMID:2168890
                           R;Burgess, W.H.; Mehlman, T.; Marshak, D.R.; Fraser, B.A.; Maciag, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 7216-7220, 1986
A;Title: Structural evidence that endothelial cell growth factor beta is the precursor
A;Reference number: A94127; MUID:87016918; PMID:3532107
                                                                                                                                                                                                                                                     A,Molecule type: protein
A,Residues: 2-155 <BUX>
A,Note: this form was designated beta endothelial cell growth factor
A,Rocession: C25043
                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 16-155 <BU2>
A,Note: this 16-11 was designated acidic fibroblast growth factor
A,Accession: A25043
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A,Residues: 22-30, XY, 32-38 <KU2>
A,Note: this form was designated brain-derived growth factor A
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A;Molecule type: mRNA
A;Residues: 1-18 <PH2>
2,'GE',5-155 <CRA>
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                                                                                                                                                          acidic fibroblast growth factor precursor - bovine
NyAlternate names: aFGF; eye-derived growth factor II; heparin-binding growth factor I;
C;Species: Bos primigenius taurus (cattle)
C;Dacession: JH0613; S02102; S02661; S22065; B24663; A94281; S03953; A91010; A24477; B25
R;Renaud, F.; Desset, S.; Bugra, K.; Halley, C.; Philippe, J.M.; Courtois, Y.; Laurent, A;Title: Heterogeneity of 3' untranslated region of bovine acidic FGF transcripts.
A;Reference number: JH0613; MUID: 92246990; PMID: 1374244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA

*Residues: 16-65 cABR.

R; Gimenez-Gallego, G.; Rookey, J.; Bennett, C.; Rios-Candelore, M.; DiSalvo, J.; Thomas,

Science 230, 1385-1388, 1985

Science 230, 1385-1388, 1985

*A; Title: Frain-derived acidic fibroblast growth factor: complete amino acid sequence and

A; Reference number: A94281; MUID:86070224; PMID:4071057
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A; Residues: 16-155 <GIM>
R; Quinkler, W.; Maæbberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Schape
Eur. J. Biochem. 181, 67-73, 1989
A; Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea
A; Reference number: S03953; MUID:89231704; PMID:2714282
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Reference number: A91010; MUID:86055750; PMID:4065099
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Residues: 16-30, XY, 32-34, XX, 36-44 <BOH>
Residues: 16-30, XY, 32-34, XZ, 36-44 <BOH>
Residues: 16-30, XZ, 32-34, YZ, 36-4993, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMEL:X13221; NID:g347; PIDN:CAA31610.1; PID:g348
R;Alterio, J.; Halley, C.; Brou, C.; Soussi, T.; Courtois, Y.; Laurent, M.
FEBS Lett. 242, 41-46, 1988
A;Title: Characterization of a bovine acidic FGF cDNA clone and its expression in brain A;Reference number: S02661; MUID:89078619; PMID:2449564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;cross-references: EMBL:X66446; NID:g411; PIDN:CAA47063.1; PID:g412
R;Abraham, J.A.; Mergia, A.; Whang, J.L.; Tumolo, A.; Friedman, J.; Hjerrild, K.A.; Gosp
Science 233, 545-548, 1986
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A;Residues: 58-155 <REN>
R;Halley, C.; Courtois, Y.; Laurent, M.
Nucleic Acids Res. 16, 10913, 1988
A;Title: Nucleotide sequence of bovine acidic fibroblast growth factor cDNA.
A;Reference number: S02102; MUID:89083506; PMID:3205724
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A;Residues: 1-155 <ALT>
A;Cross-references: EMBL:X14032; NID:g322; PIDN:CAA32192.1; PID:g323
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A;Residues: 16-45 <QUI>
R;Bohlen, P.; Esch, F.; Baird, A.; Gospodarowicz, D.
EMBO J. 4, 1551-1956, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Philippe, J.M. BMBL Data Library, May 1992 submitted to the EMBL Data Library, May 1992 A;Reference number: $22065 A;Accession: $22065
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A; Residues: 1-155 <HAL>
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C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 16-Jul-1999 C;Accession: S26649; S78446
R;Yan, G.; Nikolaropoulos, S.; Wang, F.; McKeehan, W.L.
In Vitro Cell. Dav. Biol. 27, 437-438, 1991
A;Title: Sequence of rat keratinocyte growth factor (heparin-binding growth factor type A;Reference number: S26649
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A;Molecule type: MRNA
A;Residues: 1-16, 'P. 18-100, 'M',102-123,'Q',125-150,'S',152-194 <YAW>
A;Residues: 1-16, 'P. 18-100, 'M',102-123,'Q',125-150,'S',152-194 <YAW>
A;Cross-references: EMEL:X56551; NID:956707; PIDN:CAA39892.1; PID:956708
C;Superfamily: fibroblast growth factor
C;Reyords: extracellular protein; growth factor; heparin binding; mitogen
C;Ri-31/Domain: signal sequence #status predicted <SIG>
F;32-194/Product: fibroblast growth factor 7 #status predicted <MAT>
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A;Cross-references: EMBL:Z47555; NID:g623215; PIDN:CAA87635.1; PID:g623216
C;Superfamily: fibroblast growth factor
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
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Best Local Similarity 27.5%; Pred. No. 0.00024;
Matches 39; Conservative 30; Mismatches 47; Indels '
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Best Local Similarity 34.78
Warches 35; Conservative
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R;Yan, G.
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A,Molecule type: mRNA
A,Residues: 1-194 <YAN>
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                                                                                                                                                                                                                                                 C; Keywords: acetylated amino end; angiogenesis; growth factor; heparin binding; mitogen P;2-155/Product: beta endothelial cell growth factor #status experimental ceCB> P;16-155/Product: acidic fibroblast growth factor #status experimental cMAT> P;22-155/Product: alpha endothelial cell growth factor #status experimental cECA> P;24-28,113-116/Region: heparin binding #status predicted F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: the hydrophobic core residues are packed around the internal symmetry axis C;Comment: This protein belongs to the fibroblast growth factor family. C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 KISRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETGQFLAMDTDGLLYGS-QTPNEECLFLERLEENHYNTYISKKHAEKHWFVGLKKNGR-- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acidic fibroblast growth factor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: JH0476; S20072
R;Schmidt, M.; Sharma, H.S.; Schott, R.J.; Schaper, W.
Bloochen. Biophys. Res. Commun. 180, 853-869, 1991
A;Title: Amplification and sequencing of mRNA encoding acidic fibroblast gro
A;Reference number: JH0476; MJD:92062117; PMID:1719973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GNYKKPKILIYCSNGGH---FIRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 LQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 LPLGNYKKPYLLYCSNGGY---FLRILPDGTVDGTKDRSDQHIQLQLCAESIGEVYLKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Cross-references: EMBL:X60317; NID:g1873; PIDN:CAA42869.1; PID:g1874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.0%; Score 144.5; DB 1; Length 1 ilarity 35.0%; Pred. No. 0.00012; Conservative 12; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.9%; Score 143.5; DB 2; Length 33.6%; Pred. No. 0.00014; ive 12; Mismatches 64; Indels
                                                 sidues 18-27) and bovine substance P beta (residues 98-107)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Keywords: growth factor; heparin binding
F;22-28/Region: nuclear location signal
F;133/Binding site: heparin (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibroblast growth factor 7 precursor - rat N;Alternate names: keratinocyte growth factor C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                  A,Introns: 57/1; 91/3
C,Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 APRGPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKLGPRTHFGQKAILFLPLP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 GPAR-----FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPRTHYGOKAILFLPLP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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nes 49; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132
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A; Molecule type: protein
A;Residues: YX, 33-44 «RUB»
A;Residues: YX, 33-44 «RUB»
A;Residues: YX, 33-44 «RUB»
A;Residues: YX, 33-44 «RUB»
B;Relley, M.J.; Pech, M.; Seuanez, H.N.; Rubin, J.S.; O'Brien, S.J.; Aaronson, S.A.
B;Relley, M.J.; Pech, M.; Seuanez, H.N.; Rubin, J.S.; O'Brien, S.J.; Aaronson, S.A.
A;Reiley, M.J.; Red. Sci. U.S.A. 89, 9287-9221, 1992
A;Title: Emergence of the Keratinocyte growth factor multigene family during the great A;Reference number: A46289; MUID:93028449; PMID:1409637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: sequence extracted from NCBI backbone (NCBIN:115887, NCBIP:115889)
R; Aaronson, S.A.; Bottaro, D.P.; Miki, T.; Ron, D.; Finch, P.W.; Fleming, T.P.; Ahn, J.,
Ann, N. Y. Acad. Sci. 638, 62-77, 1991
A; Title: Keratinocyte growth factor. A fibroblast growth factor family member with unuss
A; Reference number: 151958; MUID:92152720; PMID:1664700
                                                       A;Accession: A36301
A;Molecule type: mRNA
A;Residues: 1-194 <FIN>
A;Residues: 1-194 <FIN>
A;Cross-references: GB:M60828; NID:gl86738; PIDN:AAA63210.1; PID:gl86739; GB:M25295
A;Cross-references: GB:M60828; NID:gl86738; PIDN:AAA63210.1; PID:gl86739; GB:M25295
B;Rubin, J.S.; Osada, H.; Finch, P.W.; Taylor, W.G.; Rudikoff, S.; Aaronson, S.A.
Broc. Natl. Acad. Sci. US.A. 86; 802-8866; 1989
A;Title: Purification and characterization of a newly identified growth factor specific A;Reference number: A31453; MUID:89128865; PMID:2915979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense mRNA
A;Title: Human KGF is FGF-related with properties of a paracrine effector of epithelial
A;Reference number: A36301; MUID:89368897; PMID:2475908
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A;Note: the human genome contains about 16, intron-containing, partial copies C;Superfamily: fibroblast growth factor
C;Keywords: extracellular protein; growth factor; heparin binding; mitogen F;1-31/Domain: signal sequence #status predicted <81G>
F;1-31/Domain: signal sequence #status predicted <81G>
F;1-31/Domain: signal sequence factor 7 #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB:S81661; NID:9245438; PIDN:AAB21431.1; PID:9245439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 RFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.5%; Score 139; DB 1; ilarity 26.8%; Pred. No. 0.00042; Conservative 31; Mismatches 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GDB:131444; OMIM:148180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPGNKSPHRDPAPRGPARFLPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         basic fibroblast growth factor - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 --Ġĸĸткквокт----Àн̀̀ть́м 191
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A;Molecule type: nucleic acid
A;Residues: 1-189 < 800.
A;Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 97-194 < KEL>
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les 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: I51958
                                                                                                                                                                                                                                                                                                  A; Accession: A31453
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Matches
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C;Species: Mus musculus (house mouse)
C;Date: 02-Unl-1996 #sequence_revision 02-Unl-1996 #text_change 16-Jul-1999
C;Accession: 148610; S3327
R;Mason, I.J.; Fuller-Pace, F.; Smith, R.; Dickson, C.
Mcch. Dev. 45, 15-30, 1994
A;Title: FGF-7 (keratinocyte growth factor) expression during mouse development suggests
A;Reference number: 148610; MUID:94242659; FMID:8186145
A;Accession: 148610
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 28-Mar-1991 #sequence revision 07-Jul-1995 #text_change 08-Dec-2000 C;Accession: A36301; A345289; I51958
R;Finch, P. M.; Rubin, J.S.; Miki, T.; Ron, D.; Aaronson, S.A. Science 245, 752-755, 1989
      20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
                              CyAccession: S49501
RyMitchell, J.B.A.; McImnes, C.J.
Bubmitted to the EMBL Data Library, October 1994
A;Description: Cloning of a cDNA encoding ovine keratinocyte growth factor.
A;Reference number: S49501
A;Stecus: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-194
A;Cross-references: EMBL:Z46236; NID:g559503; PIDN:CAA86306.1; PID:g559504
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-194 <RES>
A;Cross-references: EMBL:222703; NID:g297755; PIDN:CAA80403.1; PID:g297756
C;Superfamily: fibroblast growth factor
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                                                                                                                                                                                                                                                                                                                                                                                    12.7%; Score 141; DB 2; Length 194; ilarity 26.8%; Pred. No. 0.00029; Conservative 32; Mismatches 46; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 RFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
12.6%; Score 140; DB 2;
Best Local Similarity 26.8%; Pred. No. 0.00035;
Matches 38; Conservative 31; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 RFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYQS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibroblast growth factor 7 precursor [validated]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 LPGNKSPHRDPAPRGPARFLPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 LPGNKSPHRDPAPRGPARFLPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GKKTKKEOKT----AHFLPM 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKGKKTKKEQKT----AHFLPM 191
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174
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acidic fibroblast growth factor - chicken
NyAlternate names: endothelial cell growth factor
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus S02639
Rischmuerch, H.; Risau, W.
Development 111, 1143-1154, 1991
A;title: Differentiating and mature neurons express the acidic fibroblast growth factor cispecies number: A60130; MUID:91347925; PMID:1715259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: mRNA
A;Residues: 1-155 c8CH>
A;Cross-references: G8.563263; NID:g234372; PIDN:AAB19629.1; PID:g234373
A;Cross-references: G8.563263; NID:g234372; PIDN:AAB19629.1; PID:g234373
B;Risau, W.; Gautschi-Sova, P.; Boehlen, P.
EMBO 7. 7, 959-962, 1988
A;Title: Endothelial cell growth factors in embryonic and adult chick brain are related thickerence number: 802639; MUID:88296438; PMID:3402441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 39
S31622
basic fibroblast growth factor - short-tailed opossum (Monodelphis domestica) (fragment)
C;Species: Monodelphis domestica
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C;Accession: S31622
                                                                                                                C;Comment: This protein is a potent mitogenic factor for NIH 3T3 fibroblasts in the absen
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 KTSRFLCORPDGALYGSLHFDPEACSFRELLLEDGYNVYOSEAHGLP---LHLPGNKSPH 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                               38 LOFGGOVRORYLYTDDAQOTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 LQFGGQVRQRYLYTDDAQQTEAHLEIREDGTVGGAADQSPESL-LQLKALKPGVIQILGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LPLGNYKKPKLLYCSNGGH---FLRILPDGKVDGTRDRSDQHIQLQLSAEDVGEVXIKST
                                                                                                                                                                                                                                                                                                                                                                                          18 LPLGNYKKPKLLYCSNGGY---FLRILPDGRVDGTKDRSDQHIQLQLYAESIGEVYIKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                            11; Gaps
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11.5%; Score 127.5; DB 2; Length 155;
Best Local Similarity 32.6%; Pred. No. 0.0027;
Matches 45; Conservative 15; Mismatches 67; Indels 11
                                                                                                                                                                                                           Length 155;
                                                                                                                                                                                                                                                                            Indels
A,Reference number: JW0055; MUID:98262939; PMID:9600090
A,Accession: JW0055
A;Molecule type: mRNA
A;Residues: 1-155 <GRI>
                                                                                                                                                                                                                 Score 131.5; DB 2;
Pred. No. 0.0013;
4; Mismatches 67;
                                                                                                                                                                                                                                                                            14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 22-30,'X',32-44,'X',46-48 <RIS>
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 SPHRDPAPRGPARFLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 LGPRTHYGOKAILFLPLP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 RDPAPRGPAR---FLPLP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 LGPRTHFGOKALLFLPLP 151
                                                                                                                                                                                                                       11.8%;
33.3%;
                                                                                                                                                                                                                                                Best Local Similarity 33.3%
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A60130
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                                                                                                                                                                                                                          Query Match
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-Jan-2001
C;Accession: JW055
R;Grieb. T.W.; Ring, M.; Brown, E.; Palmer, C.; Belle, N.; Donjerkovic, D.; Chang, H.; Y
Biochem. Biophys. Res. Commun. 246, 182-191, 1998
A;Title: Primary structure of ovine fibroblast growth factor-1 deduced by protein and cD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RiKimelman, D.; Kirschner, M.
18611 51, 869-877, 1987
Aritle: Synergistic induction of mesoderm by FGF and TGF-beta and the identification of
A;Reference number: A29618; MUID:88052890; PMID:3479265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  natural
   A;Note: sequence extracted from NCBI backbone (NCBIN:131000, NCBIP:131001)
R;Mitrani, E.; Gruenbaum, Y.; Shohat, H.; Ziv, T.
Development 109, 387-393, 1990
A;Title: Fibroblast growth factor during mesoderm induction in the early chick embryo. A;Reference number: S23636, MUID:90382254; PMID:2401202
A;Accession: S23636
A;Accession: S23636
A;Accession: Uppeliminary
A;Accession: S23636
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 95-128 <ANT>
A;Residues: 95-128 <ANT>
A;Cross-references: EMBL:X56804; NID:g62855; PIDN:CNA40139.1; PID:g62856
C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-155 <KIM>
A;Cross-references: GB:M18067; NID:g214177; PIDN:AAA49726.1; PID:g214178; GB:M21092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             basic fibroblast growth factor - African clawed frog
C;Species: Xenopus lacvis (African clawed frog)
C;Species: Xenopus lacvis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A40117; A25618
R;Kimelman, D.; Abraham, J.A.; Haaparanta, T.; Palisi, T.M.; Kirschner, M.W.
Science 242, 1053-1056, 1988
A;Title: The presence of fibroblast growth factor in the frog egg: its role as a 1 A;Reference number: A40117; MUD:89058621; PMID:3194757
A;Starus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LEIREDGTVGGAADQS-PESILQIKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 ACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPR-GPAR----FLPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 ECFFFERLESNNYNTYRSRKYS-DWYVALKRTGQXKPGPKTGPGOKALLELPEPM 185
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.4%; Score 138; DB 2; Length 189; Best Local Similarity 35.4%; Pred. No. 0.0005; Matches 40; Conservative 18; Mismatches 47; Indels
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A,Residues: 95-110,112-155 <KI2>
C,Superfamily: fibroblast growth factor
C,Keywords: growth factor
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Best Local Similarity
Matches 38; Conserv
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R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A;5000; MUID:99065613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: H88481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: GB:chr_III; PIDN:AAB53825.1; PID:g485091; GSPDB:GN00021; CESP:C05D1
R;Kusewitt, D.F.; Sabourin, C.L.K.; Budge, C.L.; Ley, R.D. submitted to the EMBL Data Library, September 1992
A;Description: Characterization of cDNA encoding basic fibroblast growth factor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 LRIHPDGRVDGIREKSDPNIKLQLQAEERGVVSIKGVCANRYLAMKEDGRLL-ALKYVTE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 YLYTDDAQQTEAHLEIREDGTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 GALYG--SIHFDPEACSFRELLLEDGYNVYQSEAHG---LPLHLPGNKS--PHRDP---A 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein let-756 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H88481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DSDETG-----FEHSGLWVSVLAGLLLGACOAHPI--PDSSPLLQFGGQVRQR
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-164 < KUS>
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                                                                                         A; Reference number: S31622
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Gene: let-756
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Sequence 24235, A
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3, Appli
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32717, A
23226, A
27502, A
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(without alignments)
288.145 Million cell updates/sec
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6: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-18109
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Maximum Match 100%
Listing first 45 summaries
                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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100.0%; Score 89; DB 4; Length 181; 100.0%; Pred. No. 5.1e-06; ative 0; Mismatches 0; Indels

Query Match Best Local Similarity 100. Matches 15; Conservative

JS-09-390-207-5

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US-09-390-207-2

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; Sequence 2, Application US/09390207
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVERTION Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0

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Query Match 100.0%; Score 89; DB 4; Length 209; Best Local Similarity 100.0%; Pred. No. 5.9e-06; Matches 15; Conservative 0; Mismatches 0; Indels

SEQ ID NO 2 LENGTH: 209 TYPE: PRT ORGANISM: Homo sapiens

US-09-390-207-2

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| 48.3 410 1 US-08-123-343A-7 Sequence 7, 48.3 410 3 US-09-431-573-4 Sequence 5, 48.3 410 3 US-09-431-573-5 Sequence 5, 48.3 420 4 US-09-431-573-5 Sequence 50. 48.3 586 4 US-09-252-991A-28601 Sequence 28. 48.3 586 4 US-09-252-991A-1250 Sequence 28. 48.3 586 4 US-09-252-991A-1250 Sequence 28. 48.3 586 4 US-09-252-991A-25003 Sequence 25. 48.3 656 4 US-09-252-991A-25003 Sequence 25. | 38 | 43 | 48.3 | 410 | ч | US-08-123-343A-5 | |
| 48.3 410 3 US-09-431-573-4 Sequence 4, 48.3 410 3 US-09-431-573-5 Sequence 5, 48.3 410 3 US-09-252-991A-30229 Sequence 5, 48.3 586 4 US-09-252-991A-28601 Sequence 28, 48.3 586 4 US-09-252-991A-28601 Sequence 28, 48.3 586 4 US-09-252-991A-28603 Sequence 28, 48.3 656 4 US-09-252-991A-25003 Sequence 27, 48.3 656 4 US-09-252-991A-25003 Sequence 27, 48.3 656 4 US-09-252-991A-25003 Sequence 27, 48.3 656 4 US-09-252-991A-25003 Sequence 28, 28.3 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0.2 | 39 | 43 | 48.3 | 410 | rd | US-08-123-343A-7 | ۲, |
| 48.3 410 3 US-09-431-555 Sequence 5, 48.3 410 3 US-09-431-555 Sequence 5, 48.3 520 4 US-09-252-991A-3029 Sequence 30. 48.3 599 4 US-09-252-991A-28601 Sequence 173 48.3 599 4 US-09-252-991A-17250 Sequence 173 48.3 599 4 US-09-252-991A-25003 Sequence 273 48.3 656 4 US-09-252-991A-25003 Sequence 275 MATCON: ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS CE: 99-37 CTATION NUMBER: US/09/390,207 Q ID NOS: 41 tentIn Ver. 2.0 ome sapiens | 40 | 43 | 48.3 | 410 | e | US-09-431-573-4 | 4, |
| 48.3 420 4 US-09-252-991A-30229 Sequence 30: 48.3 586 4 US-09-252-991A-28601 Sequence 28: 48.3 586 4 US-09-252-991A-17250 Sequence 28: 48.3 656 4 US-09-252-991A-17250 Sequence 28: 48.3 656 4 US-09-252-991A-25003 Sequence 25: 64.530 MATION: ALIGNMENTS ALIGNM | 41 | 43 | 48.3 | 410 | m | US-09-431-573-5 | 'n |
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| 48.3 599 4 US-09-252-991A-17250 Sequence 177 48.3 656 4 US-09-252-991A-25003 Sequence 2504530 Marton: pplication US/09390207 ALIGNMENTS MATION: bomason, Arlen tu, Benxian ENTION: Fibroblast Growth Factor-Like Polypeptides CE: 99-371 CTATION NUMBER: US/09/390,207 Q ID NOS: 41 tentIn Ver. 2.0 | 43 | 43 | 48.3 | 586 | 4 | US-09-252-991A-28601 | 28 |
| 48.3 656 4 US-09-252-991A-25003 Sequence 255 pplication US/09390207 04530 MATION: homson, Arlen iu, Benxian ENTION: Fibroblast Growth Factor-Like Polypeptides CE: 99-371 ICATION NUMBER: US/09/390,207 Q ID NOS: 41 tentIn Ver. 2.0 | 44 | 43 | | 599 | 4 | US-09-252-991A-17250 | 17 |
| RESULT 1 Sequence 5, Application US/09390207 Sequence 5, Application US/09390207 Patent No. 6504530 GENERAL INFORMATION: APPLICANT: Thomeson, Arlen APPLICANT: Liu, Benxian TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides CURRENT APPLICATION NUMBER: US/09/390,207 CURRENT PILING DATE: 1999-09-07 NUMBER OF SEQ ID NOS: 41 SOFTWARE: PatentIN Ver. 2.0 SEQ ID NO 5 LENGTH: 181 TYPE: PRT TYPE: PRT TYPE: PRT | 45 | 43 | | 929 | 4 | US-09-252-991A-25003 | 25 |
| RESULT I RESULT 1 VG-09-390-207-5 Sequence 5, Application US/09390207 Patent No. 6504530 GENERAL INFORMATION: APPLICANT: Liu, Benxian TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides FILE REFERENCE: 99-371 CURRENT APPLICATION NUMBER: US/09/390,207 CURRENT PILING DATE: 1999-09-07 NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5 IENGTH: 181 TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT | | | | | | | |
| Sequence 5, Application US/09390207 Patent No. 6504530 Patent No. 65 | RESULT 1 | -207-5 | | | | | |
| Fatent No. 6504530 GENERAL INFORMATION. APPLICANT: Thomason, Arlen TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides TITLE OF INVENTION: Pibroblast Growth Factor-Like Polypeptides TITLE OF INVENTION: Pibroblast Growth Factor-Like Polypeptides CURRENT APPLICATION NUMBER: US/09/390,207 CURRENT FILING DATE: 1999-09-07 NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5 IENGTH: 181 TYPE: PRT TYPE: PRT | Sequence | e 5, A | pplicati | On US/ | 093 | 90207 | |
| GENERAL INFORMATION: APPLICANT: Thomason, Arlen APPLICANT: Thomason, Arlen TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides FILE REPERENCE: 99-371 CURRENT APPLICATION NUMBER: US/09/390,207 CURRENT APPLICATION NUMBER: 1999-09-07 NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5 ILENGTH: 181 TYPE: PRT TYPE: PRT TYPE: PRT | ; Patent | No. 65 | 04530 | | | | |
| APPLICANT: Thomason, Arlen APPLICANT: Thomason, Arlen APPLICANT: Liu, Benxian TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides FILS REFERENCE: 99-371 CURRENT APPLICATION NUMBER: US/09/390,207 CURRENT FILING DATE: 1999-09-07 NUMBER OF SEQ ID NOS: 41 SOFTWARE PATENTIN Ver. 2.0 SOFTWARE PATENTIN Ver. 2.0 SEQ ID NO 5 LENGTH: 181 TYPE: PAT TYPE: PAT CORGANISM: Home sapiens | GENERAL | INFOR | MATION: | | | | |
| APPLICANT: Liu, Benxian TITLE OF INVENTION: Fairoblast Growth Factor-Like Polypeptides TITLE OF INVENTION: Fairoblast Growth Factor-Like Polypeptides FILE REFERENCE: 99-371 CURRENT APPLICATION NUMBER: US/09/390,207 CURRENT FILING DATE: 1999-09-07 NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5 LENGTH: 181 TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT | APPLIC | ANT: T | homason, | Arlen | _ | | |
| ; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides ; FILE REFERENCE: 99-371 ; CURRENT APPLICATION NUMBER: 1999-09-07 ; CURRENT FILING DATE: 1999-09-07 ; NUMBER OF SEQ ID NOS: 41 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 5 ; LENGTH: 181 ; TYPE: PRT ; TYPE: PRT ; COGANISM: Homo sapiens | , APPLIC | ANT: L | iu, Benx | cian | | | |
| ; FILE REFERENCE: 99-371 ; CURRENT APPLICATION NUMBER: US/09/390,207 ; CURRENT FILING DATE: 1999-09-07 ; NUMBER OF SEQ ID NOS: 41 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 5 ; LENGTH: 181 ; TYPE: PAT ; CRAMISM: Homo sapiens | TITLE | OF INV | ENTION: | Fibrob | las | t Growth Factor-Like Poly | peptides |
| CURRENT APPLICATION NUMBER: US/09/390,207 CURRENT FILING DATE: 1999-09-07 NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin Ver: 2.0 SEQ ID NO 5 LENGTH: 181 TYPE: PRT CREAKISM: Homo sapiens | ; FILB R. | EFEREN | CE: 99-3 | 171 | | | |
| LING DATE: 1999-09 SEQ ID NOS: 41 Patentin Ver. 2.0 81 Homo sapiens | CURREN | T APPL | ICATION | NUMBER | P :: | 8/09/390,207 | |
| SEQ ID NOS: 41 PatentIn Ver. 81 Homo sapiens | ; CURREN | T FILI | NG DATE: | 1999- | -60 | 07 | |
| Patentin Ver. 81 Homo sapiens | , NUMBER | OF SE | SON CI O | : 41 | | | |
| ; SEQ ID NO 5 ; LENGTH: 181 ; TYPE: PRT ; ORGANISM: Homo sapiens | SOFTWA | RE: Pa | tentIn V | 'er. 2. | 0 | | |
| ; LENGTH: 181 ; TYPE: PRT ; ORGANISM: Homo sapiens | SEQ ID | NO 5 | | | | | |
| ; TYPE: PRT ; ORGANISM: Homo sapiens | FLENGT | H: 181 | | | | | |
| ; ORGANISM: Homo sapiens | ; TYPE: | PRT | | | | | |
| | ; ORGAN | ISM: H | omo sapi | ens | | | |

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Sequence 21588, Application US/09252991A

Sequence 21588, Application US/09252991A

Sequence 21588, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILLE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 33142
      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196,136

FILE REFERENCE: 107196,136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18109

LENGTH: 187
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,136

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29952

LENGTH: 286
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57.3%; Score 51; DB 4; Length 187;
Best Local Similarity 57.1%; Pred. No. 2.2;
Matches 8; Conservative 1; Mismatches 5; Indels
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Patent No. 6551795
Marc J. Rubenfield et al
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-21588
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US-09-252-991A-29952
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APPLICANT:
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US-09-522-991A-22856

j Sequence 22856, Application US/09252991A

patent No. 6551795

general information:
    APPLICATION:
    APPL
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Pred. No. 2.5;
0; Mismatches 5; Indels
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; Patent No. 6551795
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 66.7°
Matches 10; Conservative
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Gendence 14335, Application US/09252991A

Sequence 24325, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERBANCE:

TORRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

IBROTH: 632
                                                                                                       Sequence 23280 Application US/09252991A

Sequence 23280 Application US/09252991A

Sequence 23280 Application US/09252991A

Sequence 23280 Application US/09252991A

Sequence 23280 Application US/09252991A

TITLE OF INVENTION: AUGUST CACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AUGUST CACID AND THERAPEUTICS

TITLE OF INVENTION: AUGUST CACID AND THERAPEUTICS

TITLE OF INVENTION: AUGUST CACID AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
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Pred. No. 60;
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Patent No. 5955652
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 HLPDRAHPRRRPAPQ 373
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Best Local Similarity 55...
Best Accountable 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ecker, Joseph
Alonso, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 53.3
Matches 8; Conservative
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81 PGGRATHPDPAP 92
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US-09-252-991A-24235
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US-09-252-991A-30648

Sequence 30648, Application US/09252991A

Sequence 30648, Application US/09252991A

Setent NO. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: MALCIA ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 209

LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25664
LENGTH: 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 4; Length 330; Pred. No. 23;
                                                                                                                                        Score 46; DB 4; Length 307; Pred. No. 21;
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                                                                                                                                                                                             2; Mismatches
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ORGANISM: Pseudomonas aeruginosa
                                                         TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                             Query Match 51.7%;
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                        100 PGDRPPGRRPAPR 112
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Best Local Similarity
7, Conserv
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US-09-252-991A-25664
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              ; SEQ ID NO 21588
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3 PGNKSPHRDPAP 14

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UPN-2949
         NAME: Beardell, L.-.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-310
TELEPHONE: 215-568-343
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 11294 amino acids
TYPE: ... linear
Beardell, Lori Y.
                                                                                                                                                                                                                                                                                         50.6%;
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Best Local Similarity 61.53
Matches 8; Conservative
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Best Local Similarity 61.5
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                                                                                                                                                                                                     TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-400-348-3
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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USA
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ANTI-SENSE: NO
US-08-261-822A-3
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COUNTRY: US
ZIP: 19103
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APPLICANT: Ecker, Joseph
APPLICANT: ALONS, JOSE
TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE
TITLE OF INVENTION: AND PATHOGENS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6355778ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                 NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5955652ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                           PLANT GENES FOR SENSITIVITY TO ETHYLENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 2; Length 1294; Pred. No. 1.4e+02;
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                                                                                                                                                                                               ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/819,288
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                               AND PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/09400348
; Patent No. 6355778
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34, 293
REPRENCE/DOCKET NUMBER: UPN-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear; MOLECULE TYPE: protein US-08-819-288-3
                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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US-09-400-348-3
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Sequence 3, Application US/08261822A
Sequence 3. Application US/0826182A
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCES. 82
CORRESPONDENCE ADDRESS.
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
CITTLE Philadelphia
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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Score 45; DB 4; Length 1294;
Pred. No. 1.4e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REALABLE FORD

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,822A
FILLING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34.293
TELEPONE: (215) 568-3100
TELEPONE: (215) 568-3100
TELEPAN: (215) 568-3100
TELEPAN: (215) 568-3100
TELEPAN: (215) 568-3100
SEQUENCE CHARACTERISTICS:
                                                      2; Mismatches
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Sequence 27502, Application US/09252991A

Sequence 27502, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-17

PRIOR FILING DATE: 1998-07-27

WOMBER OF SEQ ID NOS: 33142

LENGTH: 441
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                  DB 4; Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                               Indels
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1; Mismatches
                                                             Query Match

50.0%; Score 44.5; D

Best Local Similarity 56.2%; Pred. No. 43;

Matches 9; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                         Sequence 23226, Application US/09252991A Patent No. 6551795
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141 HLPGADRRHLHRAPHQRPAGR 161
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Pseudomonas aeruginosa
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32717
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216 PGGEDPHRRPRGPAPR 231
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                                                                                                                                                                3 PGNKSPH----RDPAPR 15
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Best Local Similarity 56.2'
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Best Local Similarity
Matches 9; Conserv
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US-09-252-991A-23226
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
APPLICANT: MAC J. RUBENFICH.
APPLICANT: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3217
ILENGTH: 372
TYPE: PRT
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                                                                                                                      APPLICANT: Trustees of The University of Pennsylvania TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene TITLE OF INVENTION: and Pathogens WUMBER OF SEQUENCES: 82 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07744A
FILING DATE: 15-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.6%; Score 45; DB 5; Le:
Best Local Similarity 61.5%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32717, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,822
FILLING DATE: June 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
NAME: Beardell, Lori Y.
TELECHATION NUMBER: 34,293
TELECHATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFRAX: (215) 568-349
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                           PCT-US95-07744A-3; Sequence 3, Application PC/TUS9507744A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1321 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 939 HLPNNKSGYWDPS 951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-32717
                                                                                                                                                                                                                                                                                                                                                                     19103
                                                                                                                                                                                                                                                                                                   CITY: Phil
STATE: PA
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                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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APPLICANT: LADNER, MARTHA B.
APPLICANT: LADNER, MARTHA B.
APPLICANT: MARTHIN, GEORGE A.
APPLICANT: MARTHIN, GEORGE A.
APPLICANT: CONNE, MAZEL YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING PACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
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Pred. No. 77;
2; Mismatches 3; Indels
                                                      Score 44; DB 1; Length 552;
Pred. No. 77;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FRADABLE FORM:
MEDILIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/999,280A
FILING DATE: 28-DEC-1992
CLASSIFICATION: 435-C1992
ATTORNEY AGENT INFORMATION:
NAME: MGGATTIGLE UT., Philip L.
REFERENCE/DOCKET NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.007
TELECOMMUNICATION NUMBER: 0681.007
                                                                                                                                                                                                                                                                            ; Sequence 24, Application US/07999280A; Patent No. 5573930; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 22, Application US/08426279; Patent No. 5672343; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LADNER, MARTHA B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
                                                            Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 552 amino acids
amino acid
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Best Local Similarity 58.3
Matches 7; Conservative
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, MOLECULE TYPE: protein US-07-999-280A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Emveryville STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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ZIP: 94662-8097
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US-08-426-279-22
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                                               Sequence 8325, Application US/09489039A

Sequence 8325, Application US/09489039A

Sequence 8325, Application US/09489039A

Patent No. 66108DA

Patent No. 66108DA

APPLICANT:
Patent OF INVENTION:
APPLICANTION:
APPLICANTION:
APPLICANTION:
FILE REFERENCE: 2709.2004001

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-27

PRIOR PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8325

LENTH: 490
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APPLICANT: LADNER, MARTHA B.
APPLICANT: LADNER, DANELLE A.
APPLICANT: MARTHI, GEORGE A.
APPLICANT: MARTHI, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: KOTHS, KIRSTON E.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
                                                                                                                                                                                                                                                                                                                                                                                                                              49.4%; Score 44; DB 4; Length 490; 46.7%; Pred. No. 68; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Intellectual Property - R440, P.O. Box 8097
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Patent No. 5573930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (510) 601-2718
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: n/a
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Emveryville STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                US-09-489-039A-8325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 20
US-07-999-280A-22
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Gaps

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US-08-401-013-22

J Sequence 2.2, Application US/08401013

Patent No. 5681719

GENERAL INFORMATION:

APPLICANT: LANDER, WARTHA B.

APPLICANT: MARTHY, GEORGE A.

APPLICANT: AMASAKI ERNEST S.

APPLICANT: KOYNE, WALE YEE

APPLICANT: KOYNE, WALE YEE

APPLICANT: KOYNE, WALE YEE

APPLICANT: ACONNE, WALE YEE

APPLICANT: ACONNE, WALE YEE

APPLICANT: ACONNE, WALE YEE

APPLICANT: ACONNE, WALE YEE

APPLICANT: ACONNE, WALE YEE

APPLICANT: ACONNE, WALE YEE

APPLICANT: ADDRESS:

ADDRESSEE: CHIKON CORPORATION

STREET: INCELLECTUAL PROPERTY - R440, P.O. BOX 8097

CUTY: EMVERYALINE STATE

COUNTY: U.S.A.

ZIP: 94662-8097

COMPUTER: LIMP CCOMPATIBLE

CONFUTER: LIMP CCOMPATIBLE

CONFUTER: LIMP CCOMPATIBLE

CONFUTER: LIMP CCOMPATIBLE

CONFUTER: DATEATION ATTA:

APPLICATION WHERE: US/08/401,013

FILING DATE: 28-DEC-1992

ATTORNEY/AGENT: UNCARFE: US 07/999,280

FILING DATE: 28-DEC-1992

ATTORNEY/AGENT: NUCHER: US 07/999,280

FILING DATE: LOWNER: 13,395

REGISTRATION NUMBER: 31,395

REGISTRATION NUMBER: 13,395

REGISTRATION NUMBER: 13,395

REGISTRATION NUMBER: 13,395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,279
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: MCGARTIGN G. Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 31,395
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (510) 601-2718
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TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: n/a
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                            TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
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202 PASASPHQPPAP 213
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 24
US-08-401-013-22
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| Sequence 24, Application US/08426279 |
| Patent No. 5672343 |
| GENERAL INFORMATION |
| APPLICANT: NOBLE, JANELLE A. |
| APPLICANT: MASTRIN, GEORGE A. |
| APPLICANT: MASSAKI ERNEST S. |
| APPLICANT: COYNE, MAZIE YEE |
| APPLICANT: KOTHE, KIRSTON E. |
| APPLICANT: KOTHE, KIRSTON E. |
| TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1 |
| NUMBER OF SEQUENCES: 24 |
| NUMBER OF SEQUENCES: 24 |
| STREET: Intellectual Property - R440, P.O. Box 8097 |
| STREET: Intellectual Property - R440, P.O. Box 8097
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KORABARI, ENDEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: MAZIE YEE
TITLE OF INVENTION: UNF FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON COURSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                 STREET: Intellectua.

STREET: Emveryville

CITY: Emveryville

COMPUTER: California

COMPUTER: U.S.A.

ZIP: 94662-8097

COMPUTER: Plopy disk

COMPUTER: PROMABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: DAD COMPATIBLE

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRIY APPLICATION NUMBER: US/08/426,279

FILING DATE: 21-APR-1995

CLASSIFICATION: 530

ATTORNEY/AGART INFORMATION:

NAME: McGarrigle Jr., Philip L.

REGISTRATION NUMBER: 0681.013

TELECOMMUNICATION INFORMATION:

TELEFANORE: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOLIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (510) 655-3542
TELEEX: n/a
INFORMATION FOR EXD ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 552 amino acida
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : |||: |||
202 PASASPHQPPAP 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Emveryville STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 23
US-08-426-279-24
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TOPOLOGY:
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US-08-426-570-24
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.4%; Score 44; DB 1; Length 552; 58.3%; Pred. No. 77; 3; Indels :ive 2; Mismatches 3; Indels
                                                                                                                                                                                                          Score 44; DB 1; Length 552;
Pred. No. 77;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Intellectual Property - R440, P.O. Box 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,013
FILING DATE: 08-MAR-1995
CLASSIFICATION NUMBER: US 07/999,280
FILING DATE: 28-MAR-1995
ATFORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 31,395
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
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APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAMASAKI, ERNEST S.
APPLICANT: CONNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/08401013
Patent No. 5681719
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 552 amino acids
amino acid
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202 PASASPHQPPAP 213
                             LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PGNKSPHRDPAP 14
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SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acid
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                                                                                                                                                                                                                                                                                                                                               3 PGNKSPHRDPAP 14
                                                                                                                  , MOLECULE TYPE: protein US-08-401-013-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Enveryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-401-013-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-401-013-24
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Gaps
                                                                      APPLICANT: NOBLE, GEORGE A.
APPLICANT: MARIIN, GEORGE A.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: COYNE, MAZIE YEE
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: WITHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1.
NUMBER OF SEQUENCES: 24
NUMBER OF SEQUENCES: 24
NUMBER OF SIGNEMESS:
ADDRESSEE: CHIRON CORPORATION
CTREET: Intellectual Property - R440, P.O. BOX 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.4%; Score 44; DB 3; Length 552; 58.3%; Pred. No. 77; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: CHIRON CORPORATION
Intellectual Property - R440, P.O. Box 8097
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 94662-98097
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEALTH Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,570
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0681.012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/08426570 Patent No. 6103224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LADNER, WARTHA B.
APPLICANT: NOBLE, JAMELIA A.
APPLICANT: NOBLE, JAMELIA A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: CAWASAKI, ERNEST S.
APPLICANT: CAWASAKI, ERNEST S.
APPLICANT: KAWASAKI, RUBER YE
APPLICANT: KOTHS, KIRSTON E.
Sequence 22, Application US/08426570 Patent No. 6103224
                                                 GENERAL INFORMATION:
APPLICANT: LADNER, JANELLE A.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: KAWAGAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 552 amino acids
amino acid
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202 PASASPHQPPAP 213
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Best Local Similarity 58.3
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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APPLICANT: NOBLE, JANELLE A.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: CANASAKI, ERNEST S.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: KAWASAKI, ERNEST F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CANDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
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49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                       DB 3; Length 552; 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Intellectual Property - R440, P.O. Box 809
CITY: Enveryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,876
FILING DATE: 21-APR-1995
FILING DATE: 21-APR-1995
                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.011
TELEPHONE: (510) 601-2718
TELEPHONE: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/08425876
Patent No. 6117422
GENERAL INFORMATION:
                                                                      22:
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
(510) 601-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acide
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 PASASPHOPPAP 213
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TELEX: n/a
INFORMATION FOR SEQ ID NO:
                         (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                 202 PASASPHQPPAP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , TOPOLOGY: linear
, MOLECULE TYPE: protein
US-08-425-876-24
                           TELEFAX: (510) 655-354
TELEX: n/a
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                           3 PGNKSPHRDPAP 14
                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-425-876-22
     TELEPHONE:
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APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON B.
APPLICANT: KOTHS, KIRSTON B.
APPLICANT: KOTHS, CAPPESS: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Enweryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE PORM:
MEDILUM TYDE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-COS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,876
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 3; Length 552;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                         COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,570
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTONEY/AGENT INFORMATION:
NAME: MCGATTIGLE UT., Philip L.
REGISTRATION NUMBER: 31,395
REGISTRATION NUMBER: 31,395
REFREENCE/DOCKET NUMBER: 31,395
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000-2718
TELECOMMUNICATION 1000-2718
TELEFRAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/08425876
Patent No. 6117422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (510) 655-3542
TELEX: n/A
INFORMATION FOR EQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 552 amino acids
amino acid
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PGNKSPHRDPAP 14
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                    Emveryville
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                   RY: U.S.A.
94662-8097
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                                                                        COUNTRY:
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NEW FORMS OF COLONY STIMULATING FACTOR-1
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         NUMBER OF SECURISES:
ADDRESSE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
STREET: Enveryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
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ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emveryuille
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2, Mismatches
                                                                                                                                                                                                                                                                      SOFTWAKE: FEGERALIN RELEGGE #1.0, VET CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/999,280
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: MGGARTIGLE Ur., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.007
FELECOMMUNICATION INFORMATION:
THERCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTH, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-401-632-22; Sequence 22, Application US/08401632; Patent No. 6204020; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELGEAX: (5Lv,
TELBFAX: n/a
TELEFAX: n/a
; INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
"VPE: amino acid
"TPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.4%;
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 58.3
Matches 7; Conservative
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NUMBER OF SEQUENCES:
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                                                                                  gequence 22, Application US/08426243

parent No. 6146851

GENERAL INFORMATION.

APPLICANT: LADNER, MARTHA B.

APPLICANT: MARTIN, GEORGE A.

APPLICANT: KAMASAKI, ENGST S.

APPLICANT: KAMASAKI, ENGST S.

APPLICANT: COYNE, MALTH YEE

APPLICANT: KOTHE, YEE

TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ANDRESS:
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TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.4%; Score 44; DB 3; Length 552; 58.3%; Pred. No. 77;
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                                                                                                                                                                                                                                                                                                                                                                                    E: CHIRON CORPORATION Intellectual Property - R440, P.O. Box 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM THE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE:
COMPUTER: DATE:
COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/999,280
APPLICATION NUMBER: 07/999,280
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
RAME: MCGARTIGLE U., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0691.007
TELECHONE: (510) 601-2118
TELEPHONE: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/08426243
Fatent No. 6146851
GENERAL INFORMATION:
APPLICANT: IADDER, MARTHA B.
APPLICANT: MOBLE, JANELLE A.
APPLICANT: MARTHY, GEORGE A.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: COYNE, MAZIE YEE
APPLICANT: MALBERECK, ROBERT F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 552 amino acids
amino acid
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Best Local Similarity 58.3-
Local 7, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Emveryville STATE: California
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US-08-426-243-24
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                                                         RESULT 30
US-08-426-243-22
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Sequence 22814, Application US/09252991A
Patent No. 6551795
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US-09-252-991A-26118
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Best Local Similarity 53.8%;
Matches 7; Conservative 2
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                                                          3 PGNKSPHRDPAP 14
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US-09-252-991A-22135
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US-09-252-991A-22814
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APPLICANT: NOBLE, JANELLE A.
APPLICANT: NARTHN, GEORGE A.
APPLICANT: KAWASALT, ERREST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: NOTHS, XIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                Score 44; DB 3; Length 552;
Pred. No. 77;
2; Mismatches 3; Indels
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ADDRESSEB: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOUTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,632
FILING DATE: 09-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INPORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.009
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
ZIR: 94662-8097
COMPUTER REALABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/08401632
Patent No. 6204020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                     49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 552 amino acids
amino acid
                                                                                                                                                                                                                                                                                         202 PASASPHOPPAP 213
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                                                                                                                                                                                                                                                                                                                                                                       3 PGNKSPHRDPAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-401-632-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Emveryville : California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-401-632-24
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US-08-401-632-24
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Sequence 2618, Application US/09252991A

Sequence 2618, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 2618

LENGTH: 969
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield STORD AND ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22814
LENGTH: 172
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Query Match

49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels
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1 Similarity 64.7%; Pred. No. 31;
11; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Steller, Hermann
APPLICANT: Abrams, John M.
APPLICANT: Abrams, John M.
APPLICANT: White, Kristin
TITLE OF INVENTION: Cell Death Genes of Drosophila
TITLE OF INVENTION: Melanogaster and Vertebrate Analogs
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: MA
                                                                                                                                                                                                                                MEDIUM TYPE: Floppy Gib.
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,343A
FILING DATE: 17-SEP-1993
CLASSIFICATION: 800
PRIOR APPLICATION 1800
PRIOR APPLICATION PROPER: US/08/04,957
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,343A
FILING DATE: 17-SEP-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,957
   ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08123343A Patent No. 5593879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 48.3
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GNKSPHRDPAP 14
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                                                                                                                                          COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                               Lexington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-123-343A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Sequence 26511, Application US/09252991A | Sequence 26511, Application US/09252991A | Sequence 26511, Application US/09252991A | Patent No. 6551795 | Patent No. 6551795 | Patent No. 6551795 | Seneral INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PRESENCE: 111LE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PRESENCE: 107196-136 | FILE REPRESENCE: 107196-136 | FILE REPRESENCE: 1999-02-18 | SPRIOR APPLICATION NUMBER: US/09/252,991A | CURRENT FILING DATE: 1998-02-18 | PRIOR APPLICATION NUMBER: US 60/094,190 | PRIOR FILING DATE: 1998-07-27 | NUMBER OF SEQ ID NOS: 33142 | SPRIOR APPLICATION NUMBER: US 60/094,190 | PRIOR FILING DATE: 1998-07-27 | NUMBER OF SEQ ID NOS: 33142 | LENGTH: 356
Sequence 22135, Application US/0925291A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: MACT G. RUBenfield et al.
APPLICANT: MACT G. RUBenfield et al.
APPLICANT: MACT G. RUBENFIELD:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

LENGTH: 247
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Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 4; Length 247; Pred. No. 46;
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APPLICANT: Abrams, John M.
APPLICANT: Grether, Megan E.
APPLICANT: White, Kristin
TITLE OF INVENTION: Cell Death Genes of Drosophila
TITLE OF INVENTION: Melanogaster and Vertebrate Analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22135
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Best Local Similarity 53.3%;
Matches 8; Conservative
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Best Local Similarity 61.5'
Matches 8; Conservative
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US-09-252-991A-26571
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; Patent No. 623524
; Patent No. 623524
; GENERAL INFORMATION:
; APPLICANT: STELLER, HERMAN
; APPLICANT: AGAPITE, UULE
; APPLICANT: AGAPITE, UULE
; APPLICANT: BERGMANN, MADREAS
; TITLE OF INVENTION: INHIBIT MAPK MEDIATED ANTI-APOPTOTIC SIGNALS
; TITLE OF INVENTION: INHIBIT MAPK MEDIATED ANTI-APOPTOTIC SIGNALS
; TITLE REFERENCE: INT-04019
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,108
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIN Ver: 2.0
; SEQ ID NO 4
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48.3%; Score 43; DB 1; Length 410;
Best Local Similarity 63.6%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 4; Indels
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Best Local Similarity 63.6%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 4; Indels
FILING DATE: 15-JAN-1993

ATTORNEY/AGENT INFORMATION:
NAME: Granthan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5907A
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
FELEPHONE: 617-861-6240
FELEPRAX: 61861-9540
FELEPRAX: 61861-9540
FELEPRAX: G1861-9540
FELEPRAX: G1861-9540
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US-09-431-573-4
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US-09-431-573-4
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Sequence 33, Application US/09901938
Sequence 33, Application US/09901938
Patent No. US20020156001A1
GENERAL INFORMATION:
APPLICANT: ECONS, Michael
APPLICANT: WHITE, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-901-938-33
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Sequence 33, Appl
Sequence 78, Appli
Sequence 78, Appli
Sequence 78, Appl
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Sequence 78, Appl
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                                                                                                       March 2, 2004, 16:07:28 ; Search time 5.4 Seconds
(without alignments)
625.639 Million cell updates/sec
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Sequence 78,
Sequence 78,
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| cgm2 6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgm2 6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgm2 6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgm2 6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgm2 6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgm2 6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgm2 6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-901-938-33

US-09-755-695-2

4 US-10-230-163-78

4 US-10-230-163-78

1 US-10-230-38-78

1 US-10-230-414-78

US-10-218-631-78

US-10-218-631-78

US-10-218-631-78

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US-10-218-849-78

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US-10-218-849-78

US-10-227-883-78
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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US-10-23-23-78

US-10-23-23-78

US-10-219-481-78

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US-10-227-881-78

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US-10-227-881-78

US-10-23-25-78

US-10-23-25-78

US-10-23-25-78

US-10-23-225-78

US-10-23-225-78
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ALIGNMENTS

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Gaps
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Sequence 7, Application US/10060765

publication No. US20020164713A1

GENERAL INFORMATION:
APPLICANT: Itoh, No. US20020164713A1uyuki

APPLICANT: Itoh, No. US20020164713A1uyuki

TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS

FILE REPERENCE: PP-16758.001/201130.408

CURRENT APPLICATION NUMBER: US/10/060,765

CURRENT FILING DATE: 2002-01-29

PRIOR APPLICATION NUMBER: US/09/715,805

WUMBER OF SEQ ID NOS: 17

SOFTHARR: EASTERO for Windows Version 4.0

SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 16;
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100.0%; Pred. No. 4.8e-08;
tive 0; Mismatches 0;
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Matches 16; Conserv
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US-10-060-765-7
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Gaps

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100.0%; Score 86; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 208
                                                                                                                                                                                                                                                                                                                    1 RORYLYTDDACOTEAH 16
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                                                                                      TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-695-2
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Sequence 33, Application US/10379334

Publication No. US20030181379A1

GENERAL INFORMATION:

APPLICANT: BCOOS, Michael

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

APPLICANT: WHITE, Kenneth

CURRENT FILIANT: NOVEL FIEROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE

FILE REFERENCE: 053884-5001

CURRENT APPLICATION NUMBER: US/09/901,938

PRIOR APPLICATION NUMBER: 60/219,137

PRIOR APPLICATION NUMBER: 60/219,137

PRIOR APPLICATION NUMBER: 60/219,137

PRIOR PILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0

SEQ ID NO 33

LENGTH: 136
     APPLICANT: STROM, Tim
APPLICANT: MEITINGER, Thomas
APPLICANT: MEITINGER, Thomas
TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
FILE REFERENCE: 053884-5001
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 33
LENGTH: 136
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100.0%; Score 86; DB 9; I
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0;
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Patent No. US20020081663A1;
GRURRAL INFORMATION:
APPLICANT: CONKIIN, DATTELL C.
TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGFII;
FILE REFERENCE: 00-03
CURRENT APPLICATION NUMBER: US/09/755,695;
CURRENT PILING DATE: 2001-05-11;
PRIOR APPLICATION NUMBER: US 60/174,526;
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 6
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Matches 16; Conservative
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CORGANISM: Homo Sapiens
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PRIOR FILING DATE: 1938-11-17
PRIOR APPLICATION NUMBER: 60/10801
PRIOR PILING DATE: 1938-11-17
PRIOR PILING DATE: 1938-11-18
PRIOR PILING DATE: 1938-11-18
PRIOR APPLICATION NUMBER: 60/11326
PRIOR PILING DATE: 1938-12-22
PRIOR PILING DATE: 1938-12-23
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APPLICANT: GAIMAIA, TACCTIA
APPLICANT: SECHAN: VANCE IN.
APPLICANT: STEPAN: VANCE IN.
APPLICANT: STEPAN: TACKTORY
WEARABE, COLIN L.
APPLICANT: WEACAMADE, CALL BANK
TITLE OF INVENTION: SECRETED AND INTERESTRIANT
TITLE OF INVENTION: ACIDS SECRETED AND SECRETED AND INTERESTRIANT
THE REPERENCE: PS3.0PC-04-99
PRIOR FILING DATE: 200-06-29
PRIOR PELICATION NUMBER: 06/06313
PRIOR PLICATION NUMBER: 60/063549
PRIOR PELICATION NUMBER: 60/063549
PRIOR PLICATION NUMBER: 60/063549
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PRIOR PLICATION NUMBER: 60/063557
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100.0%; Score 86; DB 14; Length 208; 100.0%; Pred. No. 8.3e-07; artive 0; Mismatches 0; Indels (
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                          Sequence 78, Application US/10230163 Publication No. US20030036635A1 GENERAL INFORMATION:
                                                                                                                              1 RORYLYTDDAQOTEAH 16
                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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PRIOR FILING DATE: 1998-06-28

PRIOR APPLICATION NUMBER: 60/00695

PRIOR APPLICATION NUMBER: 60/091982

PRIOR PILING DATE: 1998-06-25

PRIOR APPLICATION NUMBER: 60/091982

PRIOR PILING DATE: 1998-06-26

PRIOR PILING DATE: 1998-06-07

PRIOR PILING DATE: 1998-08-04

PRIOR PILING DATE: 1998-08-04

PRIOR PILING DATE: 1998-08-04

PRIOR APPLICATION NUMBER: 60/09516

PRIOR PILING DATE: 1998-08-10

PRIOR PILING DATE: 1998-08-17

PRIOR PILING DATE: 1998-08-17

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PRIOR PELLING DATE: 1999-04-21
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APPLICATION NUMBER: 60/127887
FILING DATE: 1999-04-05
APPLICATION NUMBER: 60/130232
                                   FILING DATE: 1998-12-22
APPLICATION NUMBER: 60/113605
APPLICATION NUMBER: 60/113296
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Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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APPLICANT: Godowski, Paul 5,
APPLICANT: Godowski, Paul 6,
APPLICANT: Godowski, Paul 19,
APPLICANT: Godowski, Paul 19,
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Mactin L.
APPLICANT: Smith, Victoria
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Augustin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
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APPLICANT: Watanabe, Colin L.
APPLICANT: MANER: 10502-04-09
FRIGR APPLICATION NUMBER: 10/119,480
FRIGR APPLICATION NUMBER: 60/06287
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Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Sequence 78, Application US/10230338; Publication No. US20030044934A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 78, Application US/10218631; Publication No. US20030045687A1
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                                                                                                            APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Grimaldi, J. Chr
                                                                                                                                                              Desnoyers, Luc
Gerritsen, Mary
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                               Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P. APPLICANT: Desnoyers, Luc APPLICANT: Gerritsen, Mary APPLICANT: Goddard, Audrey
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CORGANISM: Homo Sapien
US-10-230-338-78
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Sequence 78, Application US/10216159A Publication No. US20030069397A1
                                    PPLICATION NUMBER: 60/064103
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PRIOR FILING DATE: 1997-10-28
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                    APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C14
CURRENT APPLICATION NUMBER: U5/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-0-17
PRIOR FILING DATE: 1997-0-28
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-12-17
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PRIOR PRIOR PRIOR DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-25
PRIOR PLICATION NUMBER: 60/079294
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APPLICANT: Goddard, Audrey
APPLICANT: Goddweki, Paul J.
APPLICANT: Gormand, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victorin L.
APPLICANT: Smith, Victorin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC9
CURRENT APPLICATION NUMBER: US/10/230,414
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: US/119,480
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100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
   Stephan, Jean-Philippe F.
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US-10-230-414-78
; Sequence 78, Application US/10230414
; Publication No. US20030050448A1
; GENERAL INFORMATION
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PRIOR APPLICATION NUMBER: 60/059113
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PRIOR APPLICATION NUMBER: 60/062287
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-78
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   APPLICANT:
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AL INFORMATION:

#ILONI: Besnoyers, Luc

#PLICANI: Besnoyers, Luc

#PLICANI: Gendard, Andrey

#PPLICANI: Gendard, Markery

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PRIOR PILLING DATE: 1997-10-31
PRIOR PILLING DATE: 1997-12-17
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100.0%; Score 86; DB 14;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0;
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FILING DATE: 1998-09-10
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APPLICANT: Gerritsen, Marcy
APPLICANT: Geddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan J. Jean-Philippe F.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLCI
CURRENT FILING DATE: 2002-08-12
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PSS30P1C72
CURRENT APPLICATION NUMBER: US/10/227,873
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100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                             Query Match
100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels (
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SEQ ID NO 78
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Publication No. US20030073816A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 78, Application US/10218849
Publication No. US20030073814A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RORYLYTDDAQQTEAH 16
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Chrii
APPLICANT: Grimaldi, J. Chrii
APPLICANT: Grimaldi, J. Chrii
APPLICANT: Smith, Victoria
APPLICANT: Srephan, Jean-Phi
APPLICANT: Rean-Phi
APPLICANT: Matanabe, Colin L.
                                    TYPE: PRT
, ORGANISM: Homo Sapien
US-10-216-159A-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo Sapien
US-10-218-849-78
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US-10-227-873-78
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US-10-218-849-78
SEQ ID NO 78
LENGTH: 208
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CURRENT FILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/06287

PRIOR PLILNG DATE: 1397-09-17

PRIOR PLILNG DATE: 1397-10-21

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US-10-227-883-78

Sequence 78, Application US/10227883

Publication No. US20030073817A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Gerriteen, Mary

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Sarith, Victoria

APPLICANT: Sarith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3530PIC78

CURRENT APPLICATION NUMBER: US/10/227,883

CURRENT APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

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Best Local Similarity 100.0
Matches 16, Conservative
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US-10-227-883-78
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PRIOR APPLICATION UNMER: 60/064103
PRIOR PELING DATE: 1997-10-31
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APPLICATION NUMBER: 60/099816 FILING DATE: 1998-09-11 APPLICATION NUMBER: 60/100385 APPLICATION NUMBER: 60/063549 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/064103 LING DATE: 1998-09-10

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Gaps

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Indels

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APPLICANT: Suttry, Victoria

APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watcanabe, Colin L.
APPLICANT: Watcanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REFERENCE: P3530P1032
CURRENT PHILMS DATE: 2002-08-28
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PRIOR PILING DATE: 1997-09-17
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PRIOR FILING DATE: 1998-03-26
PRIOR PELICATION NUMBER: 60/079656
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 86; DB 14; Length 208; 100.0%; Pred. No. 8.3e-07;
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Gerritean, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Voan-Philippe F.
Watanabe, Colin L.
Wood, William I.
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR PLING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 78, Application US/10230434; Publication No. US20030078380A1; GENERAL INFORMATION:
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APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22
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Best Local Similarity 100.03
Matches 16; Conservative
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; ORGANISM: Homo Sapien
US-10-219-076-78
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
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APPLICANT: Smith, Victoria
APPLICANT: Scephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/19, 480
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Publication No. US20030078379A1
GENERAL INFORMATION:
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Gerritsen, Mary
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FILING DATE: 1999-08-17
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APPLICATION NUMBER: 60/149638
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Desmoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwell, Paul J.
APPLICANT: Godwell, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Mondalid, J. Christopher
APPLICANT: Mondalid, J. Christopher
APPLICANT: Mondalid, J. Calin L.
APPLICANT: Mondalid, J. Calin L.
APPLICANT: Mondalid, Colin L.
APPLICANT: Mondalid, Colin L.
APPLICANT: Mondalid, ACID SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE DETENBRENCE: P3530PLG1
TITLE REFERENCE: P3530PLG1
TITLE REPERENCE: P3530PLG1
TITLE OF INVENTION: ACIDS ENCOCING THE SAME
TILING DATE: 1097-00-10
PRIOR PILING DATE: 1097-00-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
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PRIOR PILING DATE: ö ö Gaps Gaps ; 0 .. 0 100.0%; Score 86; DB 14; Length 208; 100.0%; Pred. No. 8.3e-07; Length 208; Indels Indels Query Match
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Mismatches ; sequence 78, Application US/10219464; Publication No. US20030088065A1; GENERAL INFORMATION: US-10-219-075-78
; Sequence 78, Application US/10219075
; Publication No. US20030088064A1
; GENERAL INFORMATION: 1 RORYLYTDDAQQTEAH 16 44 RORYLYTDDAQQTEAH 59 1 RORYLYTDDAOOTEAH 16 44 RORYLYTDDAQQTEAH 59 Query Match Best Local Similarity 100.0 Matches 16; Conservative ; TYPE: PRT ; ORGANISM: Homo Sapien US-10-219-075-78 RESULT 18 US-10-219-464-78 ð g

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CURRENT FILING DATE:
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: ACOLOW, William I.
TILLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 1935-10-19
FRIOR FILING DATE: 2002-04-09
FRIOR APPLICATION NUMBER: 60/06313
FRIOR APPLICATION NUMBER: 60/063549
FRIOR APPLICATION NUMBER: 60/063649
FRIOR FILING DATE: 1997-10-31
FRIOR FILING DATE: 1997-10-31
FRIOR FILING DATE: 1997-10-31
FRIOR FILING DATE: 1998-03-20
FRIOR FILING DATE: 1998-03-20
FRIOR FILING DATE: 1998-03-26
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Publication No. US2030088066A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Godwski, Paul J.

APPLICANT: Goriffsen, Mary

APPLICANT: Gorowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Watanabe, Colin L.

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APPLICANT: Watanabe, Colin L.
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PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
LENGTH: 208
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Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Homo Sapien
US-10-219-464-78
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US-10-219-466-78
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APPLICANT: GCGOWSKI, Paul J.
APPLICANT: GCGOWSKI, Paul J.
APPLICANT: GTGMAIGI, J. Christopher
APPLICANT: GTMAIGI, J. Christopher
APPLICANT: Smith, Victorial
APPLICANT: Smith, Victorial
APPLICANT: Smith, Victorial
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: MATANABE ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/219,479
CURRENT APPLICATION NUMBER: US/10/119,480
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/063913
PRIOR FILING DATE: 1997-0-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR APPLICATION NUMBER: 60/06387
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PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06387

    See File Wrapper or PALM.

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100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0
PRIOR PELILARY DAILS: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/65313
PRIOR APPLICATION NUMBER: 60/65287
PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/65287
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PRIOR PELING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/669873
PRIOR PELING DATE: 1997-10-31
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Publication No. US20030088067A1
GENERAL INFORMATION:
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CORGANISM: Homo Sapien
US-10-219-466-78
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CURRENT APPLICATION WINBER: US/10/219,481

CURRENT PLING DATE: 2002-08-13

PRIOR PELICATION NUMBER: US/10/219,480

PRIOR PELICATION NUMBER: 00/059113

PRIOR PELICATION NUMBER: 60/05287

PRIOR PELICATION NUMBER: 60/062287

PRIOR PELICATION NUMBER: 60/062287

PRIOR PELICATION NUMBER: 60/063287

PRIOR PELICATION NUMBER: 60/063549

PRIOR PELICATION NUMBER: 60/06349

PRIOR PELICATION NUMBER: 60/06349

PRIOR PELICATION NUMBER: 60/069913

PRIOR PELICATION NUMBER: 60/069913

PRIOR PELICATION NUMBER: 60/079294

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                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246 SEQ ID NO 78 LENGTH: 208
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PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
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No. US20030088068A1
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Best Local Similarity 100.0
Matches 16; Conservative
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Gerritsen, Mary
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ORGANISM: Homo Sapien
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; ORGANISM: Homo Sapien
US-10-219-479-78
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Publication No.
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100.0%; Score 86; DB 14; Length 208;

Query Match

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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanab, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: COLIN L.
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: 2002-09-28
FRIOR PILING DATE: 1002-04-09
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/06313
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06349
PRIOR PILING DATE: 1997-10-31
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PRIOR APPLICATION NUMBER: 60/06349
PRIOR PILING DATE: 1999-03-20
PRIOR PILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/07928
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   Pred. No. 8.3e-07; Mismatches 0;
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Publication No. US20030088071A1
GENERAL INFORMATION:
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Publication No. US20030088070A1
GENERAL INFORMATION:
Best Local Similarity 100.0%; P. Matches 16; Conservative 0;
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CORGANISM: Homo Sapien
US-10-230-260-78
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; Sequence 78, Application US/10216165; Publication No. US20030092886A1; GENERAL INFORMATION:
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FILING DATE: 1998-03-25
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US-10-232-233-78
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APPLICANT: Smith, Victoria
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APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Collin L.
APPLICANT: Watanabe, Collin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: BCREEFED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC104
CURRENT APPLICATION NUMBER: U0/119,480
FRIOR APPLICATION NUMBER: 00/06213
FRIOR APPLICATION NUMBER: 60/06213
FRIOR FILING DATE: 1997-09-17
FRIOR APPLICATION NUMBER: 60/063549
FRIOR FILING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/063549
FRIOR FILING DATE: 1997-10-28
FRIOR FILING DATE: 1997-12-17
FRIOR APPLICATION NUMBER: 60/069873
FRIOR FILING DATE: 1998-03-20
FRIOR FILING DATE: 1998-03-20
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APPLICANT: Goddard, Audrey,
APPLICANT: Goddweki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P353091C108
CURRENT APPLICATION NUMBER: 10510/232,233
CURRENT FILING DATE: 2002-08-29
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SEQ ID NO 78
LENGTH: 208
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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US-10-232-231-78
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Matches 16; Conserv
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GENERAL INVENTATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Gedridard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Coli L.

APPLICANT: Matanabé, Coli L.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Matanabé, Coli L.

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APPLICANT: Mumber: 10/119, 480

PRIOR APPLICATION NUMBER: 60/06213

PRIOR FILING DATE: 1997-10-17

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PRIOR APPLICATION NUMBER: 60/063549

PRIOR FILING DATE: 1997-10-20

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PRIOR PILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 2002-04-09
PRIOR PLICATION NUMBER: 60/059113
PRIOR PAPLICATION NUMBER: 60/06213
PRIOR PILING DATE: 1997-09-17
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APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimadi, J. Christopher
APPLICANT: Grimadi, J. Christopher
APPLICANT: Grimadi, J. Christopher
APPLICANT: Grimadi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Medd, William I.
APPLICANT: Wead, William I.
APPLICANT: Wood, William I.
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APPLICANT: WOOD AND APPLICANTON WOORER: 00/062287
PRIOR APPLICATION NUMBER: 00/062287
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 00/06349
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 00/06391
PRIOR PILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 00/079294
PRIOR PILING DATE: 1998-03-26
PRIOR APPLICATION WOMBER: 00/079286
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PRIOR APPLICATION NUMBER: 60/703728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
LENGTH: 208
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Best Local Similarity 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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R APPLICATION NUMBER: 60/079728
R FILING DATE: 1998-03-27
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R FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085579
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/08441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 78, Application US/10218956 Publication No. US20030092887A1 GENERAL INFORMATION:
   PRIOR APPLICATION NUMBER: 60/079656
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                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo Sapien
US-10-216-165-78
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R APPLICATION NUMBER: 60/091695

R FILING DATE: 1998-07-07

R FILING DATE: 1998-07-07

R FILING DATE: 1998-07-07

R FILING DATE: 1998-08-04

R APPLICATION NUMBER: 60/095318

R APPLICATION NUMBER: 60/095318

R FILING DATE: 1998-08-04

R APPLICATION NUMBER: 60/095916

R FILING DATE: 1998-08-10

R APPLICATION NUMBER: 60/096146

R FILING DATE: 1998-08-11

R APPLICATION NUMBER: 60/096146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLING DATE: 1998-08-31
PPLICATION NUMBER: 60/099596
TLING DATE: 1998-09-09
PPLICATION NUMBER: 60/099598
TLING DATE: 1998-09-09
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APPLICATION NUMBER: 60/100848
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/100919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101738
FILING DATE: 1998-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/099812
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099816
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PPLICATION NUMBER: 60/100038
LLING DATE: 1998-09-11
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APPLICATION NUMBER: 60/101477
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FILING DATE: 1998-09-24
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FILING DATE: 1998-09-25
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APPLICATION NUMBER: 60/101922
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                                                               APPLICATION NUMBER: 60/089905
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/090472
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APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/097986
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APPLICATION NUMBER: 60/098544
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FILING DATE: 1998-09-10
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LING DATE: 1998-09-10
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TLING DATE: 1998-09-15
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APPLICATION NUMBER: 60/086392
FILING DATE: 1998-05-22
                       FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/089532
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PRIOR PILING DATE: 1998-10-30
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PRIOR APPLICATION NUMBER: 60/106905
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PRIOR PILING DATE: 1999-01-12
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PRIOR PELICATION NUMBER: 60/136773
PRIOR PELICATION NUMBER: 60/13677
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PRIOR PELICATION NUMBER: 60/13679
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PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
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APPLICATION NUMBER: 60/169445
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CURRENT APPLICATION: ACLDS ENCODING THE SAME
FILE CORRENT APPLICATION NUMBER: US/10/219,468

CURRENT APPLICATION NUMBER: US/10/19,480

PRIOR APPLICATION NUMBER: 00/059113

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-28

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PRIOR FILING DATE: 1997-10-38

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-12-17

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                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                           Query Match
100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Inc.
APPLICANT: Gerritsen, Mary
APPLICANT: Geddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watenabe, Colin L.
APPLICANT: Watenabe, Colin L.
APPLICANT: Wood, William I.
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION WUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 78, Application US/10219468; Publication No. US20030092888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RORYLYTDDAQQTEAH 16
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 16; Conserv
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44 RORYLYTDDAQQTEAH 59

RESULT 28

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APPLICANT: Stephan, Jean-Philippe F. APPLICANT: Watanabe, Colin L. APPLICANT: Watanabe, Colin L. APPLICANT: Watanabe, Colin L. APPLICANT: Watanabe, Colin L. APPLICANT: Wood, William I. ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3530PIC115 US/010/233,205 CURRENT APPLICATION NUMBER: 10/119,480 PRIOR APPLICATION NUMBER: 10/119,480 PRIOR PILING DATE: 2002-04-09 PRIOR FILING DATE: 2002-04-09 PRIOR FILING DATE: 1997-09-17 PRIOR PILING DATE: 1997-09-17 PRIOR PILING DATE: 1997-10-17 PRIOR PILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baker, Kevin P.
APPLICANT: Besnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goodard, Audrey
APPLICANT: Goodwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 78, Application US/10233205
Publication No. US20030096362A1
GENERAL INFORMATION:
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 16; Conserv
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CURRENT APPLICATION NUMBER: US/10/219,478
CURRENT FILING DATE: 2002-08-13
FRIOR APPLICATION NUMBER: 10/119,480
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FRIOR APPLICATION NUMBER: 60/052113
FRIOR FILING DATE: 1997-09-17
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FRIOR APPLICATION NUMBER: 60/07924
FRIOR FILING DATE: 1998-03-20
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APPLICANT: Goddard, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Granaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: State Colin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: ACTOR STEED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACTOR ENCODING THE SAME
FILE REFERENCE: P3530PLC30
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerriteen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
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                                                        Sequence 78, Application US/10219478
Publication No. US20030092889A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 16; Conservative
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ORGANISM: Homo Sapien
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; ORGANISM: Homo Sapien
US-10-219-072-78
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ANT: Debroyers, Luc
ANT: Gerritesn, Mary

JANT: Gerritesn, Mary

CANT: Gerritesn, Mary

CANT: Gerritesn, Mary

CANT: Gerritesn, Mary

CANT: Gerritesn, Mary

LICAN: Granaldi, J. Christopher

JICAN: Gurney, Auterin

LICAN: Gurney, Martin L.

JULICAN: Granaldi, J. Christopher

JULICAN: Stephan, Dean-Philippe F.

JULICAN: Stephan, Descrippe R.

JULICAN: Stephan, Descrippe R.

JULICAN: Wood William I.

TIE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

UNREAN PAPLICATION SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

UNREAN PAPLICATION SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

UNREAN PAPLICATION NUMBER: 06/059113

PRIOR FULING DATE: 2002-08-13

PRIOR FULING DATE: 2002-08-13

PRIOR PLING DATE: 2002-08-13

PRIOR PLING DATE: 2002-08-13

PRIOR PLING DATE: 2002-08-13

PRIOR PLING DATE: 2002-03-25

PRIOR PLING DATE: 3002-03-25

PRIOR PLING DATE: 1002-03-25

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PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-25
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Publication No. US20030096959A1
GENERAL INFORMATION:
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; ORGANISM: Homo Sapien
US-10-233-205-78
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Best Local Similarity
Matches 16; Conserv
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APPLICANT: Goddwaff, Madry
APPLICANT: Goddwaff, Audrey
APPLICANT: Goddwaff, Audrey
APPLICANT: Goddwaff, Audrei
APPLICANT: Goddwaff, Austin J.
APPLICANT: Granaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SOURCES ENCODING THE SAME
FILE REFERENCE: P3530PLG59
CURRENT APPLICATION NUMBER: US/10/19, 470
CURRENT FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/06287
PRIOR PELICATION NUMBER: 60/06313
PRIOR FILING DATE: 1997-10-21
PRIOR PILING DATE: 1997-10-31
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100.0%; Score 86; DB 14; Length 208; 100.0%; Pred. No. 8.3e-07;
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US-10-219-474-78
; Sequence 78, Application US/10219474
                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 78, Application US/10219470; Publication No. US20030096960A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RORYLYTDDAQQTEAH 16
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo Sapien
   Query Match
Best Local Similarity
Matches 16; Conserv
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US-10-219-528-78
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LENGTH: 208
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CURRENT PADELICATION NUMBER: US/10/219,474
CURRENT FILING DATE: 2002-08-13
FRIOR PRINC PELING DATE: 2002-08-09
FRIOR PELING DATE: 1970-09-07
FRIOR PELING DATE: 1997-09-17
FRIOR PELING DATE: 1997-09-17
FRIOR PELING DATE: 1997-10-28
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APPLICANT: Benoyers, Luc
APPLICANT: Benoyers, Luc
APPLICANT: Gerriteen, Mary
APPLICANT: Godowski, Audrey
APPLICANT: Godowski, Peul J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C36
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100.0%; Score 86; DB
Best Local Similarity 100.0%; Pred. No. 8.3
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                     Goddard, Audrey
Goddowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Publication No. US20030096961A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                      Desnoyers, Luc
Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo Sapien
US-10-219-474-78
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APPLICANT: Desnoyers, Inc.
APPLICANT: Desnoyers, Inc.
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria L.
APPLICANT: Smith, Victoria L.
APPLICANT: Smith, Victoria L.
APPLICANT: Smith, Victoria L.
APPLICANT: Smith, Victoria L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
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APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Mod, William L.
APPLICANT: MATANABER: US/10/19,528
CURRENT APPLICATION NUMBER: US/10/19,480
PRIOR APPLICATION NUMBER: 60/06313
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06387
PRIOR APPLICATION NUMBER: 60/06387
PRIOR FILING DATE: 1997-10-18
PRIOR FILING DATE: 1997-10-28
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CURRENT PAPPLICATION NUMBER: US/10/219,524

CURRENT PEDILOGYTON NUMBER: US/10/219,524

CURRENT PEDILOGYTON NUMBER: 10/119,480

PRIOR PILING DATE: 2002-04-09

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-10-17

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PRIOR PILING DATE: 1997-10-28

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Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 78, Application US/10219528
Publication No. US20030096963A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo Sapien
US-10-219-524-78
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PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/10147
PRIOR APPLICATION NUMBER: 60/101738
PRIOR APPLICATION NUMBER: 60/101741
PRIOR PILING DATE: 1998-09-24
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R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/084441

R RFILING DATE: 1998-05-06

R APPLICATION NUMBER: 60/085323

R APPLICATION NUMBER: 60/085323

R APPLICATION NUMBER: 60/085579

R RELING DATE: 1998-05-15

R APPLICATION NUMBER: 60/086392

R RELING DATE: 1998-05-12

R APPLICATION NUMBER: 60/086392

R RILING DATE: 1998-05-17

R APPLICATION NUMBER: 60/089538

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R APPLICATION NUMBER: 60/089905
RR FILING DATE: 1998-06-18
RR APPLICATION NUMBER: 60/090472
RR APPLICATION NUMBER: 60/090557
RR APPLICATION NUMBER: 60/090557
RR FILING DATE: 1998-06-24
RR APPLICATION NUMBER: 60/090591
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/091982
BILING DATE: 1998-07-07
APPLICATION NUMBER: 60/095302
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FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099598
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APPLICATION NUMBER: 60/09911
APPLICATION NUMBER: 60/099812
APPLICATION NUMBER: 60/099812
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APPLICATION UNDHER: 60/09816
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/100038
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APPLICATION NUMBER: 60/100385
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APPLICATION NUMBER: 60/100390
FILING DATE: 1998-09-15
APPLICATION NUMBER: 60/100627
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PILING DATE: 1998-09-16
PILING DATE: 1998-09-18
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APPLICATION NUMBER: 60/101738
FILING DATE: 1998-09-24
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FILING DATE: 1998-08-04
APPLICATION NUMBER: 60/095916
FILING DATE: 1998-08-10
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FILING DATE: 1998-08-11
APPLICATION NUMBER: 60/096791
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APPLICATION NUMBER: 60/099803
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APPLICATION NUMBER: 60/097986
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FILING DATE: 1998-08-31
APPLICATION NUMBER: 60/081819
                                                                   FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082804
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimald, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: BCREED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC74
CURRENT APPLICATION NUMBER: US/10/227,880
CURRENT FILING DATE: 2002-08-26
PRIOR FILING DATE: 2002-08-26
PRIOR FILING DATE: 1997-09-17
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100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                 PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/14569B
PRIOR APPLICATION NUMBER: 60/14622
PRIOR FILING DATE: 1999-07-28
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PRIOR PRIURG DATE: 1999-11-06
PRIOR APPLICATION NUMBER: 60/16945
PRIOR APPLICATION NUMBER: 60/16945
PRIOR PRIURG DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
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Publication No. US20030096964A1
GENERAL INFORMATION:
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FILING DATE: 1998-03-25
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godweki, Paul J. Christopher
APPLICANT: Gurmaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wad anales Colin L.
APPLICANT: Wad Amiliam I.
APPLICANT: Wood, William I.
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FILE REPERENCE: P350PL60
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PRIOR APPLICATION NUMBER: 60/149320
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PRIOR PLING DATE: 1999-12-07 Sequence 78, Application US/10227881; Publication No. US20330096965A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P. 1 RORYLYTDDAQQTEAH 16 44 RORYLYTDDAQQTEAH 59 Desnoyers, Luc Gerritsen, Mary Query Match 100. Best Local Similarity 100. Matches 16; Conservative RESULT 37 US-10-227-881-78 ò g

FILING DATE: 1998-04-22

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APPLICANT: Beacery Est inc
APPLICANT: Generiteen, Mary
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APPLICANT: Generiteen, Marstin L.
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Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels (
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Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels (
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Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
Wood, William I.
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Godowski, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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; Sequence 78, Application US/10232223
PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
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Publication No. US20030096967A1
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ORGANISM: Homo Sapien
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us-10-060-765-7.rapb

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Publication No. UGZ0030096968A1

SARERAL TROMATION

APPLICANT: Baker, Kevin P.

APPLICANT: Gadard, Audrey

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APPLICANT: Galard, Audrey

APPLICANT: Galard, Audrey

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

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PRIOR FILING DATE: 1997-10-17

PRIOR APPLICANTON NUMBER: 60/06287

PRIOR APPLICANTON WUMBER: 60/06393

PRIOR APPLICANTON WUMBER: 60/06393

PRIOR PLIING DATE: 1997-110-17

PRIOR PLIING DATE: 1997-12-17

PRIOR PLIING DATE: 1997-12-17

PRIOR PLIING DATE: 1990-03-25

PRIOR FILING DATE: 1990-03-25

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100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0
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; ORGANISM: Homo Sapien
US-10-232-223-78
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Search completed: March 2, 2004, 16:19:58 Job time : 6.4 Becs

44 RQRYLYTDDAQQTEAH 59

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                              - protein search, using sw model
                       Copyright
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OM protein

2, 2004, 15:50:07; Search time 9.6 Seconds (without alignments) 470.913 Million cell updates/sec March Run on:

US-10-060-765-7 86 Title: Perfect score: Sequence:

1 RQRYLYTDDAQQTEAH 16

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 29Jan04:* 1: geneseco1980s.* geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

CTIMMEDIES

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| 4 | 86 | 100.0 | 181 | 4 | AAU00965 | Human |
| · ru | 86 | 100.0 | 208 | 4 | AAE05078 | Human |
| ν. | 86 | 100.0 | 208 | Ŋ | AAU83630 | Human |
| 7 | 98 | 100.0 | 208 | Ŋ | ABG32358 | Human |
| α | 86 | 100.0 | 208 | w | AAE17601 | Human |
| σ | 86 | 100.0 | 208 | 9 | ABU80777 | Human |
| 10 | 98 | 100.0 | 208 | φ | AB033743 | Novel |
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| 13 | 98 | 100.0 | 208 | 9 | ABJ72266 | |
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| 191 | 98 | 100.0 | 208 | 7 | ADA37038 | Human |
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| 23 | 98 | 100.0 | 208 | 7 | ADB78051 | Nove |
| 24 | 86 | 100.0 | 7 | ۲ | ADB87117 | Human |
| 25 | 86 | 100.0 | | 7 | ADB84699 | Adb84699 Human PRO |
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ALIGNMENTS

Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation; hepatic cell, cirrhosis; infertility; impotence; testicular cancer; leukemia; lymphoma; autoimmune disease; thymus proliferative disorder. Epitope-bearing portion of human fibroblast growth factor-21 (FGF-21). AAB68418 standard; peptide; 16 AA. 23-JUL-2001 (first entry) AAB68418; AAB68418

Homo sapiens.

WO200136640-A2

25-MAY-2001.

16-NOV-2000; 2000WO-US031745.

18-NOV-1999; 99US-0166540P. 11-MAY-2000; 2000US-0203633P.

(CHIR) CHIRON CORP. (KYOU) UNIV KYOTO.

Itoh N, Kavanaugh WM;

WPI; 2001-343823/36.

New nucleic acid molecule useful for treating disease, e.g. infertility, impotence, or testicular cancer.

Claim 17; Page 39; 61pp; English.

The present sequence represents an epitope-bearing portion of human fibroblast growth factor-21 (FGF-21). FGF proteins regulate growth and differentiation of a variety of cell types. FGF-21 mucleic acids and polypeptides are useful for treating diseases and disorders characterised by inadequate numbers of hepatic cells, preferably cirrhosis of the liver. They may also be used in the treatment of infertility, impotence, and testicular cancer, as well as leukemia, lymphoma, autoimmune disease, or proliferative disorders of the thymus

Sequence 16 AA;

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Gaps

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Indels

Pred. No. 2.5e-07; Mismatches 0;

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RESULT 2 ABB81312

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an active variant (1) of a fibroblast corresponding at least one mutation in the beta-8-beta-9 loop, having enhanced specificity for one receptor subtype compared to the corresponding wild type FGF, by decreasing the biological activity mediated by at least one receptor subtype while retaining the activity mediated through another receptor subtype will has gytostatic, vulnerary, osteopathic and antiarthritic activities. (1) has gytostatic, vulnerary, of vasculogenesis or angiogenesis. (1) is useful for preparing a medicament and for treating a disease or disorder related to normal or abnormal FGF receptors (FGFRs), especially skeletal disorders, cancer, to chooper the compared of the compared of processes. (1) is useful in detection and treatment of various FGFR processes. (1) is useful in detection and treatment of various FGFR compared disorders including skeletal disorders e.g. achondroplasia, and osteoporosis, and cartiage defects, multiple companies and expression systems suitable for pharmaceutical production, targeting of chades or other agents to tissues and cells having specific FGFR subtypes, and serve as template for the formation of improved agonists and cancer. The present sequence represents a FGF core structure amino acid cancer. The present sequence represents a FGF core structure amino acid cores.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of fibroblast growth factor, useful for treating skeletal disorders including osteoporosis, malignancies and to enhance wound and fracture healing.
                                                                                                                                                                                                                                                                                                                                                                                     Fibroblast growth factor 9; FGF-9; cytostatic; vulnerary; osteopathic; antiarthritic; vasculogeneeis; angiogenesis; FGFR; skeletal disorder; fibroblast growth factor receptor; cancer; bone fracture healing; bone growth; wound healing; achondroplasia; hypochondroplasia; extilage defect; multiple myeloma.
                                                      Gaps
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                Length 16;
                                                    0; Indels
                  Score 86; DB 4; I
Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                                                                                    Human FGF21 core structure amino acid sequence.
                                                      Mismatches
                                                                                                                                                                                                                                     ABB81312 standard; protein; 124 AA.
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                    100.0%;
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                                                                                                                                                                                                                                                                                                                (first entry)
                                                          Conservative
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"And 16; Conserv?
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DB 5; Length 124;

100.0%; Score 86;

Sequence 124 AA;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fibroblast growth factor-19X polypeptides and polynucleotides useful for diagnosis, prevention, treatment of proliferative, differentiative, tumorigenic disorders such as tumor, psoriasis, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes the protein and coding sequences of thuman fibroblast growth factor (FGF) 19 homologue FGF19X, the former which is shown here. The sequences can be used in the prognosis and treatment of proliferative diseases such as cancer, restenosis, psoriasis, rheumatoid arthritis and Dupuytren's contracture, as well to stimulate cell growth for treating neurological disorders such as Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                           Human; fibroblast growth factor 19; FGF19X; embryonic development; proliferative disorder; cancer; restenosis; psoriasis; rheumatoid arthritis; Dupuytren's contracture.
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                                                                                                                                      Human fibroblast growth factor 19 homologue FGF19X.
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Herrmann JL;
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Pred. No. 3.1e-07;
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Rastelli L,
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AAB73069 standard; protein; 153 AA.
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19-JUL-2000; 2000US-00619251.
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N-PSDB; AAF76715.
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(first entry)

24-MAY-2001

Fibroblast Growth Factor; FGP; treatment; cirrhosis; mucositis; diabetes; inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis; renal tubule damage; gastrointestinal abnormality; wasting syndrome; neurodegenerative disease; hematopoietic cell reconstitution; cachexia; chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy; multiple sclerosis; short stature; delayed maturation; excessive growth; acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia; androgen target organ abnormality; respiratory distress syndrome; stroke; cancer; atherosclerosis; hypercholesterolaemia; excessive fictors. osteoarthritis; muscle atrophy; sarcopenia; wrinkles; increased fatigue; decreased stamina; decreased cardiac function; immune system dysfunction; Parkinson's disease; Alzheimer's disease; decreased cognitive function; Human Fibroblast Growth Factor-like (FGF-like) polypeptide fragment senile dementia; human.

Homo sapiens.

WO200118172-A2.

J5-SEP-2000; 2000WO-US024373.

07-SEP-1999; 99US-00391861. 23-AUG-2000; 2000US-00644052.

(AMGE-) AMGEN INC.

Thomason AR, Liu B;

WPI; 2001-226743/23

Novel isolated fibroblast growth factor-like polypeptide useful for treating, preventing or ameliorating cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease, diabetes, obesity, stroke and

Claim 14; Page 116-117; 138pp; English

The sequence represents a fragment of a fibroblast growth factor-like (FGF-like) polypeptide. FGF-like protein and its associated nucleic acid play a role in modulating body growth, maturation or life-span. They are also useful for treating, preventing or ameliotating disorders such as cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease, diseases, damage to renal tubules as a result of acute tubular necrosis, haematopoietic cell reconstitution following chemotherapy, wasting syndromes (e.g., cancer associated cachexia), damage to the corneal of epithelium, lens or retinal tissue, multiple sclerosis, myopathies, short stature, delayed maturation, alopecia, abnormalities of androgen target organs, connection, alopecia, abnormalities of androgen target organs, bronchopulmonary dysplasia, acute respiratory distress syndrome, tumours of the eye or other tissues, atherosolerosis, hypercholesterolemia, stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia, baldness, wrinkles, increased taigue, decreased stamina, decreased baldness, wrinkles, increased fatigue, decreased stamina, decreased cardiac function, immune system dysfunction, cancer, Parkinson's disease, senile dementia, Alzheimer's disease, and decreased cognitive function

Sequence 181 AA;

Gaps o; 100.0%; Score 86; DB 4; Length 181; 100.0%; Pred. No. 3.8e-07; Indels . 0 Mismatches 0; Local Similarity 100. Query Match Best Loca Matches

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ROKYLYTDDAQQTEAH 32 1 RORYLYTDDAQQTEAH 16

AAE05078 standard; protein; 208 AA. AAE05078

AAE05078;

(first entry) 18-SEP-2001 Human fibroblast growth factor (FGF) homologue, zFGF11 protein.

proliferation; mesenchymal cell; osteoblastic lineage cell; osteoporosis; chromosomal disorder; chondrosarcoma; atherosclerosis; obesity; fracture; bone formation; diabetes mellitus; neural cell development; anglogenesis; amyotrophic lateral sclerosis; cerebrovascular stroke; neuropathy; ulcer; congenital disorder; wound healing; cardiac function; glomerulonephritis; surfactant production; anorectic; ischaemia; neogenesis; hyperplasia; hypertension; cytostatic; vasotropic; therapy. fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis;

Homo sapiens.

1. .27 /label= Signal_peptide Location/Qualifiers Protein Peptide

28. 208 /label= Human_mature_zFGF11_protein 44. 46. "Heparin binding domain" Binding-site

WO200149849-A1

12-JUL-2001

05-JAN-2001; 2001WO-US000324.

05-JAN-2000; 2000US-00477886.

(ZYMO) ZYMOGENETICS INC.

Conklin DC, Chen Z;

WPI; 2001-441880/47.

N-PSDB; AAD09151.

Novel rFGF11 polypeptide and polynuclectide, a member of fibroblast growth factor family, for stimulating proliferation of mesenchymal, osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,

Claim 1; Page 63; 69pp; English.

The present sequence is human fibroblast growth factor (FGF) homologue, CC zFGF11 protein. zFGF11 gene is located on chromosome 19. zFGF11 is useful for stimulating proliferation of mesenchymal cells, osteoblastic lineage cells. zFGF11 is useful for identifying chromosomal disorders associated with abnormal expression of zFGF11 protein. zFGF11 is also useful for stimulation, inhibition or proliferation of myocytes, smooth muscle cells adipocytes, chondrocytes, neural tube-derived stem cells neural cells and neuronal progenitors, pancreatic cells, prostate-crest stem cells and neuronal progenitors, pancreatic cells, prostate-crest stem cells and neuronal progenitors, pancreatic cells, prostate-crest stem cells and obtaining close defects, fractures, catheroscis, restenosis and obbeity. Stimulation of osteoblasts costeoporosis and other deficiencies in bone structure and formation.

CC sFGF11 is useful for treating disorders associated with diabetes costeoporosis, cerebrovascular stroke, neuropathy associated with lack of menoral cell development or degeneration, amyotrophic lateral sclerosis, cerebrovascular stroke, neuropathy associated with lack of menoral differentiation and congenital disorders of the nervonal differentiation and congenital disorders of the oper circulation such as diabetic food ulcers, improving cardiac concentration, modulating surfactant production in the lumn of cutous spatem or lack and subsective conduction of ischaemia-reperfusion events, particularly in the heart or brain and for inducing skeletal muscle neogenesis and/or hyperplasia, kidney regeneration and/or for

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treating of systemic and pulmonary hypertension. Antagonists of zFGF11 are useful for inhibiting disorders associated with kidney epithelium such as glomerulonephritis
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One hundred and twenty two nucleic acids encoding PRO polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, W
                                                                                                                                                                                      Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; tectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.
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                                            Score 86; DB 4; Length 208; Pred. No. 4.4e-07;
                                                           Indels
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                                                           Mismatches
                                                                                                                             AAU83630 standard; protein; 208 AA.
                                                                                                                                                                          Human PRO protein, Seq ID No 78.
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2000US-0220624P.
2000US-0220638P.
2000US-0220664P.
2000US-0220666P.
                                            100.08;
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2000US-0227133P.
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2000WO-US020710.
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                                                                          1 RORYLYTDDAQQTEAH 16
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                                                                                                                                                           (first entry)
                                                                                        44 RORYLYTDDAQQTEAH
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                                                            16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grimaldi JC, Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-172001/22
                                            Query Match
Best Local Similarity
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                              Sequence 208 AA;
                                                                                                                                                                                                                                             WO200208288-A2
                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2000;
10-NOV-2000;
28-NOV-2000;
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22-AUG-2000;
23-AUG-2000;
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                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                           08-MAY-2002
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                                                                                                                                             AAU83630;
                                                             Matches
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The invention relates to one hundred and twenty two nucleic acids canceding PRO polypeptides. The sequences of the 122 PRO polynucleotides encoding PRO polypeptides. The PRO nucleic acids, polypeptides, and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, epecially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in periorte calls, for stimulating the release of tumour necrosis factor-alpha from human blood, stimulating or inhibiting the proliferation of normal human blood, for stimulating or inhibiting the proliferation of normal human blood, stimulating or inhibiting the proliferation of normal human blood, weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AU83592-AAU83713 represent human PRO protein sequences of the invention
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                           related disorder and for diagnosing tumors such
useful for treating a PRO related disorder and for diagnosing tumors sucl
as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
or liver tumor.
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100.0%; Pred. No. 4.4e-07;
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/label= Signal_sequence
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                                                                                                                                                           Claim 11; Fig 78; 359pp; English.
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Best Local Similarity 100.
Matches 16; Conservative
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(CHEN/) CHEN
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WPI; 2002-626540/67.

N-PSDB; ABK91310.

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Yue H, He A, Nguyen DB, Walia N, Gandhi AR, Azimzai Y_{\it i}O, Tang YT, Lu Y, Baughn MR, Duggan BM, Lee S, Hafalia A;
                                                                                                                                                                                                                                              AAE17601 standard; protein; 208 AA.
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23-JUN-2000; 2000US-0213465P.
14-NOV-2000; 2000US-0249019P.
                                         Claim 4; Fig 1; 35pp; English.
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                                                                                                                                                                                      16; Conservative
                             cerebrovascular stroke.
                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                             Sequence 208 AA;
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Bandman O, T
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                                                                                                                                                 human zFGF11
                                                                                                                                                                                       Matches
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The present invention relates to new extracellular messenger polypeptides and polymucleotides encoding them. XMES is useful in the diagnosis, cand polymucleotides encoding them. XMES is useful in the diagnosis, treatment and prevention of neurological disorders (e.g. epilepsy, cartone, or Alzheimer's disease), autoimumue/inflammatory disorders (e.g. acquired immune deficiency syndrom. AIDS, Addison's disease, or allergies), developmental disorders (e.g. renal tubular acidosis, anaemia or Cushing's syndrome), endocrine disorders (e.g. hypophysectomy, cor cushing's syndrome), and call proliferative disorders (e.g. cancer), and in the assessment of the effects of exogenous or compounds on the expression of nucleic acid and amino acid sequences of compounds on the expression of nucleic acid and amino acid sequences of critacil, bacterial, fungal, parasitic, processal and helminthic infections, trauma, disorders associated with hypopituitarism, cor hypothyroidism, hyperthyroidism or gonadal steroid hormones, and companies may be used for somatic or germline gene therapy. The present sequence is human XMES-3 protein
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                                                                                  New extracellular messenger polypeptides and polynucleotides encoding them, useful for diagnosing, treating or preventing e.g. neurological, autoimmune, inflammatory, developmental and endocrine disorders.
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                                                                                                                                                                                                     claim 1; Page 111; 123pp; English.
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Best Local Similarity 100.0%; P. Matches 16; Conservative 0;
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                    WPI; 2002-154573/20.
N-PSDB; AAD28493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 208 AA;
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                                                                                                                                                                                                                                    The invention relates to an isolated human polypeptide (1) for zFGF11 (a fibroblast growth factor), and the encoding polynucleotide (II). (1) and methods of the invention stimulating proliferation of mesenchymal cells, detecting the presence of zFGF11 in a biological sample, detecting the presence of zFGF11 in a biological sample, detecting the presence of zFGF11 in a biological sample, detecting the presence of zFGF11 in a biological sample, comparing proliferation of osteoblastic lineage cells. The polypeptides, nucleic acid and/or antibodies of the invention may be used polypeptides, nucleic associated with diabetes mellitus, neural cell development or degeneration, amyotrophic lateral sclerosis, cerebrovascular stroke, neuropathy associated with lack of maintenance of cerebrovascular stroke, neuropathy associated with lack of maintenance of cerebrovascular development. Molecules of the invention may also be used useful for improving cardiac function and for promoting wound healing of the present sequence represents the amino acid sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; extracellular messenger; neurological disorder; epilepsy; XMES-3; Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke; acquired immune deficiency syndrome; ALDS; Addison's disease; cytostatic; developmental disorder; anaemia; Cushing's syndrome; endocrine disorder; vascular malformation; cell proliferative disorder; gene therapy; cancer; neuroprotective; trauma; hypopiunitarism; hypothyroidism; antihelminthic; hyperthyroidism; gonadal steroid hormone; pancreatic disorder; nootropic; diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial; antiviral; antifungal; parasitic; protozoal; allergy.
                                                      Isolated polypeptide for zFGF11 (fibroblast growth factor) useful in treatment of disorders associated with diabetes mellitus, neural cell development or degeneration, amyotrophic lateral sclerosis,
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100.0%; Pred. No. 4.4e-07;
Live 0; Mismatches 0; Indels
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Gaps

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Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood WI;

Gerritsen ME, Goddard Smith V, Stephan JF,

Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, (GETH) GENENTECH INC.

WPI; 2003-342045/32. N-PSDB; ACA66879.

The invention describes an isolated mucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide comprised sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, blosensors or plynucleotides are useful cumour, breast tumour, prostate tumours (e.g. lung tumour, or liver tumour) in a mammal, for stimulating the release of TNF-alpha from human blood, or commal human dermal fibroblast proliferation. The PRO nucleic acid or polypeptide is also useful for treating tumours or various bone and/or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for thearpeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases, and in the diagnostic calso useful in drug screening, particularly as targets for thearpeutic intervention in these diseases. The PRO polypeptides are useful or the presence of these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are useful or the presence of these diseases. The PRO polypeptides are useful or the presence of these diseases. The PRO polypeptides are useful or the presence of these diseases. The PRO polypeptides are useful or the presence of these diseases. The PRO polypeptides are useful or the presence of these diseases. The PRO polypeptides are useful or the presence of these diseases. The PRO polypeptides are useful or the presence of these diseases. The PRO polypeptides are useful or the armony of the presence of these diseases. The PRO polypeptides are useful or the armony or the processing and the processing or the armony or the process

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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the diagnostis and treatment of tumours. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABUS073-ABUS0860 represent the human PRO polypebtides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted and transmembrane protein; PRO; cytostatic; antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; fibrobiast modulator; paramaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour; oolon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; bone disorder; cartilage disorder; sports injury;
One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
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                                                                                                                                                                                                                                                                                                                                      Score 86; DB 6; Length 208; Pred. No. 4.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted and transmembrane protein PRO10196.
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                                                                   Claim 11; Fig 78; 314pp; English
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.'
Matches 16; Conservative
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transmembrane PRO polypeptide

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                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 4.4e-07;
tive 0; Mismatches 0;
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                             Sequence 208 AA;
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New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or

Claim 11; Fig 78; 314pp; English.

wounds in a mammal

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI;

Desnoyers L, C, Gurney AL,

Grimaldi JC,

Baker KP,

WPI; 2003-512315/48.

N-PSDB; ACD68631.

Wood WI;

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Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or obesity, by administering composition comprising fibroblast growth factor
                                                                                                                                                                                        nuclearized uncertained out transmembrane (PRO) polypeptides. The proceding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, agerelated macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter; diabetes; obesity; antidiabetic; anorectic; type 2 diabetes; type 1 diabetes.
                                                                            One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                 The invention describes one hundred and eighty seven nucleic acids
Watanabe CK,
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100.0%; Pred. No. 4.4e-07;
iive 0; Mismatches 0;
 Stephan JF,
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 Smith V,
                                                                                                                                                    Claim 11; Fig 78; 314pp; English
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10-JAN-2002; 2002US-0347991P.
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   Gurney AL,
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                                    WPI: 2003-393229/37.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 208 AA;
                                                      N-PSDB; ACA68535
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   Grimaldi JC,
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The present sequence represents human fibroblast growth factor 21 (FGF-21). FGF-21 is located to chromosome 19, more specifically to 19q13.1-creating a meanmal exhibiting type 2 diabetes or type 1 diabetes, or treating a meanmal exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal composition chesity which comprises administering to the mammal a composition comprising FGF-21 which has at least 95% amino acid sequence identity to the 20% amino acid sequence given in ABP96156. Also described: (1) inducing an increase in glucose uptake in adjocyte cells by administering FGF-21 to induce an increase in glucose uptake, and (2) administering FGF-21 to induce an increase in glucose uptake; or comprised to a mammal using FGF-21 having 95% amino acid sequence or or obesity in a mammal using FGF-21 having 95% amino acid sequence identity to ABP96156. FGF-21 has antidiabetic and anoractic activities. The method is useful for treating a mammal for obesity. The method is preferably useful for treating type 1 or type 2 diabetes, and for treating domestic animals for obesity. The method is preferably the animals for obesity. The method is preferably the animals for obesity in type 2 diabetes, and for treating domestic animals for obesity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding for a PRO protein, useful for the manufacture of a medicament for diagnosing or treating tumors or for measuring or detecting expression of an associated gene.
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
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100.0%; Pred. No. 4.4e-07;
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                               Sequence 208 AA;
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Grimaldi JC,
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proliferation and the detection of the presence of a tumour within a mammal. Furthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or for measuring or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO protein of the invention
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Best Local Similarity 100.
Matches 16; Conservative
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44 RORYLYTDDAQQTEAH 59

ABJ72394 standard; protein; 208 AA.

06-NOV-2003 (first entry) ABJ72394;

Human PRO10196 protein

PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte; tumour necrosis factor; proliferation; differentiation; gene therapy; dermal fibroblast.

Homo sapiens.

US2003027988-A1.

06-FEB-2003

26-AUG-2002; 2002US-00227884.

01-JUN-2001; 2001MO-US017800. 29-JUN-2001; 2001MO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Desnoyers L, Grimaldi JC, Baker KP,

WPI; 2003-503301/47. N-PSDB; ABT44547.

New PRO protein encoding nucleic acid, useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a tumor in a mammal

Claim 11; Fig 78; 324pp; English

The invention relates to a novel isolated PRO protein encoding nucleic acid. The nucleic acid of the invention may be useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a tumour in a mammal. Furthernore, the molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells, the release of tumour necrosis factor (TNF)-alpha from human blood, the proliferation or differentiation of chondrocyte cells and for inhibiting the proliferation of normal human dermal fibroblast cells. Finally, the molecules may be utilised during gene therapy. The current sequence is that of the human PRO protein of the invention RESULT 14
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Gaps

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Length 208; 0; Indels

100.0%; Score 86; DB 6; 1 100.0%; Pred. No. 4.4e-07; ive 0; Mismatches 0;

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Best Local Similarity Matches 16; Conserva

Query Match

Sequence 208 AA;

44 RQRYLYTDDAQQTEAH 1 RORYLYTDDAQQTEAH

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Score 86; DB 6; Length 208; Pred. No. 4.4e-07;
  100.08;
  Query Match
Best Local Similarity
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The invention relates to an isolated nucleic acid encoding a PRO polypeptide. Nucleic acids that encode PRO can be used to generate either transgenic animals or knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy for replacing defective gene, in chromosome identification, as chromosome markers, or in generating probes to isolate till length PRO cDNA. The PRO polypeptides are useful for chondrocyte stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation and for detecting the presence of tumour in an mammal. The PRO polypeptides are useful as molecular markers for protein electrophoresis and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in fisue typing, Anti-PRO antibodies are useful in diagnostic assays for PRO antibodies are useful in diagnostic assays for PRO antibodies are useful in diagnostic assays for PRO antibodies are useful in diagnostic assays for protein electrophoresis of a human secreted/transmembrane PRO polypeptide
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Smith V, Stephan JF, Watanabe CK, Wood WI;
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 Gaps
                                                                                                                                                                                                                                                                                                              Human, chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
human dermal fibroblast stimulation; tumour; tissue typing;
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 Indels
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 Mismatches
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                      1 RORYLYTDDAQQTEAH
                                                                         44 RORYLYTDDAQQTEAH
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Grimaldi JC, Gurney AL,
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suffering from systemic inflammatory response syndrome (SIRS).

suffering from systemic inflammatory response syndrome (SIRS).

respiratory distress, acute lung injury, acute respiratory distress syndrome, multiple organ dysfunction syndrome, sepsis and chronic bondrius.

Parturcive pulmonary disease (e.g. emphysema and chronic bronchitis).

The SIRS includes pancreatitis, ischaemia, multiple trauma and tissue injury, haemorrhagic shock, immune-mediated organ injury, shock and renal failure. FSF12 regulates glucose levels in response to nutrient dispersion; affects the overall metabolic state and counter-acts negative side effects that occur during the body's stress response to sepsis; reduces morbidity and mortrality that occurs in critically ill patients; and stimulates glucose uptake and enhances insulin sensitivity. The present sequence represents the human FGF-21 amino acid sequence, which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for the reduction of mortality and morbidity in critically ill patients, which involves the administration of fibroblast growth factor 21 (FGF-21) (I). (I) has antiinflammatory, respiratory, antibacterial, immunosuppressive, vasotropic, haemostatic and nephrotropic activities, and can be used as a glucose level regulator, a glucose uptake stimulator, and an insulin sensitivity enhancer. (I) can be used in the manufacture of a medicament for the reduction of morbidity and mortality in critically ill patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of fibroblast growth factor 21 for reduction of mortality and morbidity in patients suffering from e.g. systemic inflammatory response syndrome and acute respiratory distress syndrome.
                                                                                                                                                                                                           mortality; morbidity; fibroblast growth factor 21; FGF-21; antiinflammatory; respiratory; antibacterial; immunosuppressive; vasotropic; haemostatic; nephrotropic; glucose level regulator; glucose uptake stimulator; insulin sensitivity enhancer; systemic inflammatory response syndrome; respiratory distress; acute lung injury; acute respiratory distress syndrome; multiple organ dysfunction syndrome; sepsis; chronic bronchitis; pancreatitis; ischaemia; multiple trauma; tissue injury; haemorrhagic shock; immune-mediated organ injury; shock; renal failure.
                                                                                                                                                                             Human fibroblast growth factor 21 SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 15-16; 22pp; English.
                                              ADA37038 standard; protein; 208 AA.
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                                                                                         ADA37038;
RESULT 16
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This invention relates to one hundred and twenty two novel nucleic acids encoding human PRO membrane bound proteins or receptors. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerritgen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                                        Human membrane bound receptor/protein PRO10196 amino acid sequence.
                                                                                                                                                                                                                                     Human, PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; oytotoxic factor factor differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.
                                                                                                               ABJ72096 standard; protein; 208 AA.
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01-UUN-2001; 2001WO-US01900.
9-AUN-2001; 2001WO-US021066.
09-ARR-2002; 2002US-00119480.
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1 RORYLYTDDAQQTEAH 16
                              44 RORYLYTDDAOOTEAH
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Sequence 208 AA;

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100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; ive 0; Mismatches 0; Indels

Local Similarity 100.0

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Sequence 208 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; periovte cell proliferation; chondrocyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
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phan JF, Watanabe CK, Wood WI;
                                                        Gaps
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100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07;
                                                  Indels
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                                                  Mismatches
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                           1 RORYLYTDDAQQTEAH 16
                                                                                                                                                   44 RORYLYTDDAOOTEAH 59
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                                                     16; Conservative
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C, Gurney AL,
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N-PSDB; ADBB3567.
                            Local Similarity
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              inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4732, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of the profit of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung
                                                                                                                                                                   tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polymucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1212 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted and transmembrane protein; PRO; cytostatic; vulnexary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; oclon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
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Smith V, Stephan JF, Watanabe CK, Wo
or PR07425 polypeptide are useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                          transmembrane PRO polypeptide.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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  PRO5723, PRO5725, PRO7154,
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Grimaldi JC, Gurney AL,
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N-PSDB; ADB80673.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 208 AA;
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Claim 11; Fig 78; 305pp; English

The invention describes an isolated PRO (secreted and transmentally polypeptide are useful for stimulating the proliferation of or gene expression in useful for stimulating the proliferation of or gene expression in the collie prox35, PRO129, PRO130 or PRO405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO357, PRO529, PRO1305 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TMF)-are useful for stimulating the release of tumour necrosis factor (TMF)-are useful for stimulating the release of tumour necrosis factor (TMF)-pro133, PRO133, PRO134, PRO136, PRO1305, PRO1306, PRO1309, P The invention describes an isolated PRO (secreted and transmembrane) transmembrane PRO polypeptide.

Sequence 208 AA;

ö Gaps ö Score 86; DB 7; Length 208; Pred. No. 4.4e-07; Indels ö 0; Mismatches 100.0%;

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ADB73215 standard; protein; 208 AA ADB73215; RESULT 20

Novel human secreted and transmembrane protein PRO10196.

04-DEC-2003 (first entry)

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosals factor alpha release; (TNF) alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; ling tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy

US2003096968-A1.

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Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, 'Wood WI;
                                                                          New isolated PRO polypeptides useful as molecular weight markers in protein electrophoresis, useful for tissue typing, and for treating arthritis and tumors.
                                                                                               Claim 11; Fig 78; 308pp; English.
                                                                                                                                                                                                                                                                        transmembrane PRO polypeptide.
                     01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
             29-AUG-2002; 2002US-00232223
                                                  Desnoyers L,
                                         (GETH ) GENENTECH INC.
                                                                WPI; 2003-765525/72.
                                                                                                                                                                                                                                                                                 Sequence 208 AA;
                                                                     N-PSDB; ADB73214.
                                                       Grimaldi JC,
    22-MAY-2003.
                                                   Baker KP,
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Gaps .. 0 100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; Indels 100.0%; Pred. ... 1 RORYLYTDDAQQTEAH 16 16; Conservative Query Match Best Local Similarity Best Loc Matches à

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RESULT 21

ADB78297 standard; protein; 208 AA. ADB78297 ID ADB7

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Gaps

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(GETH ) GENENTECH INC.
                                                              WPI; 2003-765495/72.
N-PSDB; ADB78296.
                                  US2003092889-A1
                                                        Baker KP, De
Grimaldi JC,
                               Homo sapiens.
                           gene therapy
                                      15-MAY-2003.
 ADB78297;
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for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO329, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them. The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood, for stimulating the proliferation or differentiation of expression in pericyte cells or for stimulating the proliferation of or gene normal human dermal fibroblasts. The PRO nucleic acids are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PRO polypeptides and nucleic acids encoding the polypeptides, useful e.g. in gene therapy, disease diagnosis, chromosome identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant
                                                                                                                                                                                                                                                  Length 208;
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                  100.0%; Score 86; DB 7; 1
100.0%; Pred. No. 4.4e-07;
                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB84945 standard; protein; 208 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-2000; 2000US-0222425P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-AUG-2002; 2002US-00227883.
                                                                                                                                                                                                                                                                                                                                                                        1 RORYLYTDDAQQTEAH 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO polypeptide #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 44 RORYLYTDDAOOTEAH
                                                                                                                                                                                                                                                                                                                  16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desnoyers L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-730024/69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003073817-A1.
                                                                                                                                                                                            Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB84945;
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                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 22
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Compleptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

consecul for stimulating the proliferation of or gene expression in

pericyte cells. PRO237, PRO225, PRO1132, PRO4405 polypeptide are useful

for stimulating the proliferation or differentiation of chondrocyte

cells. PRO213, PRO257, PRO125, PRO1155, PRO1160 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)-

alpha from human blood. PRO982, PRO357, PRO125, PRO1306, PRO1419, PRO1414,

CC PRO1478, PRO1134, PRO826, PRO1005, PRO983, PRO1411, PRO1411, PRO1411,

CR PRO1478, PRO1330, PRO1367, PRO1305, PRO1301, PRO1414, PRO13139,

CC PRO1486, PRO1330, PRO1347, PRO1305, PRO1494, PRO1411, PRO1411, PRO13138,

CC PRO1487, PRO1370, PRO4405, PRO1405, PRO1414, PRO1311, PRO13138,

CC PRO1487, PRO1370, PRO4405, PRO1404, PRO1417, PRO1444, PRO13138,

CC PRO1487, PRO528, PRO4414, PRO1805, PRO1444, PRO1411, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, PRO1406, P
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                                                                                                                                                                                                                  Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthitic; pericyte cell proliferation; chondrocyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated PRO polypeptide useful for tissue typing, gene therapy, a molecular weight markers in protein electrophoresis, and for treating arthritis and tumors.
                                                                                                                                                               Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Fig 78; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                  04-DEC-2003 (first entry)
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I, Gurney AL,
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technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
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Sequence 208 AA;

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                           Gaps
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100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07;
                          0; Indels
                          0; Mismatches
                           16; Conservative
    Query Match
Best Local Similarity
                              Matches
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RORYLYTDDAQQTEAH 16 44 RORYLYTDDAOOTEAH 59

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RESULT 23

ADB78051 standard; protein; 208 AA.

(first entry) 04-DEC-2003 ADB78051;

Novel human secreted and transmembrane protein PRO10196.

Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; chondrocyte cell differentiation; chondrocyte cell proliferation, chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy

Homo sapiens

US2003092886-Al.

15-MAY-2003

09-AUG-2002; 2002US-00216165.

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 25-JUL-2000; 2000US-0220607P.

09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

PJ; Wood WI; Gerritsen ME, Goddard A, Godowski F Smith V, Stephan JF, Watanabe CK, Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, WPI; 2003-765494/72. Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers in protein electrophoresis, for treating

Claim 11; Fig 78; 308pp; English.

arthritis, tumor.

N-PSDB; ADB78050.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in

pericyte cells. PRO357, PRO1229, PRO1272 or PRO4405 polypeptide are useful cor stimulating the proliferation or differentiation of chondrocyte cells. PRO357, PRO355, PRO1355, PRO1365 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF) calpha from human blood. PRO982, PRO357, PRO136, PRO1419, PRO1419, PRO1414, PRO1411, PRO1411, PRO1411, PRO1411, PRO1411, PRO1411, PRO1411, PRO1411, PRO1411, PRO1412, PRO1547, PRO1347, PRO1347, PRO1340, PRO1366, PRO1366, PRO1366, PRO1366, PRO1366, PRO1366, PRO1366, PRO1366, PRO1367, PRO1366, PRO1366, PRO1367, PRO1366, PRO1367, PRO1367, PRO1366, PRO1367, PRO1366, PRO1367, PRO1367, PRO1366, PRO1367, PRO1366, PRO1367, PRO1366, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, PRO1367, PRO1368, P transmembrane PRO polypeptide.

8888888888888888888888888888888888888

Sequence 208 AA;

٥; Gaps ö 100.0%; Score 86; DB 7; Length 208; ilarity 100.0%; Pred. No. 4.4e-07; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity

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RESULT 24

ADB87117 standard; protein; 208 AA. ADB87117;

04-DEC-2003 (first entry) Human PRO polypeptide #39

Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breat; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.

Homo sapiens

US2003088067-A1

08-MAY-2003.

L3-AUG-2002; 2002US-00219479

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Godowski PJ;

Goddard A, Godowers -- Ash JF, Watanabe CK,

Gerritsen ME, Goddard Smith V, Stephan JF,

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polypeptides encoding them.

Transmembrane polypeptides) and the PRO polynucleotides encoding them. CT fro PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumour, rectal tumour or liver tumour, breast tumour, rectal tumour or liver tumour, breast tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNP) alpha from human constitution the release of tumour necrosis factor (TNP) alpha from human constitution in perioryte cells, for stimulating the proliferation of or gene expression in perioryte cells or for stimulating the proliferation of or gene constant fibroblasts. The PRO nucleic acids are useful as nicknesses and probes, in chromosome and gene mapping, in generating transgenic animals or knock-out animals which reagents, in gene therapy, in chromosome and gene mapping, in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as periorye-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the recondition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as periorye-associated tumours and bone and/or cartilage consisting analyses of propressing an electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                          One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                          Claim 11; Fig 78; 314pp; English.
                         Desnoyers L,
                                                                                                    2003-657981/62
                                                                                                                                   N-PSDB; ADB87116
                                                     Grimaldi JC,
                         Baker KP,
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ö Gaps ö 100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; cive 0; Mismatches 0; Indel8 Local Similarity 100. Sequence 208 AA; Query Match Best Loca Matches

1 RORYLYTDDAOOTEAH 16 44 RORYLYTDDAQQTEAH 59 à g

ADB84699 standard; protein; 208 AA. 04-DEC-2003 (first entry) ADB84699; RESULT 25 ADB84699

Human, PRO, secreted polypeptide, transmembrane polypeptide, tumour, cancer, lung, colon, breast, prostate, rectum, liver, tumour necrosis factor-alpha, TWF-alpha, blood, chondrocyte cell, pericyte cell, dermal fibroblast, bone disorder, cartilage disorder, arthritis, sports injury, cytostatic, antiarthritic.

Human PRO polypeptide #39

Ното варіеля

US2003092890-A1

15-MAY-2003

14-AUG-2002; 2002US-00219536.

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynucleotides encoding them. The PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation of crosmal time periotyte cells, for stimulating the proliferation of or gene cymral human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating certonlogy, in generating transgenic animals which may be used in the development and screening of therapeutically useful reagents, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in generating probes. The PRO polypeptides, or anti-PRO markers and in generating probes. The PRO polypeptides, or anti-PRO markers and in generating probes. The PRO polypeptides or anti-PRO markers and in generating a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the re-
                                                                                                                                                                                                                                                              Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                        New isolated PRO polypeptides, useful for tissue typing, gene therapy, molecular weight markers in protein electrophoresis, and for treating
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                                                                                                                                                                                                                                   Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 78; 308pp; English.
28-JUL-1999; 99US-0146222P.
24-FEB-2000; 2000MO-US005004.
02-MAR-2000; 2000MO-US015801.
01-JUN-2001; 2001WO-US011800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 RORYLYTDDAQQTEAH
                                                                                                                                                                                                                                        Desnoyers L,
                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   arthritis and tumors.
                                                                                                                                                                                                                                                                                                                    WPI; 2003-777259/73
                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADBB4698.
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                                                                                                                                                                                                                                                                      Grimaldi JC,
                                                                                                                                                                                                                                           Baker KP,
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             셤
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as

ADB83814 standard; protein; 208 AA. (first entry) 04-DEC-2003 ADB83814; RESULT 26 ADB8381

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Novel human secreted and transmembrane protein PRO10196.

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) -alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;

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LO-APR-2003.
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colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; JS2003069397-A1 Homo sapiens, gene therapy

09-AUG-2002; 2002US-00216159.

25-JUL-2000; 2000US-0220607P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-657584/62. N-PSDB; ADB83813.

New isolated polypeptides designated PRO polypeptides including polypeptides useful for stimulating the proliferation or differentiation of specific cell types, and for diagnosing cancer.

Claim 11; Fig 78; 314pp; English

The invention describes an isolated PRO (secreted and transmembrane)

Compleptide (I). PRO982, PRO1160, PRO1187 or PRO1229 polypeptide are

completed (I). PRO982, PRO1160, PRO1187 or PRO1229 polypeptide are

completed (I). PRO982, PRO2127, PRO1229, PRO1259 polypeptide are useful

constituent of completed are useful

constituent of conditional process of the pro116 polypeptide

constituent of conditional process.

CC cols. PRO211, PRO327, PRO725, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNF)
constituent blood. PRO982, PRO351, PRO1725, PRO1306, PRO1419, PRO1414,

PRO1347, PRO3137, PRO526, PRO1605, PRO1603, PRO1141, PRO1060,

CC COMPANATOR PRO1340, PRO1347, PRO1347, PRO1341, PRO1414, PRO1341,

PRO1366, PRO1330, PRO1367, PRO1305, PRO1479, PRO1441, PRO1341,

CC PRO1266, PRO1367, PRO1367, PRO1069, PRO1471, PRO1341, PRO1367,

CC PRO1867, PRO1386, PRO1367, PRO1069, PRO1471, PRO1341, PRO1367,

CC PRO1867, PRO1368, PRO1364, PRO1373, PRO1484, PRO1347, PRO1367,

CC PRO1867, PRO1368, PRO1364, PRO1373, PRO1468, PRO4364, PRO4367,

CC PRO1867, PRO1668, PRO1184, PRO1372, PRO1488, PRO4362, PRO4468,

CC PRO1867, PRO1668, PRO11844, PRO1372, PRO1488, PRO4362, PRO4408,

CC PRO1867, PRO16674, OR PRO7425, PRO1744, PRO5778, PRO4408,

CC PRO1867, PRO16674, OR PRO7425, PRO1744, PRO5778, PRO4408,

CC Inhibiting the proliferation of normal human dermal fibroblast cells.

CC Inhibiting the proliferation of normal human dermal fibroblast cells.

CC Inhibiting the proliferation of normal human dermal fibroblast cells.

CC Inhibiting the prosence of tumour in a mammal mannal. The mammal minder cells of the same cell type, where a higher level of expression of the prosence of tumour, rectal tumour or cumour, breast tumour, prostate tumour, rectal tumour or cumour, breast tumour prostate tumour, rectal tumour or cumour, breast tumour prostate tumour, rectal tumour or cumour, breast unmour, prostate tumour, rectal tumour or cumour, colon tumour breast sample of cells take mannal mannal ma transmembrane PRO polypeptide.

The invention describes an isolated PRO (secreted and transmembrane)

CD polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the pro216 pro1272 or PRO4405 polypeptide are useful for stimulating the pro11feration or differentiation of chondrocyte for stimulating the pro11feration or differentiation of chondrocyte are useful for stimulating the release of tumour necrosis factor (INF)
CD PRO241, PRO317, PRO526, PRO362, PRO3157, PRO1306, PRO1419, PRO1419, PRO1314, PRO1317, PRO526, PRO363, PRO357, PRO1206, PRO1419, PRO1419, PRO1309, PRO1409, PRO1130, PRO1130, PRO1130, PRO1309, PRO1409, PRO1130, PRO1309, PRO1409, PRO1309, PRO1409, PRO1309, PRO1409, PRO1309, PRO1409, PRO1409, PRO1401, PRO1409, PRO1401, PRO1309, PRO1409, PRO1401, PRO1409, PRO1401, PRO1401, PRO1401, PRO1409, PRO1401, PRO1401, PRO1409, PRO140

Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers, for treating arthritis, tumor.

Claim 11; Fig 78; 308pp; English.

inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which removes comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of

Sequence 208 AA;

0 Gaрв ő Query Match 100.0%; Score 86; DB 7; Length 208; Best Local Similarity 100.0%; Pred. No. 4.4e-07; Matches 16; Conservative 0; Mismatches 0; Indels

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Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                   human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) - alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
                                                                                                                                                                                                                      colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                   Novel human secreted and transmembrane protein PRO10196.
                                                                      ADB72969 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                 12-AUG-2002; 2002US-00218956.
                                                                                                                                                                                                                                                                                                                                                      29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
1 RORYLYTDDAQQTEAH 16
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                    44 RORYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-777258/73.
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                                                                                                                                                                                                                                              gene therapy.
                                                                                                                                                                                                                                                                     Homo sapiens.
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the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane polypeptides) and the PRO polymuclectides encoding them. The PRO polypeptides and polymuclectides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of
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                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, or for preparing a medicament for treating
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                                                                                                                                                                                                                                                                           Length 208;
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                                                                                                                                                                                                                                                                           100.0%; Score 86; DB 7; I 100.0%; Pred. No. 4.4e-07;
                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC36807 standard; protein; 208 AA.
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                                                                                                                                                                                                    transmembrane PRO polypeptide
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          44 RORYLYTDDAGGTEAH
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                                                                                                                                                                                                                                                                                                                     Conservative
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N-PSDB; ADC36806.
                                                                                                                                                                                                                                                                                             Local Similarity
Les 16; Conserv
                                                                                                                                                                                                                                          Sequence 208 AA;
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                                                                                                                                                                                                                                                                                 Query Match
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chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells or for stimulating the proliferation of normal human dermal fibroblasts. The PRO nucleic acide are useful as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO markers and in generating probes. The PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, gports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, PRO, secreted polypeptide, transmembrane polypeptide, tumour, cancer, lung, colon; breast, prostate, rectum, liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast, bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                          100.0%; Score 86; DB 7; 100.0%; Pred. No. 4.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC21797 standard; protein; 208 AA.
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20-JUN-2000; 2000US-0212901P
22-JUN-2000; 2000US-0213807P.
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25-JUL-2000; 2000US-0220585P
25-JUL-2000; 2000US-0220605P
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25-JUL-2000; 2000US-0220638P
25-JUL-2000; 2000US-0220664P
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26-JUL-2000; 2000US-0220893P.
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2000US-0220607P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polypeptide #39
                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                            Sequence 208 AA;
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24-AUG-2000;
10-NOV-2000;
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22-AUG-2000;
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20-DEC-2000;

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them. The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour nerrosis factor (TMF)-alpha from human blood, for stimulating the proliferation or differentiation of conditoryte cells for stimulating the proliferation of or gene cormal human dermal fibroblasts. The PRO mucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in generating probes. The PRO polypeptides or anti-PRO antibodies, are useful for preparing a medicament for treating a medicament for treating and condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO condition which is responsive to the propertical propertical propertical propertical propertical propertical propertical propertical propertical propertical propertical propertical propertical propertical pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated PRO polypeptide useful for tissue typing, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.
                                                                                                                                                                                                                                                       Godowski PJ;
~~ Wood WI;
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Smith V, Stephan JF, Watanabe CK,
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                          2001WO-US006520.
2001WO-US017092.
2001WO-US017800.
                                                                                                                      29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
2000WO-US034956
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Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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01-JUN-2001;
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Gaps
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Length 208;
                        0; Indels
100.0%; Score 86; DB 7; L 100.0%; Pred. No. 4.4e-07;
                          Mismatches
                          ;
            Local Similarity 100.
nes 16; Conservative
 Query Match
Best Local S:
Matches 16
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ADC49828 standard; protein; 208 AA. RESULT 30 ADC49828

ADC49828;

18-DEC-2003

Novel human secreted and transmembrane protein PRO10196. (first entry)

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

cuseful for stimulating the proliferation of or gene expression in

periorte cells. PRO357, PRO2129, PRO1272 or PRO4455 polypeptide are useful

cor stimulating the proliferation of differentiation of chondrocyte

cells. PRO231, PRO357, PRO7125, PRO1306, PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNRY)
cells. PRO331, PRO356, PRO951, PRO3156, PRO1306, PRO1419, PRO1416,

RRO1478, PRO1134, PRO826, PRO3105, PRO1909, PRO1101, PRO1411, PRO1806,

RRO1478, PRO1134, PRO1266, PRO1105, PRO1909, PRO1174, PRO1141, PRO1180,

RRO1478, PRO1330, PRO1307, PRO1305, PRO1417, PRO1141, PRO1180,

RRO1431, PRO325, PRO1814, PRO1106, PRO1433, PRO1444, PRO1316,

RRO1431, PRO325, PRO1841, PRO1106, PRO1433, PRO1444, PRO1326,

RRO1431, PRO325, PRO1841, PRO1106, PRO1433, PRO1444, PRO1326,

RRO1841, PRO3259, PRO788, PRO1106, PRO1433, PRO1444, PRO1432,

CC RRO1841, PRO225, PRO788, PRO11074, PRO1137, PRO1468, PRO3444,

RRO1841, PRO225, PRO788, PRO11084, PRO1433, PRO1408, PRO4408,

CC RRO1841, PRO225, PRO788, PRO11084, PRO1437, PRO1408, PRO4408,

CC RRO1841, PRO225, PRO788, PRO11084, PRO1474, PRO1414, PRO4408,

CC RRO1841, PRO225, PRO788, PRO1444, PRO1474, PRO1414, PRO4408,

CC RRO1841, PRO225, PRO7455, PRO1448, PRO4408, PRO4408,

CC COMPANION of the same and a control sample of

CC COMPANION of the same cell type presence of tumour, rectal tumour or

CC Thermour. (I) is useful as molecular weight markers, for tissue

CC Typing, or as therapeutic agents. A polymorisectide (II) encourtol sample

CC Typing, or as therapeutic agents. A polymorisectide (II) encourtol sample

CC Typing, or as therapeutic agents. A polymorisectide (II) encourtol sample

CC Typing, or as therapeutic agents. A polymorisectide (II) encourtol sample

CC Typing, or as therapeutic agence. A property and a profit or tracting transgenic animals or knock-out animals without an escreening or sece Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; New secreted and transmembrane PRO polypeptide useful for preparing medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody, e.g. cancer. liver tumour; tissue typing; chromosome mapping; gene mapping; Claim 11; SEQ ID NO 78; 314pp; English transmembrane PRO polypeptide. 25-JUL-2000; 2000US-0220605P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480. 14-AUG-2002; 2002US-00219075. Desnoyers L, C, Gurney AL, (GETH) GENENTECH INC. WPI; 2003-801154/75. N-PSDB; ADC49827 Sequence 208 AA; US2003088064-A1 Grimaldi JC, gene therapy Homo sapiens 08-MAY-2003 Baker KP,

ö Gaps ; Query Match 100.0%; Score 86; DB 7; Length 208; Best Local Similarity 100.0%; Pred. No. 4.4e-07; Matches 16; Conservative 0; Mismatches 0; Indels

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44. RQRYLYTDDAQQTEAH 59

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The invention describes an isolated PRO (secreted and transmembrane)

C polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

collegiul for stimulating the proliferation of or gene expression in

CC pericyte cells. PRO357, PRO225, PRO1272 or PRO4405 polypeptide are useful

colles. PRO231, PRO357, PRO225, PRO1155, PRO1306 or PRO1419 polypeptide

CC are useful for stimulating the release of tumour necrosis factor (TNP)-

alpha from human blood. PRO982, PRO357, PRO1306, PRO1419, PRO1419,

CC PRO347, PRO337, PRO526, PRO363, PRO531, PRO1091, PRO1419, PRO1419,

CC PRO147, PRO1330, PRO1347, PRO1065, PRO1919, PRO1414, PRO1420,

CR PRO1486, PRO1389, PRO1387, PRO1080, PRO1071, PRO1414, PRO1432,

CC PRO1286, PRO1389, PRO1387, PRO1409, PRO1431, PRO1341, PRO1326,

CC PRO1487, PRO239, PRO4341, PRO1801, PRO4333, PRO3444, PRO4432,

CC PRO1487, PRO525, PRO988, PRO1801, PRO44333, PRO3444, PRO4432,

CC PRO523, PRO5725, PRO188, PRO1194, PRO1425, PRO1489, PRO4432, PRO4489,

CC PRO5723, PRO5725, PRO7154, or PRO1404, PRO4432, PRO4489,

CC PRO5723, PRO5725, PRO7154, or PRO1405, PRO1489, PRO4432, etc.,

CC PRO5723, PRO5725, PRO7154, or PRO1404, PRO4432, etc.,

CC PRO5723, PRO5725, PRO7154, or PRO1404, PRO4432, PRO5729, PRO54040, PRO4981, PRO1275, PRO1489, PRO5432, etc.,

CC PRO5723, PRO5725, PRO7154, or PRO7425, PO1799Ptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO5725, PRO
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                                                                                                                                                                                                                                        human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                             Novel human secreted and transmembrane protein PRO10196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 78; 315pp; English
                                           ADC49027 standard; protein; 208 AA
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                  18-DEC-2003 (first entry)
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Grimaldi JC, Gurney AL,
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N-PSDB; ADC49026.
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                                                                                              ADC49027;
RESULT 31
                           ADC4902
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the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, because tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PROS17, PROS29, PRO1772 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   release;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; prostate tumour; lung tumour; liver tumour; prostate tumour; rectal tumour; liver tumour; chondrocome mapping; chromosome mapping;
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                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                         100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted and transmembrane protein PRO10196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC49544 standard; protein; 208 AA
                                                                                                                                                                                                   sport injuries). This is the a
transmembrane PRO polypeptide.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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Grimaldi JC, Gurney AL,
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N-PSDB; ADC49543.
                                                                                                                                                                                                                                                             Sequence 208 AA;
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Goddard A, Godowski PJ; ohan JF, Watanabe CK, Wood WI;

Gerritsen ME, Goddard Smith V, Stephan JF,

Desnoyers L,

Baker KP, De Grimaldi JC,

WPI; 2003-801157/75.

N-PSDB; ADC47404

(GETH) GENENTECH INC

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

New PRO polypeptide for use as molecular weight markers for protein electrophoresis purposes and for detecting the presence of tumor in

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pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful cor stimulating the proliferation or differentiation of chondrocyte cells. PRO351, PRO355, PRO155, PRO155, PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TMF) alpha from human blood. PRO982, PRO357, PRO325, PRO1306, PRO1419, PRO1419, PRO1419, PRO1414, PRO1419, PRO1414, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419
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29-AUG-2002; 2002US-00232233. 25-JUL-2000; 2000US-0220605P.

US2003088072-A1

08-MAY-2003

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                                                                                                                                                                                                                                                                                                            100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; ative 0; Mismatches 0; Indels
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                                                                                     Claim 11; Fig 78; 314pp; English.
                                                                                                                                                                                                                                                                                         transmembrane PRO polypeptide.
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Matches 16; Conservative
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transmembrane PRO polypeptide.

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gene therapy
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Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; perioyte cell proliferation; chondrooyte cell proliferation; chondrooyte cell proliferation; chondrooyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell mifferentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
Novel human secreted and transmembrane protein PRO10196.
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Homo sapiens

US2003105288-A1.

05-JUN-2003

13-AUG-2002; 2002US-00219070,

25-JUL-2000; 2000US-0220666P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-801246/75. N-PSDB; ADC47149. New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

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The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in perioryte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO351, PRO355, PRO1155, PRO136 or PRO4419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF) alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO144, PRO1419, PRO144, PRO1134, PRO1305, PRO1055, PRO183, PRO840, PRO1080, PRO1055, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, PRO1305, P
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Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                              100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07;
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                                                                                                    100.0%; Fiv
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
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Grimaldi JC, Gurney AL,
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N-PSDB; ADC78024.
                                               Sequence 208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC78025;
                                                                                                                                                                                                                                                                                                                                         RESULT 35
ADC78025
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stimulating the proliferation of normal human dermal fibroblasts cells.

PRO181, PRO229, PRO186, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,

PRO5721, PRO5725, PRO7124, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which control sample of involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample cells indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. [1] is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful cells useful as molecular weight annound are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, propertice). This is the mammal and processed in the amino acid sequence of a human secreted and transmembrane PRO polypeptide. 8888888888888888888888888888

Sequence 208 AA;

; 100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; Indels 0; Mismatches 1 RORYLYTDDAQQTEAH 16 Query Match Best Local Similarity 100.0 Matches 16; Conservative ò

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Gaps

44 RORYLYTDDAOOTEAH 59

ADD06260 standard; protein; 208 AA. ADD06260;

Novel human secreted and transmembrane protein PRO10196. (first entry) 01-JAN-2004

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy

Ношо варіепв

US2003073816-A1

17-APR-2003.

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480. 26-AUG-2002; 2002US-00227873.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-644807/61. N-PSDB; ADD06259 New PRO polypeptides and nucleic acids encoding the polypeptides, useful

The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (I). PRO982. PRO1160, PRO1837 or PRO1339 polypeptide are

cuseful for stimulating the proliferation of or gene expression in

periorte cells. PRO357, PRO225. PRO1272 or PRO4405 polypeptide are useful

cor stimulating the proliferation of differentiation of chondrocyte

cclls. PRO357, PRO352, PRO1155, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNF)
are useful for stimulating the release of tumour necrosis factor (TNF)
are useful for stimulating the release of tumour necrosis factor (TNF)
RRO143, PRO3137, PRO356, PRO3157, PRO1306, PRO1306, PRO1419, PRO1306,

RRO143, PRO1310, PRO1307, PRO1305, PRO1005, PRO1192, PRO1104, PRO13130,

RRO1266, PRO1310, PRO1307, PRO1106, PRO1192, PRO11040, PRO13130,

RRO1926, PRO1181, PRO1307, PRO1106, PRO1192, PRO11040, PRO13130,

RRO1926, PRO1181, PRO1307, PRO1106, PRO1192, PRO11040, PRO13130,

RRO1926, PRO1928, PRO7184, PRO1106, PRO1192, PRO1140, PRO1312,

RRO1934, PRO5079, PRO6079, PRO1006, PRO1192, PRO1192, PRO1140, PRO4322,

RRO1940, PRO6079, PRO6079, PRO1006, PRO1192, PRO1140, PRO4322,

RRO181, PRO323, PRO7184, PRO1144, PRO11727, PRO1140, PRO4181,

RRO181, PRO523, PRO7184, PRO1144, PRO11727, PRO1140, PRO4108,

RRO181, PRO523, PRO7184, PRO1144, PRO1174, PRO5778, PRO4408,

RRO181, PRO523, PRO7184, PRO1144, PRO1174, PRO5778, PRO4408,

RRO181, PRO523, PRO7184, PRO4981, PRO1174, PRO5778, PRO4408,

CC Inhibiting the proliferation of normal human dermal fibroblast cells. PRO

contain cells of the same cell type presence of tumour in a mammal which a comparing the presence of tumour, rectal tumour or test sample of cells taken from the mammal, and a control sample of the presence of tumour, rectal tumour relationed and gene anaphaing or gene therapy. (II) is useful as molecular weight markers, for timeur colon tumour, breast tumour in Promour Prosence and gene mapphing or gene therapy. (II) are secenting useful for treating bone and gene mappi in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping. Claim 11; SEQ ID NO 78; 314pp; English. transmembrane PRO polypeptide.

Sequence 208 AA;

Gaps ö 100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; Live 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 16; Conservative

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ADC77779 standard; protein; 208 AA. 01-JAN-2004 (first entry) ADC77779;

RESULT 37

Novel human secreted and transmembrane protein PRO10196.

Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; tumour; chondrocyte cell differentiation; tumour necrosis factor alpha (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy

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08-MAY-2003.
        e.g. cancer.
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Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood WI;

Gerritsen ME, Goddard / Smith V, Stephan JF,

01-JUN-2001; 2001WO-US017800 29-JUN-2001; 2001WO-US021066 09-APR-2002; 2002US-00119480. 13-AUG-2002; 2002US-00219466 Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, (GETH) GENENTECH INC. WPI; 2003-657980/62. N-PSDB; ADC77778 US2003088066-A1.

One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, or for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody,

Claim 11; Fig 78; 314pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

to useful for stimulating the pro229, PRO1272 or PRO4405 polypeptide are useful

pericyte cells. PRO357, PRO225, PRO1272 or PRO4405 polypeptide are useful

for stimulating the pro11feration or differentiation of chondrocyte

cells. PRO231, PRO357, PRO1255, PRO1155, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)
alpha from human blood. PRO982, PRO351, PRO125, PRO1306, PRO1194, PRO1341,

PRO137, PRO337, PRO826, PRO1005, PRO9195, PRO141, PRO1411, PRO11080,

PRO1025, PRO1134, PRO136, PRO1305, PRO1174, PRO1411, PRO1411,

PRO1286, PRO1330, PRO1341, PRO1404, PRO1474, PRO1374, PRO1376,

PRO1887, PRO1376, PRO1387, PRO1409, PRO11474, PRO1917, PRO1446, PRO1387,

PRO1887, PRO1381, PRO4189, PRO1444, PRO1373, PRO1367,

PRO1887, PRO529, PRO788, PRO1184, PRO1174, PRO1917, PRO1186,

PRO1887, PRO5225, PRO7184, or PRO1405, PRO4488, PRO4432, PRO4484,

PRO5723, PRO5725, PRO7184, or PRO7425 polypeptide are useful for

containing the pro11feration of normal human dermal fibroblast cells. PRO1881, PRO5725, PRO788, PRO1841, PRO1374, PRO5778, PRO4332, etc.,

are useful for detecting the presence of tumour in a mammal which

involves comparing the level of expression of the above PRO polypeptides

in a test sample of cells taken from the mammal, and a control sample

control cells of the same cell type, where a higher level of expression of

the PRO polypeptides in the test sample as compared to the control sample

the PRO polypeptides in the test sample as compared to the control sample

the promite of the prometry prosefule tumour, rectal lumour is a lung

the promite of the prometry prosefule tumour, rectal lumour is a lung

the promite of the prometry prosefule tumour in the presence of tumour in the health promite of tumour in the promite promite prometry prometry prometry prosefule tumour in the prometry prometry prometry prometry promet tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO329, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

Sequence 208 AA;

ö Gaps .. 0 100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07; ive 0; Mismatches 0; Indels 16; Conservative Query Match Best Local Similarity Matches 16; Conserva

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ADD50742

ADD50742 standard; protein; 208 AA.

ADD50742;

(first entry) 15-JAN-2004 Novel human secreted and transmembrane protein PRO10196

Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;

gene therapy

Homo sapiens.

US2003105291-A1.

05-JUN-2003.

26-AUG-2002; 2002US-00227877.

29-JUN-2001; 2001WO-US021066.

(GETH) GENENTECH INC

PJ; Wood WI; Gerritsen ME, Goddard A, Godowski P Smith V, Stephan JF, Watanabe CK, Desnoyers L, Grimaldi JC, Baker KP,

2003-829361/77.

N-PSDB; ADD50741.

New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.

Claim 11; Fig 78; 308pp; English.

The invertion describes an isolated PVO | Secreted and transmission of useful for stimulating the proliferation of or gene expression in useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO259, PRO1502 or PRO4405 polypeptide are useful for stimulating the proliferation of or differentiation of chondrocyte cells. PRO351, PRO357, PRO155, PRO1306 or PRO1419 polypeptide cells. PRO351, PRO357, PRO355, PRO1306 or PRO1419 polypeptide cells. PRO331, PRO357, PRO357, PRO1805, PRO1419, PRO1419, PRO1416, PRO1414, PRO357, PRO1557, PRO1057, PRO1060, PRO1060, PRO1060, PRO1414, PRO1414, PRO1414, PRO1414, PRO1414, PRO1414, PRO1414, PRO1414, PRO1414, PRO1416, PRO1466, PRO1466, PRO1444, PRO1444, PRO1464, PRO1466, PRO1466, PRO1467, PRO1467, PRO1467, PRO1467, PRO1467, PRO1467, PRO1467, PRO1464, PRO166079, PRO166079, PRO166079, PRO166079, PRO166079, PRO166079, PRO166076, PRO166079, PRO16607 The invention describes an isolated PRO (secreted and transmembrane)

PRO147, PRO137, PRO526, PRO363, PRO531, PRO1083, PRO0840, PRO1080,
PRO1476, PRO1134, PRO626, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
PRO10286, PRO1134, PRO1126, PRO1106, PRO1071, PRO1411, PRO1309,
PRO10286, PRO1330, PRO1387, PRO1305, PRO1273, PRO1274, PRO1412,
PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1979, PRO1340, PRO1328,
PRO1940, PRO6079, PRO9836 or PRO1096 POLYPEPEDIG are useful for
etimulating the proliferation of normal human dermal fibroblasts cells.
PRO9940, PRO5725, PRO7154, or PRO1425 POLYPEPEDIG are useful for
pro19529, PRO5725, PRO7154, or PRO1425, PRO1432, PRO4408,
PRO5723, PRO5725, PRO7154, or PRO1405, PRO1714, PRO5778, PRO4408,
PRO5723, PRO5725, PRO7154, or PRO4981, PRO1714, PRO5778, PRO4408,
PRO5723, PRO5725, PRO7154, or PRO4981, PRO1714, PRO5778, PRO4408,
PRO5723, PRO5725, PRO164 or PRO4981, PRO1714, PRO5778, PRO4322, etc.,
are useful for detecting the presence of tumour in a mammal which
involves comparing the level of expression of the above PRO polypeptides
involves comparing the level of expression of the above PRO polypeptides
involves comparing the level of expression of the above PRO polypeptide
is indicative of the presence of tumour in the mammal. The tumour is lung
tumour, colon tumour, breast tumour, profete tumour, rectal tumour or
tumour, breast tumour, profete tumour, rectal tumour or
liver tumour. (1) is useful as molecular weight markers, for tissue
typing, or as therapeutic agents. A polynucleotide (11) is useful
for generating transgenic animals or knock-out animals which are useful
screening useful reagents. PRO357, PRO229, PRO172 or PRO4405 polypeptide
is useful for treating bone and/or cartilage disorders (e.g., arthritis,
sport injuries). This is the amino acid sequence of a human secreted and

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typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PJ;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; perioyte cell proliferation; perioyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                Gaps
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                                                                                                                                     Length 208;
                                                                                                                     100.0%; Score 86; DB 7; Length 20: 100.0%; Pred. No. 4.4e-07; wismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                                         ADD50988 standard; protein; 208 AA
                                                                                 transmembrane PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-2002; 2002US-00219527.
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09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                  Conservative
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                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                             Sequence 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy
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                                                                                                                                                                                                                                                                                                                    ADD50988;
                                                                                                                                      Query Match
                                                                                                                                                      Local
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                               RESULT 39
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transmembrane PRO polypeptide.

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Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                               Human, PRO, secreted polypeptide, transmembrane polypeptide, tumour,
cancer, lung, colon, breast, prostate; rectum, liver;
tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
arthritis; sports injury; cytostatic; antiarthritic.
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                             100.0%; Score 86; DB 7; Length 208; 100.0%; Pred. No. 4.4e-07;
                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen ME,
Smith V, St
                                                                                                                                                                                                                                                                                                                                                             ADD50469 standard; protein; 208 AA.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                 44 RORYLYTDDAOOTEAH 59
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO polypeptide #39.
                                                                                                                                                                                                                                                                                               1 RORYLYTDDAQQTEAH
                                                                                                                                                                                                                                                                    Local Similarity 100.
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C, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                             Sequence 208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker KP, De
Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                              RESULT 40
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WPI; 2003-765528/72.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the prol16ration of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4465 polypeptide are useful for stimulating the prol1feration or differentiation of chondrocyte cells. PRO357, PRO125, PRO1155, PRO1360 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (PMF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,

New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.

Claim 11; Fig 78; 309pp; English.

Gerritsen ME, Goddard A, Godowski E Smith V, Stephan JF, Watanabe CK,

ŗ,

Desnoyers C, Gurney

Grimaldi JC,

Baker KP,

WPI; 2003-829360/77. N-PSDB; ADD50987.

N-PSDB; ADD50468.

Novel isolated PRO polypeptide useful for tissue typing, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.

Claim 11; Fig 78; 308pp; English.

The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them.
The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumour, rectal tumour or liver tumour, breast tumour, comparing the release of tumour necrosis factor (TNF) alpha from human constituting the proliferation of differentiation of condrovyte cells, for stimulating the proliferation of or gene expression in perioyte cells for stimulating the proliferation of condrovyte cells, for stimulating the proliferation of constant human dermal fibroblasts. The PRO nucleic acids are useful as commal human dermal fibroblasts. The PRO nucleic acids are useful as antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful creagents, in gene therapy, in chromosome identification, as chromosome condition which is responsive to the PRO polypeptides, or anti-PRO antibodies, such as perioyre-associated tumours and bone and/or cartiage condition which is responsive to the PRO polypeptides or anti-PRO disorders (e.g. arthritis, sports injuries), involving inducing the rectification of chondrocytes. The PRO polypeptides are useful as molecular markers and human PRO polypeptide of the invention.

Sequence 208 AA;

Gaps .; 0 Query Match 100.0%; Score 86; DB 7; Length 208; Best Local Similarity 100.0%; Pred. No. 4.4e-07; Matches 16; Conservative 0; Mismatches 0; Indels

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2, 2004, 16:04:51

Search completed: March Job time : 10.6 secs

Q81341 vibric Callogetocs drosophila

Q9f237 bacillus fl Q0f696 saccharomyc P89057 rotavirus cal Q06696 mac musculu Q97046 drosophila Q88796 lactobacill Q98796 sulfolobus Q9776 sulfolobus Q9776 sulfolobus Q9776 sulfolobus Q9776 sulfolobus Q9776 sulfolobus Q9177 caenorhabdi Q8nrc7 corynebacte Q92644 rhizobium m Q81pf9 drosophila Q90709 drosophila Q90709 drosophila Q90709 caenays (m Q8660 cae mays (m Q6191 caenorhabdi Q23770 caenorhabdi

Q9i9q8 brachydanio Q87h76 vibrio para Q8wv14 homo sapien Q8z7n2 salmonella

Q8vyu0 jatropha cu Q8s452 jatropha cu

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 86; DB 4; Length 209; 100.0%; Pred. No. 3.3e-07; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R, Strausberg R, Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC018404; AAH18404.1; -. GO, GO.0008083; F:growth factor activity; IEA. InterPro; IPR008996; Cytok ILL_like. InterPro; IPR002948; ILL_HBGF. PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00442; FGF; Ī.
SEQUENCE 209 AA; 22284 MW; 27925C43E5167823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 21.
Homo sapiens (Human)
QBL341
QBT008
QBT008
QD66696
PB9057
QBCED4
QBYYG6
Q9YYG6
Q9YYE6
Q9QUNO
QB177
QB177
QB177
QB177
QB177
QB177
QB177
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Q8WV14
Q8Z7N2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Sc
Best Local Similarity 100.0%; P:
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
                                                                                                                                                                                                                                             1 RORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 RQRYLYTDDAQQTEAH 60
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 SEQUENCE FROM N.A.
TISSUE=Lung;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
QBVIB0
ID QBVIB0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8N683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8N683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
   Q8N683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8n683 homo sapien
Q8vi80 rattus norv
Q64469 arabidopsis
G6510 kairi virus
Q8ibcl plasmodium
G4581 caenorhabdi
P47581 lactobacill
Q7xaql houttuynia
G64468 arabidopsis
Q9f810 oryza sativ
Q7xmq2 oryza sativ
Q7xmq2 oryza sativ
Q9872 blidobacte
Q9872 blidobacte
Q98y72 klebella
Q98y73 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             067110 aquifex aeo
                                                                                                                                 March 2, 2004, 15:51:42 ; Search time 6.66667 Seconds
(without alignments)
757.244 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                OM protein - protein search, using sw model
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QBV180
Q64169
Q65610
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P71428
Q7XAQ1
Q7XAQ2
Q1468
Q9FSS1
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sp_virus:*
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1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
5: sp_nammal:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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Match Length DB
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86
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349
2349
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                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                       Run on:
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209 AA

ALIGNMENTS

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Gaps

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208 AA

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349 AA; 38724 MW; 8836B8DF2AAE2AF7 CRC64;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             N protein.
Kairi virus.
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  SQ SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE-CV. Columbia;
MEDLINE-20033487; PubMed=10617197;
Lin X., Kaul S., PubMed=10617197;
Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyma T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.2%; Score 75; DB 11; Length 208; 87.5%; Pred. No. 3.1e-05; Indels iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AC002392; AAD12024.1; -.
PIR; T00526; T00526.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR001087; Lipase_GDSL.
Pfan; PF00657; Lipase_GDSL.
Hydrolase.
                                                                                                                                                                                                                                                                                                            "Ruttus norvegicus FGF21.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB078901, BAB84299-1;
GO, GO:0008083; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok III_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22857 MW; D232445902CDB8EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative GDSL-mocif lipase/hydrolase.
  Q8VIB0;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00167; FGF; 1.
PRINKE; PR00262; ILLHBGF:
ProDom; PD000831; ILL HBGF; 1.
SWART; SM00442; FGF; 1.
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=cv. Columbia;
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=10116;
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NCBI_TaxID=80939;
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SEQUENCE FROM N.A.

WADLINE=9417233; PubMed=8126455;

ADDIA E., Pritlove D.C., Elliott R.M.;

RT "Evolutionary relationships of the Bunyavirus S genome segment.";

RT "Gen. Virol. 75:597-608 (1994).

U. Gen. Virol. 75:597-608 (1994).

DR GO; GO:0019013; C:viral nucleocapsid; IEA.

DR GO; GO:0019013; C:viral nucleocap.

BR InterPro; IPR001784; Bunya nucleocap.

DR ProDom; P0001909; Bunya nucleocap.

ProDom; P0001909; Bunya nucleocap.

The ProDom; P0001909; Bunya nucleocap.

Remi: P0001909; Bunya nucleocap.

The ProDom; P0001909; Bunya nucleocap.

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The ProDom; P0001909; Bunya nucleocap.
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Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL644507; CAD51085.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 43; DB 5; Length 1916; 42.9%; Pred. No. 2.1e+02; ive 4; Mismatches 4; Indels
Score 46; DB 10; Length 349;
Pred. No. 8.6;
3; Mismatches 4; Indels
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 1916 AA; 230013 MW; 68FF914BBA3519BD CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                        233 A.A.
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Best Local Similarity 53.3%;
Matches 8; Conservative
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Mol. Gen. Genet. 200:193-198(1985)
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01-0CT-2003
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Q7XAQ1
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Rhabditidae; Peloderinae; Caenorhabditis.
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Losiance 282:2012-2018(1998).

Exmin; 292815; CABOT294.1; -.

EXMIN; 292815; CABOT294.1; -.

R HSSP, 291713; JSHP.

R HSSP, 291713; JSHP.

R HSSP, 291713; JSHP.

R HSSP, 291713; JSHP.

R InterPro; IPRO0223; Kunitz BPTI.

InterPro; IPRO0223; Kunitz BPTI.

InterPro; IPRO0815; Morm repeat.1.

R Ffam; PF00008; thyroglobulin.1; 1.

R Pfam; PF00008; thyroglobulin.1; 1.

R Pfam; PF00008; thyroglobulin.1; 1.

R R Pfam; PF0008; thyroglobulin.1; 1.

R R SMART; SM00131; KU; 1.0.

R SMART; SM0011; TY; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 5; Length 2225; Pred. No. 2.5e+02; 3; Mismatches 3; Indels
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PROSITE; PS50279; BPTI_KUNITZ_2; 10.
PROSITE; PS00484; THYRGGLOBULIN_1; 1.
PROCEASE inhibitor; Serine procease inhibitor.
SEQUENCE 2225 AA; 242198 MW; ASDDBAR59D2A7B02A CRC64;
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                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
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01-FEE-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Transposable element ISL1.
Lactobacillus casei.
                                                                                                                              Last sequence update)
Last annotation update)
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                                                                     2225 AA
                                                                                                              Created)
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STRAIN-Group B; TRANSPOSON=ISL1;
MEDLINE=85295506; Pubmed=2993817
MEDLINE=85295506; Kiwaki M., Hi:
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99069613; PubMed=9851916;
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                                                                                                           (TrEMBLrel. 06, TrEMBLrel. 06, TrEMBLrel. 24,
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                                                                     PRELIMINARY;
                                                                                                                                                                                                             Caenorhabditis elegans.
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Best Local Similarity
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                                                                                           045881;
01-JUN-1998 (
01-JUN-1998 (
01-JUN-2003 (
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045881
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STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, magnoliids, Piperales, Saururaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ito M., Imafuku M., Tanabe Y., Aoki S., Hasebe M.;
"MADS-box genes needed for determining petal identity express in
petal-like bracts of Houttuynia cordata (Saururaceae).";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB089157; BAC80233.1; --
SRQUENCE 243 AA; 27728 MW; 7B34DBER4609D8B8 CRC64;
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                                                                                                                                                                                                                                                                       Length 93;
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SEQUENCE FROM N.A.
STRAIN=Group B; TRANSPOSON=ISL1;
STRAIN=Group B; TRANSPOSON=ISL1;
Shintizu-Kadota M.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X02734; CAA26516.1; -.
PIR; S28726; S28726.
Interprive; IPROSS14; Transposase_8.
Interprive; IPROSS14; Transposase_8; 1.
SEQUENCE 93 AA; 10745 MM; 62584573F7F83DCE CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MADS-box transcription factor.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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15;
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                                                                                                                                                                                                                                                                                                                          2; Mismatches
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                                                                                                                                                                                                                                                                       47.7%; Score 41;
61.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houttuynia cordata (Chameleon plant)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 RRKLĽQLĎĎGSQŤNPH 183
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                                                                                                                                                                                                                                                                                                                                                                                  1 RORYLYTDDAQQT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                       43 RWRKLYTEDGKOT 55
                                                                                                                                                                                                                                                                                                Best Local Similarity 61.5
Matches 8; Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Q48525;
                                                              Q7XMQ2
   RESULT 11
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                                    Q7XMQ2
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Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.B., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Bisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Selzberg S.L., Fraser C.M., Venter J.C.; the plant Arabidopsis thaliana."
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoidese, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Han B., Zhou B., Feng Q., Huang Y.C., Chen Z.H., Li Y., Zhu J.J., Tang Y.S., Zhao Q., Liu Y.L., Mu J., Yu Z., Fan D.L., Chen L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Zhu J., Liu X.H., Hu X., Lei H.Y., Zhang Y.J., Wang Y.J., Wang Y.J., Ii C., Lu Y., Chen X.C., Zhang Y., Hu H., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F., "Oryza sativa indica (Guangluai4) genomic DNA, chromosome4, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.7%; Score 41; DB 10; Length 349; 46.7%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC002392; AAD12023.1; -. PIR; T00525; T00525. GO; GO:00146787; F:hydrolase activity; IEA. InterPro; IPR001087; Lipase_GDSL. Pfam; PF00657; Lipase_GDSL. I. Hydrolase. 349 Aa; 38577 MW; OSDAC363EA5F3D2A CRC64; SEQUENCE 349 Aa; 38577 MW; OSDAC363EA5F3D2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL442007; CAC09353.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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InterPro; IPR001092; HLH basic.
InterPro; IPR001087; Lipase_GDSL.
Pfam; PF00657; Lipase_GDSL; 1.
PROSITE; PS00038; HLH_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative lipase/acylhydrolase. H0212B02.9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RORYLYTDDAQQTEA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 46.7 tes 7; Conservative
                                                                                                                                                                                                                         Nature 402:761-768(1999)
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                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
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Matches
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AC 29FSS
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Han B., Fend C., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y.J., Lu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y., Lu G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sha G. Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

BMBL, Al606692, CAR04499.1;
SRQUENCE 355 AA, 39680 MW, CFDEBEADCCD52650 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Shimizu-Kadota M., Kiwaki M., Hirokawa H., Tsuchida N.;
"ISL1: a new transposable element in Lactobacillus casei.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae, Lactobacillus.
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SEQUENCE FROM N.A.
STRAIN=Group B; TRANSPOSON=ISL1;
Shimizu-Kadota M.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00665; rve; 1.
Pfam; PF01527; Transposase 8; 1.
SEQUENCE 385 AA; 44659 WW; D905D7AC279D8FF7 CRC64;
                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.7%; Score 41; DB 10;
50.0%; Pred. No. 69;
tive 2; Mismatches 5;
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355 AA
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61.5%; Pred. No.
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STRAIN=Group B; TRANSPOSON=ISLI;
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                                                                                                                                                             OSJNBb0059K02.9 protein.
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MEDLINE=98196666; PubMed=9537320;
EMBL; AF308468; AAG42467.1; -.
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                       NON TER
SEQUENCE
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STRAIN=NCC 2705;
MEDLINE=22294977;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
"The genome sequence of Bidiobacterium longum reflects its adaptation to the human gastrointestinal tract.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
  Gaps
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Enterohacteriaceae, Klebsiella.
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                                                                                                                                                                                             Bacteria, Actinobacteria, Actinobacteridae, Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium.

NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kolko M.M., Kapetanovich L.A., Lawrence J.G.; "Alternative pathways for siroheme synthesis in Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Alkaline phosphatase isozyme conversion protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                 47.7%; Score 41; DB 16; Length 10
61.5%; Pred. No. 2.3e+02;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                            to the human gastrointestinal tract.";

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).

EMBL, AE014723; AAN24815.1;

GO, GO:0006457; P:protein folding; IEA.

InterPro; IPR01179; FKBP PPIASE.!;

PROSITE; PS00453; FKBP PPIASE.!;

Hypothetical protein; Complete proteome.

SEQUENCE 1031 AA; 111948 WW; C38B478526A9891E CRC64;
 Indels
                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Narrowly conserved hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 AA
                                                                                                        PRT; 1031 AA
  2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 183:328-335(2001).
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293 QORYLYTDLAMSS 305
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                                               43 RWRKLYTEDGKOT 55
                         1 RORYLYTDDAQQT 13
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  8; Conservative
                                                                                                        PRELIMINARY;
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Bifidobacterium longum.
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Matches 8; Conserva
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                                                                                                                   Q8G5K2;
01-MAR-2003
01-MAR-2003
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Q9EYX7
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Rhabditidae; Peloderinae; Caenorhabditis.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
InterPro; IPR003003; TTM_chemrecept2.
InterPro; IPR0010169; NmTTM_chemrecept2.
Pfam; PF01604; Ttm 5; 1.
SEQUENCE 332 AA; 38162 MW; 5D903258D5357D9F CRC64;
                                                                                       Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 332;
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NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mortimore B.J.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
MEROPS; M28.005; -.
NON TER 174 174 AA; 19047 MW; 1F3869202E11437B CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein AQ_985.
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Last annotation update)
                                                                                       46.5%; Score 40; DB 2; 50.0%; Pred. No. 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281593; CAB04743.1; -.
PIK; T25023; T25023.
                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25, T20B3.5 protein.
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les 8; Conservative
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Caenorhabditis elegans.
                                                                                                          Best Local Similarity
Matches 7; Conser
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SEQUENCE FROM N.A.
STRAIN=VF5;
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us-10-060-765-7.rspt

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Ephydroidea; Drosophilidae; Drosophila.
                           NCBI_TaxID=7227;
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CX MEDIMER-21956561; PubMed=11953381;

Li M., Shimada T., Morris J.G. Jr., Sulakvelidze A., Sozhamannan S.;

Li M., Shimada T., Morris J.G. Jr., Sulakvelidze A., Sozhamannan S.;

Li M., Shimada T., Morris J.G. Jr., Sulakvelidze A., Sozhamannan S.;

Trains with pathogenic of non-01 and non-0139 Vibrio cholerae

grains with pathogenic potential by exchange of O-antigen

piosynthesis regions. 1.

Lifet. Immun. 70:2441.2453 (2002).

RBL, AF390677; APAN226641; -

RGJ, GO:0003677; F:DNA recombination; IEA.

GO; GO:0005310; P:DNA recombination; IEA.

RICEPTO; IPRO01102; R408—HTH.

RICEPTO; IPRO01584; Rve.

R Ffam; PF00665; rve; 1.

SEQUENCE 506 AA; S8610 MW; 06887234D0D27131 CRC64;
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Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; Inthe complete genome of the hyperthermophilic bacterium Aquifex
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                 46.5%; Score 40; DB 16; Length 403; 37.5%; Pred. No. 1.2e+02; cive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae 037.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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                                                                                                        Nature 392:353-358 (1998).

BMBL; AE000717, AAC07076.1; -.

PIR, C70385, C70385.

InterPro; IPR055017; Toluene_X.

Pfam, PF03349; Toluene X, 1.

Hypothetical protein; Complete protecome.

SEQUENCE 403 AA, 45861 MW; 04804382A9F76D03 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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Best Local Similarity 63.6
Matches 7; Conservative
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SU(DX) OR CG4244.
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Matches 6: Conper
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REMINIANCE FORM N.A.

Addama M.D. Celnikers S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RADAMA M.D. Celnikers S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RADAMA M.D. Celnikers S.E., Hill R.A., Hokkins R.A., Galle R.F.,

RADAMA M. L. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Burdon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RADAMA M. K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L.,

RADAMA M. R. Benos P.V., Berman B.P., Banadari D., Bolahakov S.,

RADAMI J.F., Agbayani A., An H.J. Andrews-Péanhocch C., Baldwin D.,

RADAMI J.F., Agbayani A., An H.J. Bouck J., Brokstein P., Erctlier P.,

Burkova D., Botcham M.R., Bouck J., Brokstein P., Erctlier P.,

Burkova D., Botcham M.R., Bouck J., Brokstein P., Brottler P.,

Burkova D., Botcham M.R., Dung Z., Mays A.D., Dew I., Dietz S.M.,

Borkova D., Botcham M.R., Bouck J., Brokstein P., Brottler P.,

RADAGON K., Doup L.E., Downes W., Dugan-Rocha S., Punkov B.C., Dunn P.,

RADAMA M., Gabrielian A.B., Gary N.D., Gelbart W.M., Glasser K.,

RADAMA M., Bruscon K.A., Howland T.J., Hernandez J.R., Houck J.,

RADAMA M., Houston K.A., Howland T.J., Mel M.H., Inbeyam C.,

RADAMA M., Ralush F., Karpen G.H., Ke Z., Gelbart W.M., Glasser K.,

RADAMA M., Ralush F., Karpen G.H., Ke Z., Gubar P., Harris M.

RADAMA M., Murphy B., Minrphy L., Mizny D.M., Nelson D.L.,

RADAMA M., Moly M., Murphy B., Minrphy L., Mizny D.M., Nelson D.L.,

RADAMA M., Pittman G.S., Pan S., Pollard J., Puzi, W., Palazolo J.M.,

RADAMA M., Pittman G.S., Pan S., Pollard J., Puzi, Wang X.,

RADAMA M., Pittman G.S., Pan S., Pollard J., Puzi, Wang X.,

RADAMA M., Pittman G.S., Pan S., Pollard J., Wang X.,

RADAMA M., Pittman G.S., Pan S., Pollard J., Wang S., Yao Q.A., Ye J.,

RADAMA M., Pittman G.S., Pan S., Pollard J., Wang S., Yao Q.A., Ye J.,

RADAMA M., Pittman G.S., Pan S., Pollard J., Wasserman D.A.,

RADAMA M., Pittman G.S., Pan S., Pollard J., Wasserman D.A.,

RADAMA M., Pittman G.S., Pan S., Pollard J., Wasserman D.A.,

RADAMA M., Pittman G.S., Randers R., Wang S.,
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Revans C.A., Gocayne U.D., Amanatides P.G., Baradon R.C., Rogers Y.,

Radracon J., An H., Baldwin D., Banzon J., Beson K.Y., Busam D.A.,

Radracon J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Radracon K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Radracalez M., Houck U., Hoskins R.A., Hostin D., Howland T.J.,

Radracalez M., Houck W., Hoskins R.A., Hostin D., Howland T.J.,

Radracalez M., Houck W., Murphy B.A., Nelson C., Nelson K.A., Nunco J.,

Radraces M. Murphy B. N., Nelson C., Nelson K.A., Nunco J.,

Radraces M., Strong R., Svirskas R., Tector C., Tyler D.,

Radraces M., Strong R., Svirskas R., Tector C., Tyler D.,

Radraces M., Strong R., Svirskas R., Tector C., Tyler D.,

Radriimams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
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Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
                                                 STRAIN=Berkeley; Strain P., Hong L., Agbayani A., Carlson J., Chapleon M., Broketein P., Hong L., Farfan D., Frise E., George R., Gonzalez M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Paclebas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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"Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
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7; Conservative
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                    Alpha-glucosidase.
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SEQUENCE FROM N.A.
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01-MAY-2000
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01-JUN-2003
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 Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Calang M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Shu S., Smutniak F., Whitfield E., "Ambhurner M., Gelbart W.M., Rubin G.M., Mingall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome."; submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                               SEQUENCE FROM N.A.
Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.5%; Score 40; DB 5; Length 518; 57.1%; Pred. No. 1.6e+02; ive 1; Mismatches 5; Indels
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                                                                                                                                                                                                   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX069406; AAL39551.1; -.
EMBL; AE003584; AAN10441.1; -.
Flybase; FBG1000357; Su(dx).
GO; GO:000719; P:N signaling pathway; IGI.
GO; GO:0008587; P:wing margin morphogenesis; IGI.
GO: GO:0008586; P:wing vein morphogenesis; IGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR006047; Alpha amyl_cat.

InterPro; IPR006589; Alp amyl_cat_sub.

Pfam; PF00128; alpha-amylase; 1.

SMART; SM0042; Aamy; 1.

SMART; SM00442; Aamy; 1.
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PROSITE; PS50020; WW DOMAIN 2; 2.
SEQUENCE 518 AA; 61579 WW; 394E40BB5695856D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TYEMBLrel. 16, Created)
01-MAR-2001 (TYEMBLrel. 16, Last sequence update)
01-CCT-2003 (TYEMBLrel. 25, Last annotation update)
01ig0-1, 6-glucosidase.
Bacillus flavocaldarius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biosci, Biotechnol, Biochem, 62:1093-1102 (1998)
EMBL; AB003697; BAB18518.1; -.
PIR; JE0181; JE0181.
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MEDLINE=98357218; PubMed=9692189;
                                                                                                                                                                                                                                                                                                     InterPro; IPR000569; HECT domain.
InterPro; IPR001202; WW.RSP5_WWP.
Pfam; PF00632; HECT; 1.
SMART; SM00119; HECT; 1.
SMART; SM00119; HECTc; 1.
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Best Local Similarity
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MEDLINE=97313267; PubMed=9169871;
Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
Johnston M., Hillier L., Riles L., Dubois E., Dusterhoft A.,
Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P.,
Louis E.J., Messenguy F., Mewes H.W., Miosga T., Mostl D.,
Muller-Auer S., Nantwich U., Obermaier B., Piravandi E., Pohl T.M.,
Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M.,
Schaffe M., Schafens B., Scholler P., Schwager C., Schwarz S.,
Underwood A.P., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Nashiru O., Lee S.Y., Lee D.S.;
"Thermostable alpha-glucosidase gene from Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caldophilus GRZ4:";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF095282; AAD50603.1; -.
HSSP; P21332; P100K.
GO; GO:0004556; F:alpha-amylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR006589; Alpha amyl_cat.
InterPro; IPR006697; Alpha amyl_cat.
FMART; SM00128; Alpha-amylase; 1.
SMART; SM00642; Aamy; 1.
SEQUENCE 529 AA; 61383 MW; 9C036EICIF5118AA CRC64;
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46.5%; Score 40; DB 2; Length 529
Best Local Similarity 43.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 5; Indels
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Chromosome XII COSMID 9931.
VPS36 OR L9931.3 OR YLR417W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
43.8%; Pred. No. 1.6e+02;
tive 4; Mismatches 5;
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227 RHEHLYTEDQPETYAY 242
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                                                              RESULT 23
                                                                                          Q8CED4
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SGD; 50004409; VRS36.

GO; GO:0005768; Crendosome; IDA.

GO; GO:0016299; F:regulator of G-protein signaling activity; IMP.

GO; GO:0045014; P:negative regulation of transcription by glu. . .; IMP.

GO; GO:0045031; P:protein-Golgi retention; IMP.

GO; GO:0006632; P:protein-vacuolar targeting; IMP.

InterPro; IPR007261; Vp836.

InterPro; IPR007261; Vp836.
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Ushijima H., Morikawa S., Mukoyama A., Nishio O.;
"Characterization of VP4 and VP7 of a murine rotavirus (YR-1) isolated
Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII."; Nature 387:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.5%; Score 40; DB 3; Length 566; 53.8%; Pred. No. 1.8e+02; tive 3; Mismatches 3; Indels
                                                                                                                                                                                     Favello A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                  Waterston R.; Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cherry J.M.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
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Juned. Sci. Biol. 48:237-247(1996).

BMBL; D45215; BAA08147.1;
G0, G0:0019028; C:viral capsid; IEA.

InterPro; IPR000946; Cap VP4.

InterPro; IPR008965; Con$\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsRNA viruses; Reoviridae; Rotavirus.
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301 QYVYTRDGEEVTAH 314
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Matches 6; Conservative
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QRIIYIDDAKPTQ 64
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Matches 7; Conservative
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SERALIE-257BL/6617 IISSUE-SKin;
MEDLINE-22354683; PubMed=12466851;
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mature 420:563-573 (2002).

EMBL; ARC05500; BAC25981.1; -.

MGI:99174; Zfp27.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003676; F:mucleic acid binding; IEA.

GO; GO:0003676; F:mucleic acid binding; IEA.

GO; GO:000357; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR007097; Znf_C2H2.

Pfam; PF001352; XRAB; 1.

Pfam; PF00096; Zf-C2H2; 21.

SMART; SM00349; XRAB; 21.

SMART; SM00355; ZnF_C2H2; 21.
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01-NOV-1999 (TEMBLEEL. 12, Created)
01-NOV-1999 (TEMBLEEL. 12, Last sequence update)
01-OCT-2003 (TEMBLEEL. 25, Last annotation update)
Su(dx) procein.
Su(dx) procein.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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PROSITE; PS00208; ZINC FINGER C2H2 1; 21.
SROSIE; PS50157; ZINC FINGER C2H2 2; 22.
SROUBUCE 819 AA; 92920 MW; C6782ECCOC379C4B CRC64;
                                                                                  Last sequence update)
Last annotation update)
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53.3%; Pred. No. 2.7e+02;
tive 2; Mismatches 5;
                                                           Created)
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MEDLINE=20196006; PubMed=10731132;
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23,
25,
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19 QRSLYRDVVQETYSH 33
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PRELIMINARY;
                          Q8CED4;
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                             Zinc finger protein 27
                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
Les 8; Conserva
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RESULT 25

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Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beason K.Y., Bence P.V., Berman B.P., Bhandari D., Bolshakov S., Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., A. Burtes R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A. de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., R. Dodson K., Doup L.B., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P., R. Dorbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., R. Foeler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., A. Horrin N.L., Harrey D., Heiman T.J., Hernandez J.R., Houck J., Harris M.L., Harrey D., Heiman T.J., Hernandez J.R., Houck J., A. Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Alatai M., Kalush F., Karpen G.H., Ke Z., Kennison J.B., Ketchum K.A., Markei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Andrey D., Lei Y., Levitsky A.A., Li J., J., Lei Y., Lei Y., Lei Y., Levitsky A.A., Li J., J., Li Z., Liang Y., Lin X., Markei B. McIntosh T.C., McLeod M.P., McPherson D., R. Melson D.R., Nelson K., Nusskern D.R., Scheleb J.M., Relson K.A., Nixon K., Nusskern D.R., Scheleb T., Sandth T., Sanders R.D.C., Scheeler F., Shen H., Stirskas R., Tector C., Turner R., Venter E., Wang S., Yao Q.A., R. Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang Z.-Y., Wassarman D.A., Weinstenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., R. Thergong R.N., Robissenbach J., Walliams S.M., Woodage T., Worley K., Zhu S., Zhu X., Zhao Q., Zhan M., They G., She R.A., Myers E.W., Rubin G.M., Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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46.5%; Score 40; DB 5; Length 949;
Best Local Similarity 57.1%; Pred. No. 3.2e+02;
Matches 8; Conservative 1; Mismatches 5; Indels
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PROSITE; PS50020; WW DOMAIN 2; 2.
SEQUENCE 949 AA; 107966 Ww; 74B17A8B05AC6E6B CRC64;
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GO; GO:0008587; P:wing margin morphogenesis; IGI.
GO; GO:0008586; P:wing vein morphogenesis; IGI.
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-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
EMBL; AE003584; AAF51312.1; -.
HSSP; Q13526; AAD38975.1; -.
HSSP; Q13526; IPIN.
FlyBase; FBGI0003557; Su(dx).
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InterPro; IPR008973; C2.
InterPro; IPR000569; HBCT domain.
InterPro; IPR001202; WW.REp5_WWP.
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SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 3.
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Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 4.
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MEDITE=22480296; PubMed=1256656; MEDETE=22480296; PubMed=1256656; Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Fiers M.W. Leer R., Tarchini R., Peters S.A., Bron P.A., Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vies M., Ursing B., De Vos W.M., Siezan R.J.; Complete genome sequence of Lactobacillus plantarum WCFS1."; Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).

EMBL; AD35254; CAb63387.1; -.

EMBL; AD35254; CAb63387.1; -.

Fiam; PF00746; Gram pos_anchor.

Fiam; PF00746; Gram pos_anchor.

Fiam; PF00746; Gram pos_anchor.
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                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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                                       Q88YG6;
0-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
PRT; 2139 AA
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MEDLINE=20032073; PubMed=10562494;
                                                                                                                                                                                                                                      Cell surface protein precursor
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STRAIN=NCIMB 8826 / WCFS1;
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Best Local Similarity 77.8
Matches 7; Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              Lactobacillus plantarum.
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SEQUENCE 2139 AA
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MEDIANE=22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Xyrpides N.,
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.",
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Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.3%; Score 39; DB 16; Length 346; 58.3%; Pred. No. 1.5e+02; Live 2; Mismatches 3; Indels
                                                                                                                                                     / Match 45.3%; Score 39; DB 3; Length 327; Local Similarity 66.7%; Pred. No. 1.4e+02; nes 6; Conservative 2; Mismatches 1; Indels
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Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=226900;
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                         DC4F253E0B1ABD76 CRC64;
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Last annotation update)
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Last annotation update)
GO; GO:0009225; P:nucleotide-sugar metabolism; IEA InterPro; IPR001509; Epimerase_Dh. PF01370; Epimerase; 1.
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EMBL, AB017006, AAP09683.1; -.
ILCPPRO, IPR001466; Beta lactamase.
InterPro; IPR0010871; Beta_lactamase_A.
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                                                                                                            327 AA; 37099 MW;
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nes 7; Conservative
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REMBL; AB006752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AAK41614.1; -. REMBL; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; AB06752; A
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
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NCBI TaxID=4952;
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"Molecular cloning of the YlTGD1 gene in Yarrowia lipolytica.";
"Molecular cloning of the YlTGD1 gene in Yarrowia lipolytica.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY0406631; AAK77226.1; --
GO; GO:0008460; F:IPD2-glucose 4,6-dehydratase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
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                                                          45.3%; Score 39; DB 12; Length 259; 58.3%; Pred. No. 1.1e+02;
     259 AA; 30411 MW; 2E1C254DC626848D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Putative dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)
                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SS01380.
                                                                                                                                                                                                                                                                                                                                                        263 AA.
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                                                                                                               2; Mismatches
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217 ERFLYLDDNHQIKA 230
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                              Query Match
Best Local Similarity 58.5.
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RESULT 28
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NEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Holt R.A., Ashburner M., Henderson S.N.,
Amanatides P.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Arandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dewis S.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                        STRAIN=1021,
MEDIINE=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Finan T.M., Weidner S., Wong K., Buhrmester J., Cowie A.,
Golding B., Puehler A.;
Golding B., Puehler A.;
The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
fixing endosymbiont Sinorhizobium meliloti.";
Final. Acad. Sci. U.S.A. 98:9889-9894(2001).
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative sugar uptake ABC transporter periplasmic solute-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebbydroidea; Drosophilidae; Prosophila.
                                                                                                  protein.
RB10682 OR SME21103.
RRhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria, Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
45.3%; Score 39; DB 16; Length 439;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 4; Mismatches 2; Indels
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PROSTITE; PS00013; PROKEM LIPOPROTEIN; 1.
Plasmid; Hypothetical protein; Complete proteome.
SRQUENCE 439 AA; 47505 MW; 274E8BDC80BF57D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBIPF9;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
CG7795-PB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; B95927; B95927.

GO; GO:0046821; C:extrachromosomal DNA; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR000437; Prok lipoprot_S.

InterPro; IPR00059; SBP_bac_1.
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152 QKSLYQDEAKKTE 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                          NCBI_TaxID=382;
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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
"Labmitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

BMBL; APO6277; BAB98518.1;
"GO; GO:0005488; F:initochondrial inner membrane; IEA.

GO; GO:0005488; F:initochondrial inner membrane; IEA.

GO; GO:0006812; F:cation transporter activity; IEA.

GO; GO:0006812; F:cation transport; IEA.

RO; GO:0006812; F:cation transport; IEA.

RO; GO:0006812; F:cation transport; IEA.

InterPro; IPR00684; F:Cation transport; IEA.

InterPro; IPR00684; MgtE intracl.

InterPro; IPR001993; Mitoch_carrier.

R Ffam; PF00571; GBS; 2.

R Ffam; PF00571; GBS; 2.

R Pfam; PF00514; MgtE N; 1.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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                                                                              "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                          45.3%; Score 39; DB 5; Length 369; 70.0%; Pred. No. 1.6e+02; cive 1; Mismatches 2; Indels
                                                                                             Investigating bology."
Science 282:2012-2018(1998).
EMBL; 729596; CABD1858.3; -.
EMBL; 729596; CABD1858.3; -.
PIR; T18857; T18859.
WormPep; C02C6.3; CE29169.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
Pfam; PP00560; LRR; 4.
Pfam; PP01463; LRRCT; 1.
SMART; SM00081; LRRCT; 1.
SEQUENCE 369 AA; 42639 MW; CFB127DC68B96D3A CRC64;
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QBNRC7;

01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
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         SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE 430 AA;
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OBNRC7 RESULT 31 QBNRC7

ð g 439 AA.

PRT;

PRELIMINARY;

Q926H4 Q926H4;

RESULT 32 0926H4 ID 09 AC 09

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Gaps

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Anthropoda; Hexapoda; Insecta; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

SEQUENCE FROM N.A.

Drosophila melanogaster (Fruit fly).

Created)
Last sequence update)
Last annotation update)

01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,

LD44821p.

604 AA.

PRT;

PRELIMINARY;

DBMSAB; QBMSAB

RESULT 34 Q8MSA8

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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Gode K., Gong F., Garg N.S., Gelbart W.M., Glasser K., RA Glock R., Gong F., Gorell J.H., Gu Z., Galan P., Harris M., Harrey D., Heiman T.J., Fernandez J.R., Houck J., Rabali M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Jalai M., Ralush F., Karpen G.H., Kezi, Kennison J.A., Ketchum K.A., Ramael B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Martei B. M. Gircsh T.C., Mozled M.P., Mocherson D., Martei B., McIncosh T.C., Mozled M.P., Mocherson D., Martei B., McIncosh T.C., Mozled J., Moshrefi A., Retwork G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Markun S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ralazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G., Ranact K., Remington K., Saunders R.D., Scheeler F., Shen H., Raha B.L., Shen H., Spier E., Stardling A.C., Staen Hows, Sun E., Smith T., Rapier E., Spradling A.C., Staenleton M., Strong R., Sun E., Spradling A.C., Staenleton M., Strong R., Sun E., Shift J., Mang Z.Y., Weinsenbach J., Mulliams S.M., Woodager, Worley K.C., Wu D., Yang S., Zhu X., Smith H.O., Zheng X.H., Mensen B.M., Zhong F.N., Zhong Y., Zhou X., Zhu S., Zhu X., Smith H.O., Zheng X.H., Mensen Benome sequence of Drosophila melanogaster.", Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

A Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Banson J., An H., Baldwin D., Banzon J., Beson K.Y., Busam D.A.,

Carlson J., An H., Baldwin D., Banzon J., Beseon K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Degwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Numoo J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

William S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Mistra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Mistra S., Crosby W.A., Matthews B.B., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Galbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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46.7%; Pred. No. 2.8e+02;
tive 5; Mismatches 1; Indels
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EMBL; AE003620; AAN11163.1; --
FlyBase; FBgn0032019; CG7795.
SEQUENCE 598 AA; 67370 MW; ZB9CA0BE22421CC9 CRC64;
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelffer B.D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Barsandale J., Bayraktaroglu L., Basaley E.M.,
Besson K.Y., Bennos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Bulle C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Rosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                 Ctapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Partel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 5; Length 604; Pred. No. 2.9e+02; 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY118966; AAM50826.1; -.
Flybase; FGGM0032019; CG7795.
SEQUENCE 604 AA; 68182 MW; D8B168E7BFBA07FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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428 YLYTMIEDSEETQRH 442
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Best Local Similarity 46.7
Matches 7; Conservative
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                                                                                                                                                                                                                                                       STRAIN=Berkeley;
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Celniker S.;
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Local Similarity

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ID 061851
AC 061851;
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BEBLIA ARGOSTOL A. PAFESC401;
BEBLIA ARGOSTOL A. PAFESC401;
BEBLIA ARGOSTOL A. PAFESC401;
BEBLIA ARGOSTOL A. PAFESC401;
BEBLIA ARGOSTOL A. PAFESC401;
BEBLIA ARGOSTOL A. PAFESC401;
BEBLIA ARGOSTOL A. PAFESC401;
BEBLIA ARGOSTOL A. PAFESC401;
BEBLIA ARGOSTOL A. PAFESC401;
BEBLIA ARGOSTOL A. PAFESC401;
BEBLIA ARGOSTOL A. BAFESC401;
BEBLIA ARGOSTOL A. BAFESC401;
BEBLIA ARGOSTOL A. BAFESC401;
BEBLIA ARGOSTOL A. BAFESC401;
BEBLIA ARGOSTOL A. BAFESC401;
BEBLIA ARGOSTOL A. BAFESC401;
BEBLIA ARGOSTOL A. BAFESC401;
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BEBLIA ARGOSTOL A. BAFESC401;
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BEBLIA ARGOSTOL A. BAFESC401;
BEBLIA ARGOSTOL A. BAFESC401;
BEBLIA ARGOSTOL A. BAFESC401;
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Nakai T., Moriya A., Tonouchi N., Sakai F., Hayashi T.;
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EMBL; AB003689; BAA23595.1; -.
EMBL; AB003689; BAA33467.1; -.
PIR; JC5869; JC5869.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Gluconacetobacter.
NCBI_TaxID=28448;
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       643 AA; 72867 MW; 94FFB937EE9CBB12 CRC64;
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Last sequence update)
Last annotation update)
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Biosci. Biotechnol. Biochem. 61:1789-1790(1997)
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MEDLINE=98296257; PubMed=9630539;
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01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 46.7 tes 7; Conservative
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BETA-GLU.
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STRAIN=cv. B73;
Bergstrom D., Springer N.M., Schmitt L.T., Guthrie E., Sidorenko L.,
Kaeppler S.W., Cone K.C.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF54813; AAN41253.1; -.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Best Local Similarity 53.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                     Length 735;
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Chandler V.L., Kaeppler S.M., Kaeppler H.F., Cone K.C.;
"Sequences from the Plant Chromatin Consortium.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                               78223 MW; 463DB8116F1C55E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8H6B0;

1. MAR-2003 (TrEMBLrel. 23, Created)
01. MAR-2003 (TrEMBLrel. 23, Last sequence update)
01. UNV-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                       45.3%; Score 39; DB 2; 1
70.0%; Pred. No. 3.6e+02;
PRT; 4368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              766 AA.
                                                                                                                                                                                                                    1; Mismatches
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InterPro; IPR003516; PoetSET.
InterPro; IPR007728; Pre-SET.
InterPro; IPR001214; SET.
InterPro; IPR003606; Zn2-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50868; POST SET; 1. PROSITE; PS50867; PRE SET; 1. PROSITE; PS50280; SET; 1. SEQUENCE 766 AA; 83842 MW;
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Pfam; PF00856; SET; 1.
Pfam; PF02182; YDG SRA; 1.
SMART; SM00468; PFESET; 1.
SMART; SW00317; SET; 1.
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Best Local Similarity 70...
7, Conservative
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24 2
21 204 2
251 AA;
                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
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SIGNAL
CHAIN
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VARIANT
SEQUENCE
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Q919Q8;
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                                                           Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                         A Waterston R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBLA ARC(51, AAC(17540.2; -...)

EMBLA ARC(511, AAC(17540.2; -...)

R PIR, T33163; T33163.

R WormPep; F55F10.1; CE30377.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000166; F:MUCleotide binding; IEA.

GO; GO:000166; F:MUCleotide binding; IEA.

GO; GO:000160; P:two-component signal transduction system (p. ..;

InterPro; IPR002393; AAA ATPASE.

R InterPro; IPR002393; AAA ATPASE.

R InterPro; IPR002095; VWF_A.

R SMART; SM00327; VWA; 1.

R SMART; SM00327; VWA; 1.

R R SMART; SM00327; VWA; 1.

R PROSITE; PS50234; VWA; 1.

R PROSITE; PS50234; VWA; 1.

R HYDOCHELICAL protein; ATP-binding.

O SEQUENCE 4368 AA; 492651 MW; 6CE6A78E56A57969 CRC64;
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                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 45.3%; Score 39; DB 5; Length 436
Local Similarity 60.0%; Pred. No. 2.8e+03;
Nes 9; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                   STRAIN=Bristol N2;
Pauley A., Gattung S., Scheet P.;
"The sequence of C. elegans cosmid F55F10.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
01-AUG-1998 (TrEMBLrel. 07, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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SEQUENCE FROM N.A.
STRAINEBELSECO N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                  STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                            investigating biology. The C
Science 282:2012-2018(1998).
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01-OCT-2003 (TrEMBLrel.
Hypothetical protein.
                                                     Caenorhabditis elegans.
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                                Aypothetical protein.
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SEQUENCE FROM N.A.
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                        SEQUENCE FROM N.A.
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                                                                                   NCBI_TaxID=6239;
                                                                                                                                        Waterston R.;
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DegLane FROW N.A.

MEDLINE=2046702; PubMed=11003389;

Witved L., Holmskov U., Koch C., Telsner B., Hansen S., Skjodt K.;

Witved L., Holmskov U., Koch C., Telsner B., Hansen S., Skjodt K.;

Witved L., Holmskov U., Koch C., Telsner B., Hansen S., Skjodt K.;

Witved L., Holmskov U., Koch C., Telsner B., Hansen S., Skjodt K.;

structure predicts affinity for galactose.";

Immunogenetics 51:955-964(2000).

HSSP; P19999; 1AFB.

SZRN; ZBB-GBRE-000427-2; mbl.

GO, GO:0005529; F:sugar binding; IEA.

GO, GO:0007157; P:heterophilic cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBI_TaxID=7955;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.2%; Score 38; DB 5; Length 235
50.0%; Pred. No. 1.5e+02;
tive 1; Mismatches 7; Indels
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MANNOSE BINDING-LIKE LECTIN.
                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Blanchard M., Bradshaw H.;
Blanchard M., Bradshaw H.;
submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
EMBL; U64852; AAB0472.1; -.
WormPep; W01A11.7; CE14402.

Hypothetical protein.
SEQUENCE 235 AA; 26776 MW; C087F352ED5F9874 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M -> L.
K -> N.
12D0ABD06B6E3B11 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR008160; Collagen.
InterPro; IPR001304; Lectin.C.
Pfam; PP01391; Collagen; 2.
Pfam; PP01391; Collagen; 2.
ProDom; PD000007; Clg_helix; 1.
ProDom; PD000007; Clg_helix; 1.
PROSITE; PS00615; C.TYPE_LECTIN 1; 1.
PROSITE; PS00615; C.TYPE_LECTIN 2; 1.
Collagen; Lectin; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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Query Match
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps

0;

2 QRYLYTDDAQQT 13 |:| ||| ::| 135 QKYYVTDDVEET 146

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Search completed: March 2, 2004, 16:07:19 Job time : 8.66667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model - protein search, using OM protein March Run on:

2, 2004, 15:51:17; Search time 1.53333 Seconds (without alignments) 543.341 Million cell updates/sec

1 RORYLYTDDAQQTEAH 16 US-10-060-765-7 86 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

141681 seqs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 7 | 75 | 87.2 | | Н | FGFL MOUSE | แนย แ |
| m | 41 | 47.7 | | Н | HEM1 NEIGO | |
| 4 | 41 | 47.7 | Н | Н | DPOL_ADEG1 | |
| 2 | 40 | 46.5 | 543 | Н | ZN08_HUMAN | |
| 9 | 40 | 46.5 | 776 | Н | VP4 ROTPY | |
| 7 | 40 | 46.5 | 1587 | н | SURZ CAEEL | |
| 00 | 39 | 45.3 | 215 | Н | IF4E APLCA | |
| σ | 39 | 45.3 | 627 | Н | 2AD2_SCHPO | |
| 10 | 39 | 45.3 | 776 | Н | VP4 ROTH6 | |
| 11 | 38 | 44.2 | 457 | Н | CUSC ECOLI | - |
| 12 | 38 | 44.2 | 460 | Н | CUSC_ECO57 | - |
| 13 | 38 | 44.2 | 460 | Н | CUSC_ECOL6 | |
| 14 | 38 | 44.2 | 553 | Н | SYR STAEP | |
| 1.5 | 38 | 44.2 | 775 | H | VP4_NCDV | |
| 16 | 38 | 44.2 | 775 | Н | VP4_ROTF1 | |
| 17 | 38 | 44.2 | 775 | 7 | VP4_ROTH3 | human r |
| 18 | 38 | 44.2 | 776 | Н | VP41 ROTS1 | simian |
| 19 | 38 | 44.2 | 116 | ч | VP42_ROTS1 | simian |
| 20 | 38 | 44.2 | 776 | Н | VP4 ROTB5 | bovine |
| 21 | 38 | 44.2 | 176 | Н | VP4 ROTBC | bovine |
| 22 | 38 | 44.2 | 176 | н | VP4 ROTSF | simian |
| 23 | 38 | | 776 | Н | VP4_ROTSS | simian 1 |
| 24 | 38 | 44.2 | 792 | Н | OSTA XYLFA | xylella |
| 25 | 38 | 44.2 | 792 | Н | OSTA XYLFT | xylella |
| 26 | 38 | 44.2 | 1308 | Н | YTX2 XENLA | xendous |
| 27 | 38 | 44.2 | 3859 | - | RPOA_LELV | |
| 28 | 37 | 43.0 | 101 | Н | AFAA ECOLI | - |
| 29 | 37 | 43.0 | 273 | Н | VE08_VACCC | |
| 30 | 37 | 43.0 | 273 | Н | VEO8 VACCV | |
| 31 | 37 | 43.0 | 273 | Н | VE08 VARV | |
| 32 | 37 | 43.0 | 291 | н | SNAG_ARATH | Q9spe5 arabidopsis |
| 33 | 37 | 43.0 | 337 | Н | SYW_SYNY3 | P73655 synechocyst |

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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformarics assessment."; Genome Res. 13:2265-2270 (2003).
-:- SUBCELULAR LOCATION: Secreted (Potential).
-:- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22887296; PubMed=12875309; MEDLINE=22887296; PubMed=12875309; MEDLINE=22887296; PubMed=12875309; MEDLINE=22887296; PubMed=12875309; Clark H.F., Gurney A.L., Abaya E., Carwley C., Currell B., Deuel B., Dowd P., Chen J., Chow B., Chowley C., Currell B., Deuel B., Dowd P., Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Haung A., Kim H.S., Kilmowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Kie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDINE-10858549; MEDINE-20461777; PubMed=10858549; Nishimura T., Nakatake Y., Konishi M., Itoh N.; "Identification of a novel FGF, FGF-21, preferentially expressed in "Identification of a novel FGF, FGF-21, preferentially
                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last agenace update)
15-WAR-2004 (Rel. 43, Last amotation update)
Fibroblast growth factor-21 precursor (FGF-21) (UNQ3115/PRO10196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; ABG21975; BAA99415.1; -.
EMBL; AY359086; AAQ8944.1; -.
HSSP; PG3968; LBAR.
Genew; HGNC:3678; FGFZ1.
GO; GO:0005576; C:extracellular; TAS.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0007467; P:cell-cell signaling; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR008996; Cytok_II_llike.
                                          209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1492:203-206(2000).
                                            PRT;
                                            STANDARD;
                                                                                                                                                                                                    Homo sapiens (Human).
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Matches
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--- SUBCELLULAR LOCATION: Secreted (Potential).
--- TISSUE SPECIFICITY: Nost abundantly expressed in the liver, also expressed in the thymus at lower levels.
--- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDILTNE-20461777; PubMed=10858549;
Mishimura T., Nakatake Y., Konishi M., Itoh N.;
"Identification of a novel FGF, FGF-21, preferentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                     ; Score 86; DB 1; Length 209; ; Pred. No. 3.6e-08; 0; Mismatches 0; Indels
                                                                                                                                                                                                                   FIBROBLAST GROWTH FACTOR-21.
                                                                                                                                                                                                                                                MISSING (IN REF. 2).
27925C52A0023823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-21 precursor (FGF-21)
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                                                                                                                                                                                               POTENTIAL.
                            Pfam; PF00167; FGF; 1.
PRINTS; PR00262; ILLHBGF.
ProDom, PD000083; ILL HBGF; 1.
SMART; SN00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; FALSE_NBG.
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                                                                                                                                                                                                                                                                             209 AA; 22300 MW;
  InterPro; IPR002348; IL1_HBGF.
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                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                            209
                                                                                                                                                                  Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=10090;
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                                                                                                                                                                                                                                                                                SEQUENCE
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is in no
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STRAINS-ATC 700825 / FR 1090;
MEDLINE-99030330; PubMed=9811666;
MEDLINE-99030330; PubMed=9811666;
MEDLINE-99030330; PubMed=9811666;
MEDWINE J.A., Sung M., Gipson M., Hartman K., Dyer D.W.;
Transport of intext porphyrin by HpuMB, the hemoglobin-haptoglobin utilization system of Neisseria meningitidis.";
J. Bacteriol. 180:6043-6047(1998).
J. CATALYTIC ACTIVITY: Glutamy1-tRNA(Glu) + NADPH = glutamate-1-semialdehyde + NADP(+) + tRNA(Glu).
Semialdehyde + NADP(+) + tRNA(Glu).
Semialdehyde + NaDP(+) + Glutamy1-tRNA reductase family.
J. SIMILARITY: Belongs to the glutamy1-tRNA reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrhoeae.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 210;
non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 28 POTENTIAL.
29 210 FIBROBLAST GROWTH FACTOR-21.
210 AA; 23237 MW; AE02AABA6477E6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.2%; Score 75; DB 1; I
87.5%; Pred. No. 3.4e-06;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
36-EBB-2003 (Rel. 41, Last annotation update)
Glutamyl-tRNA reductase (EC 1.2.1.-) (GluTR).
                                                                                                                                                                                                         HSSP; P03968; IBAR.
MGD; MGI:1861377; F9f21.
InterPro; IPR008996; Cytck III_like.
InterPro; IPR008348; III_HBGF.
Pfam; PF00167; FGF; I.
PRINTS; PR00262; III_HBGF.
PRODOM; PD000831; III_HBGF.
PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP, MF 00087; -; 1.
InterPro; IPR000343; GlutR.
Pfam; PF00745; GlutR dimer; 1.
Pfam; PF05201; GlutR N; 1.
Pfam; PF05200; GlutR N; 1.
PTGRFAMS; TIGR01035; hemA; 1.
PROSITE; PS00747; GLUTR; 1.
                                                                                                                                                EMBL; AB025718; BAA99416.1; -. EMBL; AK007574; BAB25115.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF067426; AAC79428.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 kokiriropoporean 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ma.
Local St..
14;
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ID HEM1 NEIGO
AC Q9ZHD6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenovirus CELO.";
J. Virol. 70:2939-2949(1996).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         !- MISCELLANDOUS: This DNA polymerase requires a protein as a primer. :- SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Avian adenovirus gall (strain Phelps) (Fowl adenovirus 1) (CELO).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete DNA sequence and genomic organization of the avian
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MEDLINE=96186720; PubMed=8627769;
Chiocca S., Kurzbauer R., Schaffner G., Baker A., Mautner V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U46933; AAC54904.1; -.

InterPro; IPR006172; DNA_pol_B.

InterPro; IPR00486; DNA_pol_B.

PRO3175; DNA_pol_B 2; 1.

PRINTS; PR00106; DNAPOLB.

SWART; SW00486; POLBC; 1.

FROSTIF; PS00116; DNA_POLYMERASE B; 1.

Transferase; DNA-directed DNA_polymerase; DNA_replication;
                                                                                    47.7%; Score 41; DB 1; Length 415; 61.5%; Pred. No. 9.7; tive 1; Mismatches 4; Indel8
                  NUCLEOPHILE (BY SIMILARITY).
BASE (BY SIMILARITY).
054D366586CEB32F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1121 AA; 129395 MW; AS5B9B6A54D3BDE1 CRC64;
                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase (EC 2.7.7.7).
Porphyrin biosynthesis; Oxidoreductase; NADP. ACT SITE 50 NUCLEOPHILE (BY ACT_SITE 94 94 BASE (BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 AA.
                                                                                                                                                                                                                                                                                   PRT; 1121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                    50 50 M
94 94 B2
415 AA; 45453 MW;
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                                                                         Query Match
Best Local Similarity 61.5-
Best Acas 8; Conservative
                                                                                                                                                              4 YLYTDDAQQTEAH 16
                                                                                                                                                                                               82 YLYTLÓMÓETVRH 94
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                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (N) {DNA}
                                                                                                                                                                                                                                                                                   DPOL_ADEG1
Q64751;
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P17098;
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                                                       SEQUENCE
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ZNO8 HUMAN
ID ZNO8 HT
AC P17098;
DT 01-AUG-
                                                                                                                                                                                                                                                                     DPOL_ADEG1
                                                                                                                                                                                                                                                    RESULT 4
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Pfam; PF00096; zf-C2H2; 7.

Pfam; PF00096; zf-C2H2; 7.

SWART; SW00349; KRAB; 1.

SWART; SW00355; ZnF_C2H2; 7.

PROSITE; PS00028; KRAB; 1.

PROSITE; PS00028; KRAB; 1.

PROSITE; PS00157; ZNC_FINGER_C2H2_1; 7.

PROSITE; PS00157; ZNC_FINGER_C2H2_2; 7.

Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003677; F:DNA binding; NAS.
GO; GO:0008270; F:zinc ion binding; NAS.
GO; GO:0008270; F:zinc ion binding; NAS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 8 (Zinc finger protein HF.18) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 543;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61772 MW; ADD987504ECAC019 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.5%; Score 40; 53.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 KRAB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001909; KRAB.
InterPro; IPR007087; Znf_C2H2.
InterPro; IPR007086; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M29581; AAA61314.1; -.
PIR; B34612; B34612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 RGEYLYTYDSÖITDS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P08046; 1A1H.
Genew; HGNC:13154; ZNFB.
MIM; 194532; -.
                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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RESULT
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                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                    01-MAY-1992 (Rel. 22, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP9].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
| N-LINKED (GLCNAC. ) (POTENTIAL) |
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(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.5%; Score 40; DB 1; Length 776; 50.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86772 MW; B6A6C9CF81541014 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP8.
OUTER CAPSID PROTEIN VP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .)
                                                                                                                                                                                                                                   Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI TaxID=10919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUR2 CAEEL

ID SUR2 CAEEL

AC 010669; 045497; Q90365;

DT 01-N0V-1997 (Rel. 35, Created)

DT 15-MAR-2004 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC
                                                           776 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 30;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M63231; AAA47100.1; -.
PIR; A40342; VPXXXM.
InterPro; IPR000416; Cap VP4.
InterPro; IPR008985; Cona_like_lec_gl.
Pfam; PF00426; VP4; 1.
Coat protein; Glycoprotein.
Onter Protein; Glycoprotein.
Onter Protein.
                                                                                                     Created)
                                                                                                                                                                                                                         Porcine rotavirus (strain YM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 gyryrpgegirah 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                             STANDARD;
                                                                                                   01-MAY-1992 (Rel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      776 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                           VP4_ROTPY
P25174:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
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                RESULT 7
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                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                           Singh N., Han M.;
"sut-2, a novel gene, functions late in the let-60 ras-mediated
"sut-2, a novel gene, functions late in the let-60 ras-mediated
signaling pathway during Caenorhabditis elegans vulval induction.";
Genes Dev. 9:2251-2265(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IF4E_APLCA

ID IFAE APLCA

CO7210.

O7210.

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2003 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last amordatation update)

DF Bukaryotic translation initiation factor 4E (eIF4E) (eIF-4E) (mRNA DE cap-binding procein) (eIF-4F 25 kDa subunit).

OS Aplysia californica (California sea hare).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Functions in the let-60 ras signaling pathway; acts downstream of let-60 during C.elegans vulval induction.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note=No experimental confirmation available;
-i- DEVELOPMENTAL STAGE: Highest levels in embryos and larvae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1405 1587 GLN/HIS-RICH.
505 505 Y -> FLD (in isoform b).
FTIG=VSP 00413.
1587 AA, 183906 MW; Al25FGA74922BIIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dobson R.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB
Pred. No. 68;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q10669-2; Sequence=VSP_004435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q10669-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACIDIC.
                                                                                                                                                                                                                 STRAIN=Bristol N2;
MEDLINE=96018822; PubMed=7557379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U33051; AAA85507.1; -.
EMBL; Z92834; CAB07385.2; -.
EMBL; Z92834; CAB07394.2; -.
WOTMPEP; F39B2.4a; CE28023.
WOTMPEP; F39B2.4b; CE28024.
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1553 QQQYLYMQQLQQHQQH 1568
                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.5%;
Local Similarity 43.8%;
les 7; Conservative 3
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SUR-2 OR F39B2.4.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ourbin R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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VARSPLIC
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us-10-060-765-7.rsp

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with calcineurin.";
Genes Cells 6:455-473(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                "Fission yeast homologues of the B' subunit of protein phosphatase 2A: multiple roles in mitotic cell division and functional interaction
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
MEDLINE=21275457; PubMed=11380623;
Tanabe O., Hirata D., Usui H., Nishito Y., Miyakawa T., Igarashi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
delta 2 isoform (PP2A, B subunit, B' delta 2 isoform).
PARZ OR PBP2 OR SPAC6F12.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein biosynthesis; Translation regulation; Initiation factor; RNA-binding; Phosphorylation.
MOD RES 207 207 PHOSPHORYLATION (BY PKC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.3%; Score 39; DB 1; Length 215; 72.7%; Pred. No. 10; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY PKC).
9EE00CB6DE8162E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                627 AA.
                                                                                                 SEQUENCE FROM N.A., AND PHOSPHORYLATION.
TISSUE=Nerve;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                          MEDLINE=99009053; PubMed=9792652;
                                Aplysioidea, Aplysiidae, Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR001040; IIF_eIF_4E. Pagin; PRD652; IF18E; 1. ProDom; PD003697; IIF_eIF_4E; 1. PROSITE; PS00813; IF4E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF085810; AAC36720.1; -. HSSP; P07260; 1AP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 AA; 24646 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 LWTRDAQKTEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LYTDDAQQTEA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P78759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZADZ_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RK WEDLINE=172.

RADIANE=172.

RADIANE=172.

RADIANE=172.

RA MODIANE=11849401; PubMed=11859360;

RA Squarcs J., Beat N., Hayles J., Baker S., Basham D., Bowman S., Squarcs J., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin N., Harris D., Hidalgo J., Hodgeon G., Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgeon G., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Mooney P., Moule S., Munghll K., Murchy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Sauders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares S., Stevens K., Stevens K., Skelton J., Simmonds M., Squares S., Stevens K., Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Volckaert G., Aert R., Roben J., Grymonprez B., Reliens I., Borlex E., Moestl D., Hilbert H., Reinhardt R., Pohl T.M., Rabel C., Fuchs M., Frizz C., Holzer E., Moestl D., Hilbert H., Rabel C., Fuchs M., Gailbert H., Rainhardt R., Purst S.M., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Abaga R.R., Cruzado L., Jimenez J., Sanchez M., Galzon K., Pallsad V.A., Galzon B., Sanchez M., Rochet M., Gaillardin C., Tallada V.A., Galzon P., Zhorkez M., Rochet W., Morles S., Armstrong J., Forsburg S.L., Rpakovski G.V., Ussery D., Barrell B.G., Nurse P., Shancome sequence of Schizosaccharomyces pombe.";

R. Nature 415:871-880 (2002).
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SUBCELULAR LOCATION: Cytoplasmic and nuclear.
SIMILARITY: Belongs to the phosphatase 2A regulatory subunit B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE-98162722; PubMed=9501991; Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.; Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.; Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                   "Isolation and characterization of parl(+) and par2(+): two Schizosaccharomyces pombe genes encoding B' subunits of protein
SEGUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION. MEDLINE=20221714; PubMed=10757751;
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                                                                                                                                                                                                                                                                                          Genetics 154:1025-1038(2000)
                                                                                                    Jiang W., Hallberg R.L.;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       phosphatase 2A
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Virology 182:407-412 [1991].
-!- SUBCELLUIAR LOCATION: Outer capsid.
-!- PIM: VP8 is one of two trypsin cleavage products of VP4; the other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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OUTER CAPSID PROTEIN VP6 (POTENTIAL).

OUTER CAPSID PROTEIN VP5 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
EMBL; AB041232; BAB40598.1; -.
BMBL; 298533; CAB11096.1; -.
EMBL; D89107; BAA13770.1; -.
GeneDB_SPombe; SPACFT12.12; -.
GO; GO;0007043; P:cell cycle; ISS.
GO; GO:0016043; P:cell organization and biogenesis; ISS.
GO; GO:0016288; P:cytokinesis; ISS.
GO; GO:007067; P:mitosis; ISS.
InterPro; IRR002554; B56.
Ffam; PF01603; B56; I.
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10-0CT-2003 (Rel. 42, Last annotation update)
10-cr capsid protein VP4 (Hemagglutinin) (Outer (Contains: Outer capsid proteins VP5 and VP8].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.3%; Score 39; DB 1; llarity 46.2%; Pred. No. 36; Conservative 3; Mismatches
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10947;
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InterPro; IPR008985; ConA like_lec_gl.
Pfam; PF00426; VP4; 1.
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Qian Y., Green K.Y.;
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Matches 6; Conservative
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P26451;
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SECUENCE FROM N.A.
Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
Chung E., Allen E., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
Rederspiel N., Hyman R., Kalman S., Boris R.W.;
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glassner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / DH5-alpha;
MEDLINE=20461235; PubMed=11004187;
MURBON G.P., Lam D.L., Outten F.W., O'Halloran T.V.;
Mundon G.P., Lam D.L., Copper-responsive two-component system on the chromosome of Escherichia coli K-12.";
                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99420866; PubMed=10493123;
Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
"Enrichment of low abundance proteins of Escherichia coli by
hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
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Mau B., Shao Y.;
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CUSC_ECOLI STANDARD; PRT; 457 AA. P77211; Q91673; Q9X444; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Cation efflux system protein cusC precursor. Escherichia coli.
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                                                                                                                                                                                        Enterobacteriaceae; Escherichia
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5; Indels

3; Mismatches

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send. AB4070.1; -.
EMBL; AB0699; BA35206.1; -.
EMBL; AP0699; BA35206.1; -.
EMBL; AP0609; BA35206.1; -.
EMBL; AP70134: Cusc.
DR nterPro; IPR001423; Cusc.
DR nterPro; IPR001423; Cusc.
DR press. IPR001423; Prok_lipoprot_S.
DR Press. IPR001423; Prok_lipoprotein; Palmitate; Complete protecme. RW Outer membrane; Signal; Elpoprotein; Palmitate; Complete protecme. FT SIGNAL 1 1 1 B SIMILARIY.
FT CHAIN 18 457 CATION EFFLOX SYSTEM PROTEIN CUSC.
FT LIPID 18 18 N-palmitoyl cyclerine (Probable).
ILPID 18 18 S-diacylglycerol cysteine (Probable).
ILPID 18 18 S-diacylglycerol cysteine (Probable).
INTANT 6 6 L -> M (IN STRAIN KI / RS218).
T -> A (IN STRAIN KI / RS218).
T -> A (IN STRAIN KI / RS218).
T -> A (IN STRAIN KI / RS218).
T -> F (IN STRAIN KI / RS218).
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                                                                                                                                                                                                                                                                                                                                                            ABDLINE=22697381; PubMed=12813074;
MEDLINE=22697381; PubMed=12813074;
MEDLINE=22697381; PubMed=12813074;
Molecular analysis of the copper-transporting efflux system CusCFBA of Escherichia coli.";
J. Bacteriol. 185:3804-3812(2003).
J. Bacteriol. 185:3804-3812(2003).
Lo copper and silver. In pathogenic strains it allows the bacteria to invade brain microvascular endothelial cells (BWBC) thus allowing it to cross the blood-brain barrier and cause neonatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: The cus efflux system is composed of cusA, cusB, cusC and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: The cus system plays an important role in copper tolerance under anaerobic growth and, under extreme copper stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                        MEDLINE=21391920; PubMed=11399769;
Outten F.W., Huffman D.L., Hale J.A., O'Halloran T.V.;
"The independent cue and cus systems confer copper tolerance during
aerobic and anaerobic growth in Escherichia coli.";
J. Biol. Chem. 276:30670-30677 (2001).
                                                                                                                                                                                                                              Franke S., Grass G., Nies D.H.;
"The product of the ybdE gene of the Escherichia coli chromosome is involved in detoxification of silver ions.";
Microbiology 147:965-972 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anchor (Potential).
-1- INDUCTION: Transcriptionally regulated by cusR in response to copper and silver ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in aerobic growth.
-!- SIMILARITY: Belongs to the fusA/nodT family.
                                                                                                                                                                                                            MEDLINE=21178899; PubMed=11283292;
FUNCTION IN COPPER HOMEOSTASIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitis.
                                                                                                                                                                                                 STRAIN=K38;
                                                                                                                                                                        INDUCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete gamone sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).

-I. FUNCTION: Part of a cation efflux system that mediates resistance to copper and silver (By similarity).

-I. SUBGNIT: The cus efflux system is composed of cusA, cusB, cusC and cusF (By similarity).

-I. SUBGNITAR LOCATION: Attached to the outer membrane by a lipid
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STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Posfei G., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfei G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

"Melch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anchor (Potential).
-!- INDUCTION: Transcriptionally regulated by cusR in response to copper and silver ions (Probable).
-!- SIMILARITY: Belongs to the fusA/nodT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NGBI_TaxID=83334;
S -> F (IN STRAIN K1 / RS218).
R -> G (IN STRAIN K1 / RS218).
Q -> R (IN STRAIN K1 / RS218).
S -> P (IN STRAIN K1 / RS218).
G -> GWQQ (IN STRAIN K1 / RS218).
W, BB5B2B6B6719F7A1 CRC64;
                                                                                                                                                                     ;
                                                                                                                               1; Length 457;
                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                           10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Cation efflux system protein cusC precursor. CUSC OR Z0711 OR ECS0610.
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                                                                                                                                   44.2%; Score 38; 58.3%; Pred. No.
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MEDLINE=21156231; PubMed=11258796;
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EMBL; AP002552; BAB34033.1; -.
PIR; B90705; B90705
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10-0CT-2003 (Rel. 42, Last anno
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457 AA;
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
-!- FUNCTION: Part of a cation efflux system that mediates resistance to copper and silver (By similarity).
-!- SUBUNT: The cus efflux system is composed of cusA, cusB, cusC and cusF (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.P., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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INTERPRO, IPR000437; Prok_lipoprot_S.

INTERPRO; IPR000437; Prok_lipoprot_S.

INTERPRO; IPR000437; Prok_lipoprot_S.

PR03115; PS00131; PR0XAR_LIPOPROTEIN; 1.

PR05115; PS00131; PR0XAR_LIPOPROTEIN; 1.

Outer membrane; Signal; Eipoprotein; Palmitate; Complete proteome. SIGNAL 1 17

BY SIMILARITY.

CHAIN 18 460 CATTON BFPLUX SYSTEM PROTEIN CUSC.

CHAIN 18 460 CATTON BFPLUX SYSTEM PROTEIN CUSC.

Signal 18 N-palmitoyl cysteine (Probable).
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-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
   PIR; E8555; B0322.
InterPro; IPR00437; Prok_lipoprot_S.
Ffam; PF02321; OEP; 2.
PROSITE; PS0013; PROKAR LIPOPROTEIN; 1.
PROSITE; PS0013; PROKAR LIPOPROTEIN; 1.
OUTER membrane; Signal; Tipoprotein; Palmitate; Complete proteome.
SIGNAL 1 17 BY SIMILARITY.
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18 460 CATION EFFLUX SYSTEM PROTEIN CUSC.
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-!- INDUCTION: Transcriptionally regulated by cusR in response to
copper and silver ions (Probable).
-!- SIMILARITY: Belongs to the fusA/nodT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli O6.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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S-diacylglycerol cysteine (Probable)
FE79EDB715ABC922 CRC64;
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Pred. No. 38;
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LO-OCT-2003 (Rel. 42, Last sequence update)
LO-OCT-2003 (Rel. 42, Last annotation update)
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MEDLINE=22388234; PubMed=12471157;
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
ARGS OR SE0380.
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InterPro; IPR001412; IRNA-synt_I.
Pfam; PF00485; N-A=91.
Pfam; PF005746; IRNA-synt_Id_C; I.
Pfam; PF05746; IRNA-synt_Id_C; I.
PRINTS; PR01038; TRNASYNTHARG.
TIGRPAMS; TIGR00456; argS; I.
PROSTITS; PS00178; ATRALIGABE I; I.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                    Gaps
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Mol. Microbiol. 49:1577-1593 (2003).
-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA (Arg) = AMP + diphosphate + L-arginyl-trNA (Arg).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.; "Genome-based analysis of virulence genes in a non-biofilm-forming
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                                                  DB 1; Length 460;
                                                                                                       2; Indels
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460 AA; 50709 MW; 4C1D618F06AD66B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBL_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                  553 AA.
                                                                                                    3; Mismatches
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                                                  Score 38; DB
Pred. No. 38;
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InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR005148; N.
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                                                     44.2%;
58.3%;
                            148 RONYLATEEAOR 159
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                                                                                                                                                          1 RORYLYTDDAGO 12
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STRAIN=ATCC 12228;
PubMed=12950922;
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73:1939-1946(1992).

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P39033;
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-I. SUBCELLULAR LOCATION: Outer capsid.
-I. PIM: VP8 is one of two trypsin cleavage products of VP4; the other
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MEDLINE=92356070; PubMed=1322955;
Isegawa Y., Nakagomi O., Nakagomi T., Ueda S.;
A VPA sequence highly conserved in human rotavirus strain AU-1 and
faline rotavirus strain FRV-1.";
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01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8].
                                                                                                                                                                                (GLCNAC...) (POTENTIAL).
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OUTER CAPSID PROTEIN VP8.
OUTER CAPSID PROTEIN VP6.
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N-LINKED (GLCNAC. .) (POT
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                                                                                                                                                                                                                                                                  Nebraska calf diarrhea virus (strain Lincoln) (NCDV).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=39009;
                                                                                                                                     01-AUG-1990 (Rel. 15, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Outer capsid protein VP4 (Hemagglutinin) (Out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       775 A.A.
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Interpro; IPR008985; ConA_like_lec_gl
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01-AUG-1990 (Rel. 15, Last Begn
10-OCT-2003 (Rel. 42, Last anno
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QYTYTRDGEEVTAH 315
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Coat protein; Glycoprotein.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                      Viruses; dsRNA vi:
NCBI_TaxID=10932;
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P17465;
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J. Gen. Virol. 73:1939-1946(1992).
-!- SUBCELLULAR LOCATION: Outer capsid.
-!- PTM: VP8 is one of two trypsin cleavage products of VP4; the other product is VP5.
-!- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
J. Gen. Virol. 73:1939-1946(1992).
-!- SUBCELLULAR LOCATION: Outer capsid.
-!- PTM: VPB is one of two trypsin cleavage products of VP4; the other product is VP5.
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01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8].
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                                                                                         -!- SIMILARITY: Belongs to the rotaviruses VP4 protein family
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=39013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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PIR; JQ1639; JQ1639.
InterPro; IPR000416; Cap VP4.
InterPro; IPR008885; ConA_like_lec_gl.
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Coat protein; Glycoprotein.
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the European Bioinformatics Institute. There are no restrictions on
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                                                                                                                                                                                                     Coat protein; Glycoprotein.
CHAIN 1 776
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P12976;
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VP42_ROTS1
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Yeager M., Berriman J.A., Baker T.S., Bellamy A.R.;
Yeager M., Berriman J.A., Baker T.S., Bellamy A.R.;
Three-dimensional structure of the rotavirus haemagglutinin VP4 by
cryo-electron microscopy and difference map analysis.";
EMBO J. 13:1011-1018(1994).
-!- SUBCELIGIAR LOCATION: Outer capsid.
-!- STMCELIGIAR is one of two trypsin cleavage products of VP4; the other
product is VP5.
-!- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
-!- CAUTION: SEE ALSO VERSION 2 OF THIS PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-3 AND 751-776 FROM N.A. MEDILLE=87231047; PubMed=3035499; Lopez S., Arias C.F.; "I copez S., Arias G.F.; "I copez S., Arias G.F.; "The nucleotide sequence of the 5' and 3' ends of rotavirus SA11 gene
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10-OCT-2003 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8] (Version 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 4-750 FROM N.A. MEDILIBE-866459212, PubMed-10-886. S. Arias C.F., Bell J.R., Strauss J.H., Espejo R.T., Lopez S., Arias C.F., Bell J.R., Strauss J.H., Espejo R.T., "Primary structure of the cleavage site associated with trypsin
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Pred. No. 69;
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                                                                                                                                                 OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP9.
OUTER CAPSID PROTEIN VP5.
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=37137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enhancement of rotavirus SA11 infectivity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               776 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
   email to license@isb-sib.ch)
                                   EMBL; D10970; BAA01747.1; -.
PIR, JQ1638; JQ1658.
InterPro; IPR00416; Cap VP4.
InterPro; IPR008985; Cap Iike_lec_gl.
Pfam; PF00426; VP4; 1.
CACAL protein; Glycoprotein. OUTER CAP
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DT 01-OCT-1989

DT 01-OCT-2003

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OS VITUSES; GAR
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RP SEQUENCE OF
RR MEDLINE=8604

RR LOPEZ S., AR
RT "PRIMARY SET
RY "INCOLOGY 144

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=89183617; PubMed=2538804;
Mitchell D.B., Both G.W.;
Michell D.B., Both G.W.;
"Complete nucleotide sequence of the simian rotavirus SAll VP4 gene.";
Nucleic Acids Res. 17:212-2122(1989).
-!- SUBCELLUIAR LOCATION: Outer capsid.
-!- PIM: VP8 is one of two trypsin cleavage products of VP4; the other
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OUTER CAPSID PROTEIN VP8 (POTENTIAL).
OUTER CAPSID PROTEIN VP5 (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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01-077-1989 (Rel. 12, Last sequence update)
01-077-2003 (Rel. 42, Last annotation update)
01corr-2003 (Rel. 44, Hemagajutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8] (Version 2).
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-!- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
-!- CAUTION: SEE ALSO VERSION 1 OF THIS PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 776;
Pred. No. 69;
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=37137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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InterPro, IPR008985; Con_like_lec_gl.
                                                                                                                                                                            EMBL; Y00336; CRA68424.1; -.
PIR; A04129; VPXR4S.
InterPro; IPR000416; Cap VP4.
InterPro; IPR008885; ConA like lec gl.
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1- SUBCELLULAR LOCATTON: Outer capsid.

1- PTM: VP8 is one of two trypsin cleavage products of VP4; the other product is VP5.

1- SIMILARITY: Belongs to the rotaviruses VP4 protein family.

1- SIMILARITY: DRN00416; Cap VP4.

InterPro; IPR008985; Cap VP4.

InterPro; IPR008985; Cap VP4.

Coat protein; Glycoprotein.

CHAIN.
                                                                                                                                                                                                Gaps
         OUTER CAPSID PROTEIN VP4.

OUTER CAPSID PROTEIN VP8 (POTENTIAL).

OUTER CAPSID PROTEIN VP5 (POTENTIAL).
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MEDLINE=93286580; PubMed=8389807;
Taniguchi K., Urasawa I., Urasawa S.;
"Independent segregation of the VP4 and the VP7 genes in bovine rotaviruses as confirmed by VP4 sequence analysis of G8 and G10
                                             (POTENTIAL).
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OUTER CAPSID PROTEIN VP9.
OUTER CAPSID PROTEIN VP5.
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                                             N-LINKED (GLCNAC. . . ) (
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                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine rotavirus (serotype 8 / strain A5).
Viruges; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=36440;
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01-UUN-1994 (Rel. 29, Last sequence update)
01-UUN-1993 (Rel. 42, Last annotation update)
01-ter capsid protein VP4 (Hemagglutinin) (Out
                                                                                                                                   N-LINKED (GLCNAC
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Mismatches
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Pred. No.
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Pred. No.
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                                                                                                                                                    86774 MW;
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                                                                                                                                                                          44.2%;
llarity 42.9%;
Conservative
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                                                                                                                                                                                                                                           : | | | | :: | | | 302 OYTYTRDGEEVTAH 315
Coat protein; Glycoprotein. CHAIN 1 776
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776 AA;
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Best Local Similarity
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132
149
198
386
776 AA;
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P36305;
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Matches
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-- SUBCELLULAR LOCATION: Outer capsid.

-- PTM: VPR is one of two trypsin cleavage products of VP4; the other product is VP5.

-- PTM: PRIJARITY: Belongs to the rotaviruses VP4 protein family.
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                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1988 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
[Contains: Outer capsid proteins VP5 and VP8].
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Potter A.A., Cox G., Parker M., Babiuk L.A.;
"The complete nucleotide sequence of bovine rotavirus C486 gene
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Pred. No. 69;
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01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Oute
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776 AA
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InterPro; IPR000416; Cap VP4.
InterPro; IPR008985; ConA_like_lec_gl.
Pfam; PF00426; VP4; 1.
Coat protein; Glycoprotein.
CHAIN
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OUTER
PRT;
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                                                                                                                                                                               Bovine rotavirus (strain C486)
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Best Local Similarity
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P17463;
  VP4 ROTBC
P08713;
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VP4_ROTSF
ID VP4_R
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DT 01-AU
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                                                                                                        MEDLINE=89012172; PubMed=2845121;
Nishikawa K., Taniguchi K., Torres A., Hoshino Y., Green K.,
Kapikkan A.Z., Chanock R.M., Gorziglia M.;
"Comparative analysis of the VP3 gene of divergent strains of the rotaviruses simian SA11 and bovine Nebraska calf diarrhea virus.";
J. Virol. 62:4022-4026(1988).
-!- SUBCELLUIAR LOCATION: Outer capsid.
-!- FTM: VP8 is one of two trypsin cleavage products of VP4; the other product is VP5.
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01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
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MEDLINE=89012172; PubMed=2845121;
Nishikawa K., Taniguchi K., Torres A., Hoshino Y., Green K.,
Kapikian A.Z., Chanock R.M., Gorziglia M.;
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Pred. No. 69;
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OUTER CAPSID PROTEIN VP9.
OUTER CAPSID PROTEIN VP5.
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Viruses; dgRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10926;
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                   Simian 11 rotavirus (strain SA11-FEM).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
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N-LINKED
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InterPro; IPR008985; ConA like_lec_gl.
Pfam; PF00426; VP4; 1.
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PIR; B31159; VPXRT1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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                                                                                               SEQUENCE FROM N.A.
                                                          NCBI_TaxID=10925;
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RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Ra Simpson A.J.G., Reinach F.C., Arruda P., Baia G.S., Baptista C.S., Rayarea R., Alvaes L.M.C., Arruda J.E., Baia G.S., Baptista C.S., Rayareaga R., Alvaes L.D., Bordin S., Bove J.M., Briones M.R.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Carrer H., Ra Benen M.R.B., Colombo C., Costa R.F., Costa M.C.R., Costa-Neto C.M., Ra Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Raga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Raga J.S., Franca S.C., Franco M.C., Franca S.L., Gomber A., Goldman G.H., Goldman M.H.S., Gomes E.L., Kitajima J.P., RA Fraga J.S., Franca B.E., Ladjørt E.L., Kitajima J.P., RA Fraga J.S., Franca B.E., Ladjørt F., Lambais M.R., Deite L.C.C., R. Machado J.A., Marches M.V., Martins E.B., L., Marchins E.M., Marchins E.M., Marchins E.M.F., Marchins C.L., RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Monto D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Action A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Rakelia H.A., Jr., Pesquero J.B., Rakelia H.A., Jr., Pesquero J.B., Rake Rosa A.J.M., Actoberto P.G., Santelli R.V., Sawasaki H.E., At., de Rosa V.E., Jr., de Silva R.A., de Silva R.A., Jr., Salvasaki H.E., Ade Silva R.A., K., K., Silva W.A. Jr., Rake Rosa V.E., Silva W.A. Jr., Rake Rosa V.E., Rake Rosa V.E., Rake Rosa V.E., Rake Rosa V.E., Silva W.A. Jr., Rake Rosa V.E., Silva W.A. Jr., Rake Rosa V.E., Silva W.A. Jr., Rake Rosa V.E., Silva W.A. Jr., Rake Rosa V.E., Silva W.A. Jr., Rake Rosa V.E., Silva R.A., Rake Rosa A.J.M., Rake Rosa V.E., Silva W.A., Jr., Rake Rosa V.E., Silva W.A. Jr., Rake Rosa V.E., Silva R.A., Rake Rosa V.E., Silva W.A., Jr., Rake Rosa V.E., Silva W.A., Jr., Rake Rosa V.E., Silva W.A., Jr., Rake Rosa V.E., Silva W.A., Jr., Rake Rosa V.E., Silva R.A., Rake Rosa V.E., Silva W.A., Jr., Rake Rosa V.E., Silva R.A., Rake Rosa V.E., Silva R.E., Raber R.E., Raber R.E., Raber R.E., Raber R.E., Raber R.E., Raber R.E., Raber R.E., Raber R.E., R
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Xanthomonadaceae; Xylella.
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                                                                                                                                                                                                                                                                                                                                                                             OUTER CAPSID PROTEIN VP4.
OUTER CAPSID PROTEIN VP8.
OUTER CAPSID PROTEIN VP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86770 MW; 683BAAE24B329674 CRC64;
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N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
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28-FFB-2003 (Rel. 41, Created)
28-FFB-2003 (Rel. 41, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC N-LINKED (GLCNAC
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IMP OR OSTA OR XF0837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
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MEDLINE=22421331; PubMed=12533478;

WEDLINE=22421331; PubMed=12533478;

WASTINE=22421331; PubMed=12533478;

WASTIVE M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,

Myaki C.Y., Furlan L.R., Camargo L.B.A., Ferro M.T.T., da Silva F.R.,

Takita M.A., Lemos B.G.M., Machado M.A., Ferro M.T.T., da Silva F.R.,

A Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira M.J.,

Coutinho L.L., Kimura E.T., Ferro E.S., Haravava R., Kouramae E.E.,

Marino C.L., Giglioti B., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Marino C.L., Giglioti B., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Marino C.L., Giglioti B., Abreu I.L., Rormighieri E.F., Kishi L.T.,

da Cunha A.F., Ferrile R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,

de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,

C., Celestine R.C., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                   wemwinder permeaulinty. Essential for envelope biogenesis. Could be part of a targeting/usher system for outer membrane components (By similarity)
da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Taai S.M., Tsuhako M.H., vallada H., van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.; I. Setubal J.C.; I.The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).

I. FUNCTION: Determines N. hexane tolerance. Involved in outer membrane permeability. Essential for envelope biogenesis. Could B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANIC SOLVENT TOLERANCE PROTEIN.; EB97FF8CFD35A422 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.2%; Score 38; DB 1; Length 792; 61.5%; Pred. No. 70; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Outer membrane (By similarity). SIMILARITY: Belongs to the imp/ostA family.
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10-OCT-2003 (Rel. 42, Last Bequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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IMP OR OSTA OR PD1836.
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InterPro; TPR007533; OstA_C.
POTENT (PRO453; OSTA_C; 1.
Outer membrane; Signal; Complete proteome.
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Best Local Similarity 61...
8; Conservative
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Q87AI9;
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
FUNCTION: Determines N-hexane tolerance. Involved in outer membrane permeability. Essential for envelope biogenesis. Could be part of a targeting/usher system for outer membrane components (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garrett J.E., Knutzon D.S., Carroll D., "Composite transposable elements in the Xenopus laevis genome."; Mol. Cell. Biol. 9:3018-3027(1989).
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                                                                                                                                                                                                                                                                                                                                                                                   ORGANIC SOLVENT TOLERANCE PROTEIN.; 70637D6FA7B62DAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1308;
                                                                                                                                                                                                                                                                                                                                                                                                                                         44.2%; Score 38; DB 1; Length 792; 61.5%; Pred. No. 70; cive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.2%; Score 38; DB 1; Length 13C
63.6%; Pred. No. 1.2e+02;
ive 1; Mismatches 3; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein, Transposable element.
SEGURANCE 1308 AA: 149577 MW; C9A9C98CDC169C19 CRC64;
                                                                        (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JNN-1990 (Rel. 13, Created)
01-JNN-1990 (Rel. 13, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
Transposon TX1 hypothetical 149 kDa protein (ORF 2).
Transpus (African clawed frog).
                                                                          -!- SUBCELLULÂR LOCATION: Outer membrane (By 8:
-!- SIMILARITY: Belongs to the imp/ostA family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1308 AA.
                                                                                                                                                                                                                                                                                               HAWAP, MF 01411; -; 1.

Interpro; IRR007643; OstA_C.

Pfam; PF04453; OstA_C; 1.

Outer membrane; Signal; Complete proteome.

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InterPro; IPR000477; RVTSe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=89384562; PubMed=2550791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF03372; Exo_endo_phos; 1. Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                 EMBL; AE012560; AA029668.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              23 792 O
792 AA; 90768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M26915; AAA49976.1; -.
PIR; B32494; B32494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 RYLYDDGKWOTRA 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1308 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTX2 XENLA
P14381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: WITH THE POLYMERASE PROTEIN OF OTHER CORONAVIRUSES AND
                                                                                                                                                                                                                                                                                                                MEDINE-93297139; PubMed-8517032;
Meulenberg J.J.M., Hulst M.M., de Meijer E.J., Moonen P.L.J.M.,
den Besten A., de Kluyver E.P., Wensvoort G., Moormann R.J.M.;
Helystad virus, the causative agent of pordine epidemic abortion and
respiratory syndrome (PEARS), is related to LDV and EAV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         suggested. Also contains a protease domain. CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                      Viruses; seRNA positive-strand viruses, no DNA stage; Nidovirales;
                                                                                                                                                                                                            Lelystad virus (LV) (Porcine reproductive and respiratory syndrome
                                                                                                                         01-0CT-1993 (Rel. 27, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 43, Last annotation update)
POL polyprotein (ORF1A) [Contains: RNA-directed RNA polymerase (EC 2.7.7.48); Helicase; Protease (EC 3.4.21.-)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF TOROVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kroese M.V., Moormann R.J.M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                              PRT; 3859 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cys Ser_trypein.
Peptidase C31.
Peptidase C32.
Peptidase C33.
Peptidase C33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 3327-3859 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M96262; AAA46273.2; -. EMBL; M96262; AAA46274.1; -. EMBL; L04493; AAA47101.1; -.
                                                                                                                                                                                                                                                  Arteriviridae, Arterivirus.
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        Virology 192:62-72(1993)
                         ORYLYADPSPO 888
QRYLYTDDAQQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR008742;
InterPro; IPR008743;
InterPro; IPR008760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; C31.001; -.
MEROPS; C32.001; -.
MEROPS; C33.001; -.
MEROPS; S32.UPW; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A36861; A36861.
PIR; A45392; A45392.
PIR; B36861; B36861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR009003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR008741;
                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       REVISION TO 3327.
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                                                                                                  RPOA LELV
                                                                                                                                                                                                                                 virus)
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-!- FUNCTION: REGULATES THE TRANSCRIPTION OF GENES INVOLVED IN THE BIOSYNTHESIS OF AFIMBRIAL ADHESIN-III.

-!- SIMILARITY: HIGH TO E.COLI DAAA; SOME, TO E.COLI PAPB.

-!- CAUTION: It is uncertain whether Met-1 or Met-17 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garcia M.-I., Labigne A., le Bouguenec C.L.; "Nucleotide sequence of the afimbrial-adhesin-encoding afa-3 gene "Nucleotide sequence of the afimbrial flanking IS1 insertion sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_PSvir.
InterPro; IPR005159; WCM-
InterPro; IPR005159; WCM-
InterPro; IPR005159; WCM-
Pfam; PF05410; Peptidase_C31; 1.
Pfam; PF05411; Peptidase_C32; 1.
Pfam; PF05412; Peptidase_C33; 1.
Pfam; PF05412; Peptidase_C33; 1.
Pfam; PF05412; Varial helicase1; 1.
Pfam; PF01443; Viral helicase1; 1.
Pfam; PF03716; WCCH; 1.
Pfam; PF03716; WCCH; 1.
                                                                                                                                                                                                                                                                                            (BY SIMILARITY) (BY SIMILARITY) (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 1; Length 3859; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                  TRYPSIN-LIKE SERINE PROTEASE. CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                         421758 MW; 8C5E945AC6895CEE CRC64;
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                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
T -> V (IN REF. 3).
V -> I (IN REF. 3).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFA-III adhesin operon regulatory protein.
                                                                                                                                                         Serine protease; Zinc-finger.
                                                                                                                                                                                                                                                                                  POLYMERASE
                                                                                                                                                                                                CYS-RICH.
                                                                                                                                                                                                                           HELICASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95095929; PubMed=8002584;
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54.5%;
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es 6; Conserv
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1203
1724
1724
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1810
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3506
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3859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFAA ECOLI
ID AFAA ECOLI
AC P53515;
                                                                                                                                                            Hydrolase;
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DOWAIN
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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protective mechanisms.";
FEBS Lett. 319:80-83(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||:|||:|:
157 RYVYTDNAK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RYLYTDDAQ 11
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                        Orthopoxvirus.
NCBI_TaxID=10254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLETE GENOME
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                  01-NOV-1991
                                         01-NOV-1991
01-NOV-1991
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ID VEOS VARV
                                                                                          Protein E8.
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                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P., Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
                                                                                                                                                                           Transcription regulation; Activator; Trans-acting factor; Plasmid.
SEQUENCE 101 AA; 11743 MW; F55914BC263BDD6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.0%; Score 37; DB 1; Length 273; 66.7%; Pred, No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                    Score 37; DB 1; Length 101;
                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005057; POX_E8.
Pfam; PP03394; POX_E8; 1.
PIRSF; PIRSF015690; VAC_E8K; 1.
SEQUENCE 273 AA; 31935 MW; 648DEADFF23EC9DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete DNA sequence of vaccinia virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P21049;
01-FFB-1991 (Rel. 17, Created)
01-FFB-1991 (Rel. 17, Last sequence update)
16-PCG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 AA.
                                                                                                                                                                                                                                                                                pred. No. 10;
1; Mismatches
                                                         EMBL, X76688, CAA44114.1, ALT_INIT.
PIR, D5545, D55545.
INTECPEO, IRRO043356, Fim_regulat.
Pfam, PF03333, PapB; 1.
PRINTS, PR01554; FIMREGULATRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91021027; PubMed=2219722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M35027; AAA48047.1; -. PIR; C42509; C42509.
                                                                                                                                                                                                                                                                                        58.3%;
                                                                                                                                                                                                                                                                 43.0%;
                                         EMBL; X76688; CAA54113.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 179:247-266 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 1 RORYLYTDDAOQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             2 RERYLYLADTPO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 RYVYTDNAK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RYLYTDDAQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orthopoxvirus.
NCBI_TaxID=10249;
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VE08_VACCV
ID _VE08_VACCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; C42509;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein E8
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VE08 VACCC
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273 AA.

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                             Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECRING FROM N.A.
STRAIN=India-1967 / Isolate Ind3;
STRAIN=India-1967 / Isolate Ind3;
MEDILINE=9415.2114; PubMed=8109158;
Shchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,
Sandakhchiev L.S.;
Hanalysis of the nucleotide sequence of a 43 kbp segment of the
"Analysis of thrins India-1967 strain.";
Virus Res. 30:239-258(1993).
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MEDLINE-94088747; PubMed-8264798;
Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                          Gershon P.D., Jones E.V., Moss B., Ahn B.-Y.; submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPO, INTRODS057; POX_E8.
PEAM; PF03394; POX_E8; 1.
PIRSF, PIRSF015690; VAC_E8R; 1.
SEQUENCE 273 AA; 31888 MW; 6C274DCEE6353629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.0%; Score 37; DB 1; 66.7%; Pred. No. 32; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
(Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 20, Last annotation update)
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MEDLINE=93202281; PubMed=8384129;
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Query Match
Best Local Similarity
      S_{2}
                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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C STRAINE-CV. Collumbia;

MAYER T.V. Collumbia;

MAYER KF.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

MAYER KF.X., Schueller C., Wambutt R., Entian K.-D., Terryn N.,

A Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Meichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

A Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,

Reichert B., Portetelle D., Perez-Alonsoo M., Boutry M., Bancroft I.,

A Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,

Langham S.-A., McCullagh B., Bilham L., Robben J.,

Van der Schueren J., Grymonprez B., Chuang Y.-O., Vandenbussche F.,

Bracken M., Weltjens I., Vor M., Bastiaens I., Aert R., Defcor E.,

Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNAG ARATH STANDARD; PRT; 291 AA.

SNAG ARATH STANDARD; PRT; 291 AA.

OSSEPS; OSSUNB;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
6amma-soluble NSF attachment protein (Gamma-SNAF) (N-ethylmaleimide-sensitive factor attachment protein (gamma-SNAF) (N-ethylmaleimide-sensitive factor attachment protein (gamma).

GSNAP OR AT4G20410 OR F9F13.60.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;
eurosids II, Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia;
STRAIN=cv. Columbia;
MEDILINE=20193631; PubMed=10727946;
MEDILINE=20193631; PubMed=10727946;
MEDILINE=20193631; PubMed=10727946;
Weightional and molecular identification of novel members of the
ubiquitous membrane fusion proteins alpha- and gamma-SNAP (soluble
Nethylmalaimide-sensitive factor-attachment proteins) families in
Dictyostellum discoideum.";
Eur. J. Biochem. 267:2062-2070(2000).
                                                 "Potential virulence determinants in terminal regions of variola
                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
Venter C.J.;
                                                                                                                                                                                                                                                                                                                                                                                43.0%; Score 37; DB 1; Length 273; 66.7%; Pred. No. 32; cive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                     EMBL; X69198; CAA48990.1; -.
EMBL; L22579; AAA60797.1; -.
PIR; B36842; B36842.
PIR; T28487; T28487.
InterPro; IPR005057; Pox_E8.
Pffam; PF03394; Pox_E8; 1.
PRSF; PRSF015690; VAC_E8R; 1.
SEQUENCE 273 AA; 31896 MW; 02859D3F756A53AE CRC64;
                                                                   smallpox virus genome.";
Nature 366:748-751(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 RYVYTDNAK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RYLYTDDAO 11
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Beneiser S., Hampel S., Feldpausen M., Lamberth S., Van den Daele H.,
Be Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Clark L., Doggett J., Hall S., Kay W., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
Radoreker H., Scharfe M., Grime M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Farrmann B., Granderath K., Daumer D., Herzl A.,
RA Gabel C., Puchs M., Yicale D., Lignori R., Pirzavandi E.,
RA Schnabl S., Hiller R., Schmidt W., Lecharry A., Casacubert E.,
RA Abefdor F., Cooke R., Berger C., Monfort A., Casacubert E.,
RA Gabel C., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Schnabl S., Hiller R., Schmidt W., Lecharry A., Rascubert E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Taron D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Accaria P., Bearn M., Wilson R., Abbott S., Stocker S.,
RA Rechon M., Murray J., Schulz K., Huang E., Spiegel L.,
RA Schomin T., Walcki J., Graves T., Harmon G., Redards J.,
RA Remerille P., Courney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
Ramer J., Fulton L., Ryan E., Andrews S., Gelsel C., Layman D.,
RA Melson J., Berghoff A., Jones K., Drome K., Cotton M., Johnson A.,
RA Melson J., Peston R., Vill D., Shekher M., Matero A., Shah R.,
RA Benta W., Marriensen R., Macrews S., Gelsel C., Layman D.,
RA Melson J., Shedt J., Ryan E., Andrews S., Gelsel C., Layman B.,
Radon J., Shedt J., Ryan E., Andrews S., Gelsel C., Layman B.,
Radon J., Shect P., Marriensen R., Macrowill M., Johnson A.,
Radore J., Marriensen R., Macrowill M., Johnson A.,
Radore J., Marriensen R., Mccoolul M., Johnson A.,
Radore J., Marriensen R., McCoolul M., Joh
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Feldmann K.A.,"
Feldmann K.A.,"
Feldmann K.A.,"
Full-length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Required for vesicular transport between the endoplasmic reticulum and the Golgi apparatus. Binds to SNARE complex and then recruits NSF to disassemble it (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic peripheral membrane protein (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SIMILARITY: Belongs to the SNAP family.
-!- CAUTION: Ref.2 sequences differ from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transport; Protein transport; Endoplasmic reticulum; Golgi stack; Multigene family.
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3EECE3B64D038BAD CRC64;
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EMBL, AL080253; CAB45807.1; ALT_SEQ.
EMBL, AL161553; CAB79041.1; ALT_SEQ.
EMBL, AV086673; AAM63730.1; -.
InterPro; IPR000744; NSF attach.
InterPro; IPR008941; TPR-like.
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129 129 A
291 AA; 32360 MW;
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SIP2 YEAST
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PRINTS; PR01039; TRNA-SYNTHIRP.
TIGRFAMs; TIGM00233; trpS; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Сарв
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diphosphate + L-tryptophanyl-tRNA(Trp).
-l-SUBUNIT: Homodimer (By similarity).
-l-SUBCELLUTAR LOCATION: Cytoplasmic.
-l-SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=970661201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Mayajima N., Hirosawa M., Suquira M., Satamoto S., Kimura T., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Tabata S.; Yamada M., Tabata S.; Shimpo S., Especial S.; Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Tabata S.; Sapera S.; Shimpo S., Takeuchi C.; Wada T., Matanabe A., Saquence analysis of the genome of the unicellular cyanobacterium Synachocystis sp. strain PCG6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
30-WAX-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 3:109-136(1996).
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 203 "KMSKS" REGION.
202 202 ATP (BY SIMILARITY).
337 AA; 37763 MW; A7808E60A78D312D CRC64;
                                                                                                                                                                                                                                                                                                                Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.0%; Score 37; DB 46.7%; Pred. No. 40;
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00953; LLZ...
HAMAP; MF 00140; -; I.
InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002306; Trp_tRNA-synt_lb.
InterPro; IPR002306; Trp_tRNA-synt_lb.
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90908; BAA17700.1; ALT_INIT.
HSSP; P00953; 1D2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 46.7 tes 7; Conservative
                                                                                                                                                                       STANDARD;
   7; Conservative
                                                                      200 YLYAHDLÖQAE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
203
202
                                     4 YLYTDDAQQTE 14
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                     SYW SYNY3
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   Matches
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2 QRYLYTDDAQQTEAH 16 || |: || :: | | 232 QRGLWFDDPERPECH 246

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RESULT 34

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEGUENCE FROM N.A.
MEDLINE-97298309; PubMed-9153757;
Feuermann M., Simeonava L., Souciet J.-L., Potier S.;
"Analysis of 11.7 kb DNA sequence from the left arm of chromosome VII
reveals 11 open reading frames: two correspond to new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kail M., Juettner E., Vaux D.;
"Lambda clone B22 contains a 7676 bp genomic fragment of
Saccharomyces cerevisiae chromosome VII spanning the VAM7-SPM2
intergenic region and containing three novel transcribed open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific targets.
-!- PIM: Phosphorylated by SNF1 in vitro.
-!- SIMILARITY: Belongs to the 5'-AMP-activated protein kinase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0005679; F:SNFIA/AMP-activated protein kinase activity; IMP.
GO; GO:0007574; P:cell aging (sensu Saccharomyces); IMP.
GO; GO:0007467; P:filamentous growth; IMP.
GO; GO:0006468; P:protein amino acid phosphorylation; IMP.
GO; GO:0007165; P:signal transduction; IMP.
PF04739; AMPKBI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang X., Jiang R., Carlson M.;
"A family of proteins containing a conserved domain that mediates interaction with the yeast SNF1 protein kinase complex.";
EMBO J. 13:5878-5886(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Could be an adaptor that promote the activity of SNF1 towards
                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast 12:799-807(1996).
-!- FUNCTION: Not known; interacts with the SNF1 protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                          Drebot M.A., Jansma D., Himmelfarb H.J., Friesen J.D.; submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases
                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
SIP2 protein (SPM2 protein).
SIP2 OR SPM2 OR YGL208W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95112798; PubMed=7813428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96408772; PubMed=8813766;
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EMBL; Z15159; AAC3420.1; --
EMBL; Z72730; CAA96922.1; --
EMBL; U33754; AAC49497.1; --
PIR; S51792; S51792.
GERMONLINE; 141256; --
SGD; S0003176; SIP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-283 FROM N.A.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C;
                               WHEN THE STANKE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SEED OF THE SE
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                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=86149315; PubMed=3006051;
Hagen D.C., McCaffrey G., Sprague G.F. Jr.;
"Evidence the yeast STE3 gene encodes a receptor for the peptide pheromone a factor: gene sequence and implications for the structure of the presumed receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakayama N., Miyajima A., Arai K.;
Nucleotide sequences of STE2 and STE3, cell type-specific sterile
genes from Saccharomyces cerevisiae.";
EMBO J. 4:2643-2648(1985).
                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0004933; F:mating-type a-factor pheromone receptor act. GO; GO:0000750; P:signal transduction during conjugation with.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coupled receptor; Pheromone response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 470;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5DBF611076B8CA91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M12239; AAA35113.1; -.
EMBL; X03011; CAA26795.1; -.
EMBL; X24151; CAA52261.1; -.
EMBL; Z28177; CAA82019.1; -.
PIR; B24670; B24670.
GGERMOLILE; 139933; -.
SGD; S0001661; STE3.
GO; GO:0005887; C:integral to plasma membrane; IDA.
                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 83:1418-1422(1986)
                                                  (Rel. 06, Last sequence update) (Rel. 42, Last annotation update)
470 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94205264; PubMed=8154185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001499; STE3_GPCR
                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53708 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.08;
                                                                                       factor receptor.
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Transmembrane; G-protein
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
53
1134
1183
2228
470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
156
206
267
300
470 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                     STE3 OR YKL178C.
                                 01-JAN-1988
                                                                      10-OCT-2003
                                                                                       Pheromone A
                                                   01-JAN-1988
   STE3 YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
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MEDLINES-9638014; PubMed=8796346;

Freiberg C., Perret X., Broughton W.J., Rosenthal A.;

Freiberg C., Perret X., Broughton W.J., Rosenthal A.;

"Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.

"Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.

"Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.

Genome Res. 6:590-600(1996).

-!- FUNCTION BE REQUIRED FOR THE FORMATION OF A FUNCTIONAL

NITROGENASE FE PROPEIN. PROBABLY ACCEPTS ELECTRONS FROM FIXA/FIXB

AND REDUCES A QUINONE.

-!- COPACTOR: FAD (Potential).

-!- SIMILARITY: Belongs to the ETF-QO / fixC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perret X.;
"Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:334-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nitrogen fixation; Oxidoreductase; FAD; Flavoprotein; Plasmid
                                                                                                                                                                                                                                                                                                                                                                             Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.0%; Score 37; DB 1; Length 435; 46.7%; Pred. No. 54;
                                   Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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                                                                        Indels
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SEQUENCE 435 AA; 47536 MW; 5C41133C66F84BA61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium
   46404 MW; CBB4FCE0070A563F CRC64;
                                   43.0%; Score 37; DB 1; 58.3%; Pred. No. 51;
                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                   435 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000100; AAB91888'1; -.
InterPro; IPR001327; FAD_pyr_redox.
PRINTS; PR00368; FADPNR.
                                                                                                                                                                                                                                                                                                                                                              (strain NGR234).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORFWIDDISHIGMH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                              320 ERYYYTLDROOS 331
                                                                        Conservative
                                                                                                           2 QRYLYTDDAQQT 13
                                                                                                                                                                                                                                   STANDARD;
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                  Query Match
Best Local Similarity
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   415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                             OR Y4UP.
                                                                                                                                                                                                                                                                                                                                                              Rhizobium sp.
                                                                                                                                                                                                                                                                                                                          FixC protein.
                                                                                                                                                                                                                                   FIXC RHISN
Q53208;
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RESULT 35

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R HAMAP, ME 001273; -; 1.

R InterPro; IPR001278; Arg_tRNA-synt_lc.

R InterPro; IPR001278; Arg_tRNA-synt_lc.

R InterPro; IPR001412; tRNA-synt_ld.

R InterPro; IPR001412; tRNA-synt_ld.

R Pfam; PF00750; tRNA-synt_ld.

R Pfam; PF00750; tRNA-synt_ld.

R Pfam; PF05746; tRNA-synt_ld.

R Pfam; PF05746; tRNA-synt_ld.

R Pfam; PF05746; tRNA-synt_ld.

R PRINTS; PR01018; TRNASYNTHARG.

R TIGRRAMA; TIGRO456; arg/9; 1.

R PROSITE; PS00178; A TRNA_LIASE I; 1.

Aminoacy1-tRNA synthétase; Protein biosynthesis; Ligase; ATP-binding;
                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Arginyl-RNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21311952; PubMed-11418146;
MEDLINE-21311952; PubMed-11418146;
Ruroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Rurida M., Ohta T., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanebisa M.,
Yamashira A., Obhima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP + diphosphate + L-arginyl-tRNA(Arg).
-i- SUBUNT: Monomer (By similarity).
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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                                                                                                                                                                                                                                                                                       Bacteria, Firmicutes; Bacillales; Staphylococcus
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                                                                                                                                                                                                                                                           Staphylococcus aureus (strain N315)
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Lancet 357:1225-1240(2001)
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518 TDDIEKTKAH 527
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                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=158879;
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                               SYR STAAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGR00456; argS; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginyl--ENA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS)
ARGS OR SAVO607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
Gaps
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-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP
diphosphate + L-arginyl-tRNA(Arg).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus (strain Mu50 / ATCC 700699).
Bacteria, Firmloutes, Bacillales, Staphylococcus.
NCBL_TaxID=158878;
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   1; Mismatches
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HAMAP; MF_00123; -; 1.
InterPro; IPR001278; Arg_tRNA-synt_lc.
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Pfam; PF00750; RNA-sylt ld; 1.
Pfam; PF05746; tRNA-sylt ld C; 1.
PRINTS; PR01038; TRNASYNTHARG.
                                                                                                                                    226 YTFVQDLQQVEGH 238
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Best Local Similarity 60...
6; Conservative
                                                                  4 YLYTDDAQQTEAH 16
      6; Conservative
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518 TDDIEKTKAH 527
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Q932F6;
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SOURCE STANDARD BRANCH COURT STANDARD BRANCH

ö Gaps ; 43.0%; Score 37; DB 1; Length 553; 60.0%; Pred. No. 71; 1; Indels tive 3; Mismatches 1; Indels (Rel. 41, Created) (Rel. 41, Last sequence update) (Rel. 41, Last annotation update) 553 AA SYR STAAW Q8NXT8; 28-FEB-2003 (28-FEB-2003 (28-FEB-2003 (

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Search completed: March 2, 2004, 16:05:26 Job time: 3.53333 secs
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InterPro; IPR001278; Arg_tRNA-synt_1c.
InterPro; IPR001278; Arg_tRNA-synt_1d.
InterPro; IPR001412; tRNA-synt_1d.
InterPro; IPR001412; tRNA-synt_1.
Pfam; PF03465; N-Arg; 1.
Pfam; PF03465; RNA-synt_1d; 1.
Pfam; PF00750; tRNA-synt_1d; 1.
Prints; PR01038; TRNASNYTHARG.
ITGRRAMG; ITGR00456; argS; 1.
PR051TS; PS00178; AA_TRNA_LIGASE 1; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS) ARGS OR MW0571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                           -!- SUBUNIT: Monomer (By Similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                            SEQUENCE FROM N.A.
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Naga T., Takeuchi R., Manon K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatau K.,
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 1.8.1.8)
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Vibrionaceae; Vibrio.
                                                                                                                                                                                  CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP diphosphate + L-arginyl-tRNA(Arg).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Thiol:disulfide interchange protein dsbD precursor (Protein-disulfide reductase)
DSBD OR VV11247.
                              Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         593 AA.
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                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP004824; BAB94436.1; -.
                                                                                                                                                                      Lancet 359:1819-1827(2002)
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518 TDDIEKTKAH 527
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                                                  NCBI_TaxID=196620;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                            acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CMCP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSBD VIBVU
Q8DCZ0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Complete genome sequence of Vibrio vulnificus CMCD6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Required to facilitate the formation of correct
disulfide bonds in some periplasmic proteins and for the assembly
of the periplasmic c-type cytochromes. Acts by transferring
electrons from cytoplasmic thioredoxin to the periplasm. This
transfer involves a cascade of disulfide bond formation and
reduction steps (By similarity).
-!- CATALYTIC ACTIVITY: Protein dithiol + NAD(P) + = protein disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THIOL: DISULFIDE INTERCHANGE PROTEIN DSBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase, Redox-active center; Electron transport; NAD;
Transmembrane; Inner membrane; Cytochrome c-type biogenesis; Signal;
                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                   (By similarity).
-!- SIMILARITY: Belongs to the thioredoxin family. DsbD subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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REDOX-ACTIVE (BY SIMILARITY)
REDOX-ACTIVE (BY SIMILARITY)
REDOX-ACTIVE (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 1;
Pred. No. 76;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential.
Potential.
Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF 00399; -; 1.
InterPro; IRR003834; Ctytoch TM.
InterPro; IPR003684; Thiored.
InterPro; IPR006663; Thioredox_dom2.
Pfam; PR02683; DSDD, 1.
Pfam; PR02085; thiored; 1.
PR0SITE; PS00194; THIOREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE016801; AA009703.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64815 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 YLYTDDAQQTE 14
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            593 AA;
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| | td. |
|---------|-------------|
| 5.1.6 | Compugen Li |
| version | - 2004 |
| GenCore | (c) 1993 |
| | Copyright |

OM protein - protein search, using sw model

March 2, 2004, 16:00:38 ; Search time 2.26667 Seconds
(without alignments)
678.999 Million cell updates/sec Run on:

US-10-060-765-7 86 1 RQRYLYTDDAQQTEAH 16 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | probable GDSL-moti | hypothetical prote | hypothetical prote | н | | hypothetical prote | | CL. | | Ch. | | щ | 1 | | hypothetical prote | | probable phosphopr | beta-glucosidase (| hypothetical prote | probable membrane | 5 | | | probable resistand | | ble per | layer | layer | outer layer protei |
|---------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------|--------|---------|--------|--------|--------|--------|--------|--------------------|--------|--------------------|--------------------|--------------------|-------------------|--------|--------|--------|--------------------|--------|---------|--------|----------|--------------------|
| QI QI | T00526 | T26063 | S28726 | T00525 | T25023 | C70385 | JE0181 | B34612 | \$59382 | VPXRYM | T21986 | T21993 | C36819 | G90294 | T18857 | B95927 | T11663 | JC5869 | T33962 | AI0633 | T01629 | B64790 | B90705 | E85555 | F81042 | A81989 | VPXR4S | , JQ1638 | JQ1639 |
| DB | 1 | N | ~ | 01 | 7 | N | ~ | Ŋ | 7 | 7 | 7 | ~ | N | N | N | ~ | 7 | ~ | ~ | N | ~ | ~ | N | ~ | N | N | Н | Н | н |
| Length | 349 | 2225 | 93 | 349 | 332 | 403 | 529 | 543 | 266 | 776 | 1661 | 1663 | 259 | 263 | 278 | 439 | 627 | 735 | 235 | 285 | 344 | 457 | 460 | 460 | 580 | 580 | 747 | 775 | 775 |
| % Query Match | 53.5 | 50.0 | 47.7 | 47.7 | 46.5 | 46.5 | 46.5 | 46.5 | 46.5 | 46.5 | 46.5 | 46.5 | 45.3 | 45.3 | 45.3 | 45.3 | 45.3 | 45.3 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 |
| Score | 46 | 43 | 41 | 41 | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 39 | 39 | 39 | 39 | 39 | 39 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 |
| Result No. | | 8 | ٣ | 4, | S | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 |

RESULT 2
T26063
hypothetical protein WOIF3.3 - Caenorhabditis elegans
hypothetical protein WOIF3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26063
R;Cummings, P.
R;Cummings, P.
A;Reference to the EMBL Data Library, March 1997

| | layer | | outer layer protei | outer layer protei | outer layer protei | outer layer protei | hypothetical outer | organic solvent to | WD repeat domain p | transposable eleme | hypothetical prote | hypothetical prote | two-component hybr | orf la protein - L | afaA protein - Esc | hypothetical prote | |
|---|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
| | VPXRTZ | VPXRT1 | VPXRB3 | JQ2022 | VPXRS1 | 803611 | S24410 | B82756 | T48933 | B32494 | A99580 | T18499 | AG1897 | B36861 | D55545 | AE3288 | |
| 1 | 775 1 | 776 1 | 776 1 | 176 1 | 776 1 | 776 2 | 776 2 | 792 2 | 1051 2 | 1308 2 | 1426 2 | 1619 2 | 1645 2 | 2396 2 | 101 2 | 145 2 | |
| | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 44.2 | 43.0 | 43.0 | |
| | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 37 | 37 | |
| | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | |

ALIGNMENTS

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Gaps

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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: C70385
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: ĞB;AE000717; NID:g2983492; PIDN:AAC07076.1; PID:g2983498; GB:AE0006
A,Experimental Bource: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 392, 353-358, 1998
A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300; MUID:98196666; PMID:9537320
A,Accession: C70385
A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cypecies: Caenorhabditis elegans
Cypecies: Caenorhabditis elegans
Cypecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
Cydecession: T25023
RyMortimore, B
RyMortimore, B
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RyMortimory: DNA
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Rymortimory: CESP:T20B3.5
Rymortimory: CESP:T20B3.5
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <STO>
A;Crose.references: GB:AE002093; NID:g3176707; PIDN:AAD12023.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

46.5%; Score 40; DB 2; Length 332;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                     Length 349;
                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 5
A;Introns: 110/1; 246/3
C;Superfamily: Caenorhabditis hypothetical protein C49G7.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T20B3.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                  Query Match 47.7%; Score 41; DB 2; Best Local Similarity 46.7%; Pred. No. 17; Matches 7; Conservative 4; Mismatches 6
                                                                                                                                                                              A,Gene: T20K24.6; At2g19050
A,Map position: 2
A,Introns: 82/1; 123/3; 198/3; 281/1
C,Superfamily: myrosinase-associated protein MyAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein aq 985 - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RORYLYTDDAQQTEAH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              в ктруінтарғоотуги 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 ORRYVYWDNVHSTEA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RORYLYTDDAQOTEA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-403 < AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: CESP:T20B3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: aq 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
T25023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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A, Residues: 1-349 < ROUD
A, Residues: 1-349 < ROUD
A, Cross-references: EMBL:AC002392; NID:g3176701; PID:g3176707
A, Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Blsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: Lose valls
A;Molecule type: DNA
A;Cross-references: EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
A;Experimental source: clone W01F3
A;Experimental source: clone W01F3
A;Gene: CESP:W01F3.3
A;Gene: CESP:W01F3.3
A;Gene: CESP:W01F3.3
A;Gene: CESP:W01F3.3
A;Anap position: 5
A;Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable GDSL-motif lipase/hydrolase [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T20K24.6
S;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dete: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C;Accession: T00525; H84571
S;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
A;Reference number: Z14167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402, 761-768, 1999
A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A,Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 1 (insertion sequence ISL1) - Lactobacillus casei
C;Species: Lactobacillus casei
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X02734; NID:g1279518; PIDN:CAA26516.1; PID:g43974
A;Experimental source: insertion sequence ISL1; strain C239
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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R,Shimiru-Kadota, M.; Kiwaki, M.; Hirokawa, H.; Tsuchida, N.
Mol. Gen. Genet. 200, 193-198, 1985
A;Title: ISLI: a new transposable element in Lactobacillus casei.
A;Reference number: S28726; MUID:85295506; PMID:2993817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Mobile element: insertion sequence ISL1
C;Superfamily: Shigella flexneri conserved hypothetical protein
                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 2; Length 2225;
Pred, No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 2; Length 93;
Pred. No. 3.7;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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477 QRYFYNEDSQKCE 489
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Best Local Similarity 53.0.
Tr Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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A; Residues: 1-93 <SHI>
                                   A; Accession: T26063
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Cjaccession: A40342
R;Lopez, S.; Lopez, I.; Romero, P.; Mendez, E.; Soberon, X.; Arias, C.F.
W Virol. 65, 3738-3745, 1991
A;Title: Rotavirus YM gene 4: analysis of its deduced amino acid sequence and prediction A;Reference number: A40342; MUID:91251227; PMID:1645789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: genomic RNA
A; Residues: 1-776 < LOP.
A; Cross-references: GB:M63231; NID:g333323; PIDN:AAA47100.1; PID:g333324
C; Cross-references: GB:M63231; NID:g33323; PIDN:AAA47100.1; PID:g333324
C; Superfamily: rotavirus outer layer protein VP3
C; Superfamily: rotavirus outer layer protein; glycoprotein; hemagglutinin
F; 1-241/Product: outer layer processing #status predicted < VP6>
F; 242-247/Region: cleavage processing #status predicted
F; 248-776/Product: outer layer protein VP5 #status predicted < VP5>
F; 17, 32, 56, 97, 116, 132, 151, 178, 183, 198, 325, 670/Binding site: carbohydrate (Asn) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1
A;Introns: 37/3; 102/2; 229/3; 317/3; 375/2; 505/3; 546/1; 668/3; 833/1; 904/2; 941/3; <sup>§</sup>
                            A;Cross-references: EMBL:U20162; NID:g632669; PIDN:AAB67493.1; PID:g632672; MIPS:YLR417w
A;Experimental source: strain S288C (AB972)
C;Genetics:
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C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C,Accession: T21986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               outer layer protein VP3 - porcine rotavirus C (strain YM)
NiAlternate names: hemagglutinin; VP4 protein
NiContains: outer layer protein VP5; outer layer protein VP8
C.Species: porcine rotavirus C
C.Species: 30-Jun.1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 776;
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                                                                                                                                                                                                                                                                                                                                             DB
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                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                             Score 40; DB
Pred. No. 44;
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                                                                                                                                                                                                                                     SGD:S0004409; MIPS:YLR417w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.5%;
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Best Local Similarity 50.0.
To Conservative
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52 QRIIYIDDAKPTQ 64
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Best Local Similarity
7; Conserv?
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A; Residues: 1-1661 <WIL>
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Best Local Similarity
A;Accession: S59382
A;Molecule type: DNA
A;Residues: 1-566 <FAV>
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A;Cross-references:
A;Map position: 12R
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                                                                                                                                                                                                                          Oligo-1, 6-glucosidase (EC 3.2.1.10) - Bacillus flavocaldarius KP1228
C;Species: Bacillus flavocaldarius KD128
C;Species: Bacillus flavocaldarius KD128
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 20-Sep-1999
C;Accession: J0018
B;Kashiwabara, S.; Matsuki, Y.; Kishimoto, T.; Suzuki, Y.
Biosci. Biotechnol. Biochem. 62, 1093-1102, 1998
A;Title: Clustered proline residues around the active-site cleft in thermostable oligo-1
A;Reference number: JE0181; MUID:98157218; PMID:9692189
A;Accession: J5018
A;Molecule type: DNA
A;Residues: 1-529 *KAS>
A;Accession: J5018
A;Accession: J5018
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A;Cross-references: DNA
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Cispecies: Homo sapiens (man)

Cjate: 22-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 01-Dec-2000

Cjate: 22-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 01-Dec-2000

Cjacession: B34612

R;Lania, L.; Donti, E.; Pannuti, A.; Pascucci, A.; Pengue, G.; Feliciello, I.; La Mantia A;Title: cDNA isolation, expression analysis, and chromosomal localization of two human A;Reference number: A34612; MUID:9016993; PMID:2106481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: GB:M29581; NID:g340447; PIDN:AAA61314.1; PID:g340448; GB:J04751
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C,Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C,Keywords: DNA binding; zinc finger
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C;Accession: S59382
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N;Alternate names: hypothetical protein L9931.3
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
46.5%; Score 40; DB 2; Length 529;
Best Local Similarity 43.8%; Pred. No. 41;
Matches 7; Conservative 4; Mismatches 5; Indels
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A;Description: The sequence of S. cerevisiae cosmid 9931.
A;Reference number: S59376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                     SKRYVYVDTRSEDETH 100
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164 RGEYLYTYDSQITDS 178
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              16
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              RORYLYTDDAQQTEAH
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A;Molecule type: mRNA
A;Residues: 1-543 <LAN>
A;Cross-references: GB:W3
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ses 8; Conserv
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Best Local S:
Matches 8
                                                                              85
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9

Mismatches

3;

Conservative

7;

Matches

1627 QOQYLYMQQLQQHQQH 1642

1 RQRYLYTDDAQQTEAH

A;Accession: T21993 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

R;Dobson, R. submitted to the EMBL Data Library, March 1997 A;Reference number: Z19498

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procession: B9927.

C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: B9927
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Ritle: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Residues: 1-439 cKUR>
A;Residues: 1-439 cKUR>
A;Residues: 1-439 cKUR>
A;Residues: 1-439 cKUR>
A;Residues: 1-439 cKUR>
A;Residues: 1-439 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
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A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Residues: 1-430 cKUR>
A;Reference Unmber: A; Davis, R.W.; Dreano, S.; Rederspiel, N.A.; Fisher, R.F.
L; Hyman, R.W.; Jones, T.
C; Hyman, R.W.; Jones, T.
C; Hyman, R.W.; Jones, T.
C; Hyman, R.W.; Jones, T.
C; Hyman, R.W.; Wondenbol, W.; Vonholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, KA;Reference number: A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMb2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: 279596; NID: e1323798; PIDN: CAB01858.1; GSPDB: GN00028; CESP: C02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable sugar uptake ABC transporter periplasmic solute-binding protein precursor
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A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: 690294
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-263 < KUR>
A; Cressereferences: GB: AE006641; NID: g13814594; PIDN: AAK41614.1; GSPDB: GN00155
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C02C6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18857
R;Swinburne, J.
submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A,Introns: 9/3; 46/3; 95/2; 135/1; 176/3; 209/3
C,Superfamily: Caenorhabditis elegans hypothetical protein C02C6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 2; Length 278;
Pred. No. 29;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                 Length 263;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: T18857
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Aclecule type: DNA
A;Residues: 1-278 <WIL>
                                                                                                                                                                                                                                                                                                                 2.
                                                                                                                                                                                                                                                                                                          Score 39; DB 2; Pred. No. 28; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: clone C02C6
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                                                                                                                                                                                                                                                                                                                 45.3%;
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Best Local Similarity 70.v.
70.v.
71 Conservative
                                                                                                                                                                                                                                                                                                                                                 Local Similarity 50.0 nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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C11 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 07-May-1999
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 07-May-1999
C;Accession: 36819
R;Strayer, D.S.; Jerng, H.H.; O'Connor, K.
Virology 185, 585-595, 1991.
Virology 185, 585-595, 1991.
A;Atitle: Sequence and analysis of a portion of the genomes of Shope fibroma virus and ma A;Reference number: A41700; MUID:92074222; PMID:1660196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 1
A;Introns: 37/3; 102/2; 229/3; 317/3; 375/2; 505/3; 546/1; 670/3; 835/1; 906/2; 943/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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A;Cross-references: EMBL:Z92834; PIDN:CAB07394.1; GSPDB:GN00019; CESP:F39B2.4b
A;Experimental source: clone F39B2
                                                                                                                                                                                                                                                                                    hypothetical protein F39B2.4b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21993
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C;Superfamily: vaccinia virus D10R protein; mutT domain homology
F;123-157/Domain: mutT domain homology <MUTT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1663;
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                      Indels
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1629 <u>pópyrymo</u>prophoph 1644

g

RESULT 13

1 RQRYLYTDDAQQTEAH 16

Local Similarity
Les 7; Conserv

Matches

Query Match

A; Gene: CESP: F39B2.4b

C;Genetics:

Score 39; DB 2 Pred. No. 27; 2; Mismatches

45.3%;

Query Match
Best Local Similarity 58.37
Conservative

4 YLYTDDAQQTEA 15 YTWIDDAORVSA 36

ਨੇ g RESULT 14

A; Status: translation not shown A; Molecule type: DNA

A; Residues: 1-259 <STR>

0

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probable membrane transporter STY1164 [imported] - Salmonella enterica subsp. enterica s
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: Ano633
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher, P; Parkhill, J; Dougan, G; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Authors: Parry, C; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Hitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPDB:GN00023; CESP:F46E10.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-235 <BLA>
A;Cross-references: EMBL:U64852; PIDN:AAB04972.1; GSPDB:GN00023; CESP:W01A11.7
A;Experimental source: strain Bristol N2; clone W01A11
C; Comment: This enzyme is involved in cellulose synthesis and its degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F46E10.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 05-Nov-1999
C;Accession: T3362; F26E0
R;Johnson, D.; Bradshaw, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                      Indels
                                  C,Superfamily: beta-glucosidase
C,Keywords: glycosidase; hydrolaase
E;1-26/Domain: signal sequence #status predicted <SIG>
F;27-735/Product: beta-glucosidase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: The sequence of C. elegans cosmid F46E10. A; Reference number: Z21446
A; Accession: T33962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Wolecule type: DNA
A;Residues: 1-235 <JOH2-
A;Cresidues: 1-235 <JOH2-
A;Cresidues: 10-255 <JOH2-
A;Cresidues: 10-255 <JOHC-
A;Cresidues: Branchard; Clone F46El0
R;Blanchard, M.; Bradshaw, H.
Submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid WOLAll.
A;Reference number: Z20658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA
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50.0%; Pred. No. 37;
vative 1; Mismatches
                                                                                                                                                                                                             Pred. No. 90;
1; Mismatches
                                                                                                                                                                                 45.3%; Score 39; 70.0%; Pred. No.
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Best Local Similarity 50.00
Check 8; Conservative
                                                                                                                                                                          Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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718 TDDSQQTTMH 727
                                                                                                                                                                                                                                                                                                    7 TDDAQQTEAH 16
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A, Status: preliminary
A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable phosphoprotein phosphatase (EC 3.1.3.16) regulatory chain - fission yeast (Schi
C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Accession: T11663
A Status: preliminary; translated from GB/EMBL/DDBJ
A Status: preliminary; translated from GB/EMBL/DDBJ
A Mylecule type: DNA
A, Molecule type: DNA
A, Residues: 1-627 < BAR>
A, Cross-references: EMBL: Z98533; NID:e1071719; PID:e334113
A, Cross-references: EMBL: Z98533; NID:e1071719; PID:e334113
B, Yoshioka, S.; Kato, K.; Makai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A, Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A, Reference number: Z17323; MUID:98162722; PID:9501991
A, Reference number: Z17323; MUID:98162722; PID:9501991
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A,Residues: 27-55 <TO2-
A,Experimental source: strain BPR2001
A,Kyberimental source: strain BPR2001
A,Note: the residues and 714 and 715 are interchanged in the authors' translation
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A;Experimental source: strain BPR2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Rosidues: 215-627 < YOS>
A;Cross-references: EMBL:D89107; NID:g1749421; PIDN:BAAL3770.1; PID:g1749422
A;Experimental source: strain PR745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                           DB 2; Length 439;
50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 2
Pred. No. 75;
3; Mismatches
                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 131/3; 213/1; 278/3; 410/2
A;Note: SPAC6F12.12
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                              45.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                         152 ÓKSLÝQĎEAKKTÉ 164
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                                                                                                                                                              Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                 2 QRYLYTDDAQQTE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z17305
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               A; Contents: annotation
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                                           C;Genetics:
A;Gene: SMb21103
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
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probable resistance protein ylcB [imported] - Escherichia coli (strain O157:H7, substra C;Species: Bscherichia coli (cjDate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: E85555 B;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE005174; NID:g12513457; PIDN:AAG54905.1; GSPDB:GN00145; UWGP:Z0
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable resistance protein [imported] - Escherichia coli (strain 0157.H7, substrain RI)
                                                                                                                                                                                                                                   A;Cross-references: GB:AE000162; GB:U00096; NID:91786782; PIDN:AAC73673.1; PID:91786785
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: B90705
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and Gasternoce number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule_type: DNA
A,Rabidues: 1-460 <HA>
A,FRedidues: 1-460 <HA>
A,CROSA-references: GB:BA000007, PIDN:BAB34033.1, PID:g13360068; GSPDB:GN00154
A,CROSA-references: strain 0157:H7, substrain RIMD 0509952
C,Genetics:
A,Gene: EGs0610
C,Superfamily: nodulation protein nodT
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                                                                                                                                                                  A;Accession: B64790
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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Pred. No. 79;
3; Mismatches 2; Indels
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A,Title: The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 2; Length 457;
Pred. No. 79;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: yclB
(Superfamily: nodulation protein nodT
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TWM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.2%;
58.3%;
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Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 RQNYLATEEAQR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || || |::||:
148 RQNYLATEEAQR 159
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A,Molecule type: DNA
A,Residues: 1-460 <STO>
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: B64790
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable GDSL-motif lipase/hydrolase At2g19010 [imported] - Arabidopsis thaliana N;Alternate names: AFG protein homolog F19F24.21; hypothetical protein T20K24.2 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Peb-1999 #sequence revision 19-Feb-1999 #text_change 16-Feb-2001 C;Accession: T01629; T00521; D84571 B4571 Ex;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, April 1998 I BAC F19F24 genomic sequence. A;Reference number: Z14153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMEL:AC002392; NID:g3176701; PID:g3176703
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Residues: 1-344 <ROU>
A)Cross-references: EMBL:AC003673; NID:g3004543; PID:g3004563
A)Cross-references: EMBL:AC003673; NID:g3004543; PID:g3004563
B,Experimental source: cultivar Columbia
B,Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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            A; Cross-references: GB: AL513382; PIDN: CAD08252.1; PID: g16502299; GSPDB: GN00176
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                                                                                                                                                                          Length 285;
                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                      DB 2;
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C;Superfamily: myrosinase-associated protein MyAP
                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yclB protein - Escherichia coli (strain K-12)
                                                                                                                                                                          Score 38;
Pred. No.
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A, Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                      44.2%;
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                                                                                                                                                                                                                                                                                                                                 2 ORYLYTODAQQTE 14
                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z14167
                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                     A;Gene: STY1164
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B64790
                                                                 Genetics
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A,Gene: ylcB C,Superfamily: nodulation protein nodT

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1 RORYLYTDDAGO 12

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Outer layer protein VP4 - human rotavirus A (serotype G3, strain AU-1)
N/Alternate names: hemagglutinin; outer capsid protein VP4
N;Contains: outer layer protein VP5; outer layer protein VP8
C;Species: human rotavirus A
C;Species: human rotavirus A
C;Species: human rotavirus A
C;Species: human rotavirus A
C;Accession: U21638
R;18egawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.
J; Gen. Virol. 73, 1939-1946, 1992
A;Accession: U21638; MUID:92356070; PMID:1322955
A;Reference number: U21638; MUID:92356070; PMID:1322955
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C.Superfamily: roctavirus outer layer protein VP3

C.Superfamily: roctavirus hemagglutinin; outer capsid protein

C.Superfamily: roctavirus hemagglutinin; outer capsid evP8>

F;1-241/Product: outer layer protein VP8 #status predicted «VP8>

F;242-247/Region: cleavage processing #status predicted «VP5>

F;248-775/Product: outer layer protein VP5 #status predicted «VP5>

F;17,32,97,132,183,198,237,567,613/Binding site: carbohydrate (Asn) (covalent) #status p
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J. Gen. Virol. 73, 1939-1946, 1992
A,Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav
                                                                                                                                                                                                                 Rilopez, S.; Arias, C.F.; Bell, J.R.; Strauss, J.H.; Espejo, R.T.
Virology 144, 11-19, 1985
A,Title: Primary structure of the cleavage site associated with trypsin enhancement of
A,Reference number: A04129; MUID:86045932; PMID:2998038
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outer layer protein VP3 - simian rotavirus SA11 (fragment)
C;Species: simian rotavirus SA11
A;Note: host (monkey)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 29-Oct-1999
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44.2%; Score 38; DB 1; Length 747

Best Local Similarity 42.9%; Pred. No. 1.4e+02;

Matches 6; Conservative 3; Mismatches 5; Indels
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Pred. No. 1.4e+02;
3; Mismatches 5;
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C;Superfamily: rotavirus outer layer protein VP3
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A;Molecule type: genomic RNA
A;Residues: 1-747 <LOP>
A;Cross-references: GB:M11158; NID:g61868
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299 QYTYTRDGEEVTAH 312
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Best Local Similarity 42.99
Matches 6; Conservative
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A;Residues: 1-775 <1SE>
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A;Residues: 1-580 <PRR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83973.1; PID:g737941
A;Experimental source: serogroup A, strain Z2491
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A;Experimental source: serogroup B, strain MC58
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Local Similarity 63.6%; Pred. No. 1e+02;
hes 7; Conservative 1; Mismatches 3; Indels
                                                                                                             Query Match
44.2%; Score 38; DB 2; Length 460;
Best Local Similarity 58.3%; Pred. No. 79;
Matches 7; Conservative 3; Mismatches 2; Indels
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1; Mismatches

Best Local Similarity 63.6 Matches 7; Conservative

A; Residues: 1-580 <TET> A;Accession: F81042 A;Status: preliminary A;Molecule type: DNA

A; Gene: NMB1780

C;Genetics:

Query Match

361 ROTÝKYIDDÁE 371

RESULT 26

1 RORYLYTDDAQ 11

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361 ROTYKYIDDAE 371 1 RORYLYTDDAQ 11 Best Loca Matches

A;Gene: NMA0686; NMA0687

Query Match

RESULT 27

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A map position: segment 4
C; Superfamily: roctavirus outer layer protein VP3
C; Superfamily: roctavirus outer layer protein of Steywords: glycoprotein; hemagglutinin; outer capsid protein
F; 1-241/Product: outer layer protein VP8 #status predicted <VP8>
F; 242-247/Region: cleavage processing #status predicted <VP5>
F; 248-776/Product: outer layer protein VP5 #status predicted <VP5>
F; 248-776/Product: outer layer protein VP5 #status predicted <VP5>
F; 56,97,132,151,198,456,507,670/Binding site: carbohydrate (Asn) (covalent) #status pre
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A; Molecule type: genomic RNA
A; Molecule type: genomic RNA
A; Molecule type: GB:013395; NID:G393327
A; Cross-references: GB:013395; NID:G393327
A; Note: this translation is not annotated in GenBank entry ROBASVP4, release 113.0
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                                                                                                                                                                     (covalent) #status
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Nucleic Acids Res. 15, 4361, 1987
A;Title: The complete nucleotide sequence of bovine rotavirus C486 gene 4 cDNA.
A;Reference number: A29529; MUID:87231020; PMID:3035492
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outer layer bemagglutinin; outer capsid protein VP4
NyAlternate names: hemagglutinin; outer capsid protein VP8
Sybcies: outer layer protein VP5; outer layer protein VP8
C;Species: bovine rotavirus A
C;Bate: 24-Peb-1994 #sequence_revision 24-Peb-1994 #text_change 02-Jun-2000
C;Accession: JQ2022
R;Taniguchi, K.; Urasawa, T.; Urasawa, S.
J; Gen. Virol. 74, 1215-1221, 1993
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C,Superfamily: rotavirus outer layer protein VP3
C,Keywords: glycoprotein; hemagglutinin
F,32,56,97,132,151,183,198,456,507,596,602/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outer layer protein VP3 - bovine rotavirus A (strain C486)
N;Alternate names: hemagglutinin
C;Species: bovine rotavirus A
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
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A;Molecule type: genomic RNA
A;Residues: 1-776 <POI>
A;Cross-references: GB:Y00127; NID:g61854; PIDN:CAA68325.1; PID:g61855
C;Genetics:
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein; hemagglutinin; outer capsid protein
F;1-241/product: outer layer protein VP8 #status predicted <VP8>
F;248-776/Product: outer layer protein VP5 #status predicted <VP5>
F;248-776/Product: outer layer protein VP5 #status predicted <VP5>
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Pred. No. 1.4e+02;
3; Mismatches 5; Indele
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Best Local Similarity 42.9%;
Matches 6; Conservative
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Best Local Similarity 42.57,
Best Local 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 32
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NyAlternate names: glycoprotein VP3; hemagglutinin; outer capsid protein VP3
N;Contains: outer layer protein VP5; outer layer protein VP8
C;Species: simian rotavirus SAll
A;Note: host (monkey)
C;Decies: simian rotavirus SAll
A;Note: host (monkey)
C;Accession: B31159
R;Nishlkawa, K; Taniguchi, K; Torres, A; Hoshino, Y; Green, K; Kapikian, A.Z.; Charl
A;Nishlkawa, K; Taniguchi, K; Torres, A; Hoshino, Y; Green, K; Kapikian, A.Z.; Charl
A;Virol. 62, 4022-4026, 1988
A;Title: Comparative analysis of the VP3 gene of divergent strains of the rotaviruses si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outer layer protein VP3 - Nebraska calf diarrhea virus (strain NCDV-Lincoln)
N,Alternate names: glycoprocein VP3; hemagglutinin; outer capsid protein VP3
N;Contains: outer layer protein VP5; outer layer protein VP8
N;Contains: outer layer protein VP5; outer layer protein VP8
C;Species: Nebraska calf diarrhea virus
C;Species: Nebraska calf diarrhea virus
C;Accession: C31159
Hequence_revision 31-Mar-1990 #text_change 12-Apr-1996
C;Accession: C31159
R;Nishikawa, K.; Taniguchi, K.; Torres, A.; Hoshino, Y.; Green, K.; Kapikian, A.Z.; Chan J. Virol. 62, 4022-4026, 1988
A;Title: Comparative analysis of the VP3 gene of divergent strains of the rotaviruses shall a strain of the colaviruses of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the colaviruse of the
                                                                                                                                                                                                                                                                                     A,Map position: segment 4

(Suberfamily: roctavirus) outer layer protein VP3

(Suberfamily: roctavirus) hemagglutinin, outer capsid protein

(Steywords: glycoprotein; hemagglutinin, outer capsid prodicted <VP8>

F;1241/Froduct: outer layer protein VP8 #status predicted <VP8>

F;242-247/Region: clearage processing #status predicted <VP5>
F;248-775/Product: outer layer protein VP5 #status predicted <VP5>
F;17,32,97,132,183,198,567,613/Binding site: carbohydrate (Asn) (covalent) #status predi
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C;Superfamily: rotavirus outer layer protein VP3
C;Seywords: glycoprotein; hemagglutinin; outer capsid protein
F;1-241/Product: outer layer protein VP8 #status predicted <VP8>
F;248-775/Product: outer layer protein VP5 #status predicted <VP5>
F;548-775/Product: outer layer protein VP5 #status predicted <VP5>
F;56,97,132,151,183,198,456,507,596,602/Binding site: carbohydrate (Asn) (covalent) #sta
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                                                                                                                                                                     A; Cross-references: DDBJ:D10971; NID:g222536; PIDN:BAA01748.1; PID:g222537 C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.2%; Score 38; DB 1; Length 7/5
42.9%; Pred. No. 1.4e+02;
- Minmatches 5; Indels
                               A, Reference number: JQ1638; MUID: 92356070; PMID: 1322955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 44.2%;
Local Similarity 42.9%;
les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 42.9
Matches 6; Conservative
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C; Genetics:
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A,Molecule type: genomic RNA
A,Residues: 1-775 <NIS>
C,Genetics:
                                                                                                                    A; Molecule type: genomic RNA
A; Residues: 1-775 < ISE>
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                                                                                     A; Accession: JQ1639
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Matches

à д RESULT 34

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Apperimental source: strain 936.

Apperimental source: strain 936.

RySimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, i.E.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, i.E.A.; Carraro, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Facincani, A.D.; Frenca, A.J.S.

submitted to GenBank, June 2000

A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm A,Authors: Ferreira, M.L.; Kemper, E.L.; Kitalima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigir J.D.; Junqueira, M.L.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. Chadó, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A.Authors: Matsukuma, A.Y.; Manck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; A,Authors: Matsukuma, A.Y.; Genod, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; A,Authors: da Silva, A.C.R.; da Silva, F.R.; de Sa, R.G.; Santelli, R.V.; Sawasa A,Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira, M.A.; Meference number: A59328

A;Contents: annotation
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
R;Accession: 88756
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE003923; GB:AE003849; NID:g9105736; PIDN:AAF83647.1; GSPDB:GN001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organic solvent tolerance precursor XF0837 [imported] - Xylella fastidiosa (strain 9aSc)
                             C;Accession: S24410
R;Mattion, N.M.; Estes, M.K.
Arch. Virol. 120, 109-113, 1991
A;Tile: Sequence of a rotavirus gene 4 associated with unique biologic properties.
A;Reference number: S24410; MUID:92028406; PMID:1656916
A;Accession: S24410
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 19-Feb-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                        44.2%; Score 38; DB 2; Length 776
42.9%; Pred. No. 1.4e+02;
rative 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                  A, Cross-references: BMBL:X57319
C, Superfamily: rotavirus outer layer protein VP3
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61.5%;
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                   A;Molecule type: genomic RNA A;Residues: 1-776 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-792 <SIM>
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein; hemagglutinin; outer capsid protein
F;1-241/Product: outer layer protein VPB #status predicted <VPS>
F;248-776/Product: outer layer protein VPS #status predicted <VPS>
F;328-776/Product: outer layer protein VPS #status predicted (Aps) (covalent) #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Nishikawa, K.; Taniguchi, K.; Torres, A.; Hoshino, Y.; Green, K.; Kapikian, A.Z.; Char J. Virol. 62, 4022-4026, 1988
A;Title: Comparative analysis of the VP3 gene of divergent strains of the rotaviruses si A;Reference number: A94694; MUID:89012172; PMID:2845121
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                                                                                                                                                                                                                                                                                                       outer layer protein VP3 - simian rotavirus SA11 (strain SA11-SEM)
N'Alternate names: glycoprotein VP3; hemagglutinin; outer capsid protein VP3
N'Contains: outer layer protein VP5; outer layer protein VP8
C'Species: simian rotavirus SA11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Bimian rotavirus SA11
C.Species: Bimian rotavirus SA11
C.Species: O-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Sep-1999
C.Accession: S03611
R;Mitchell, D.B.; Both, G.W.
Nucleic Acids Res. 17, 2122, 1989
A;Title: Complete nuclectide sequence of the simian rotavirus SA11 VP4 gene.
A;Reference number: S03611; MuID:89183617; PMID:2538804
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: host (monkey)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
C;Accession: A31159
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C,Genetics:
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:M23188; NID:g515742; PIDN:AAA47355.1; PID:g515743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.2%; Score 38; DB 1; Length 776; 42.3%; Pred. No. 1.4e+02; tive 3; Mismatches 5; Indels
                                 5; Indels
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C;Species: simian rotavirus SAll
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                                    Mismatches
                                    3;
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QYTYTRDGEEVTAH 315
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302 QYTYTRDGEEVTAH 315
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                                                                                                       3 RYLYTDDAQQTEAH 16
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Best Local Similarity 42.2.
Best Local Si Conservative
                                       6; Conservative
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Best Local Similarity
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A; Residues: 1-776 <MIT>
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RESULT 35

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hypothetical protein MYPU 5450 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: A99580
B;Chambaud, I:; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUD:21267165; PMID:11353084
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A;Molecule type: DNA
A;Residues: 1-1426 <XUN>
A;Crosidues: 1-1426 <XUN>
A;Crosidues: CB:AL445566; PID:914089960; PIDN:CAC13718.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                A;Map position: 3
A;Introns: 36/3; 121/3; 205/3; 336/2; 668/3; 739/1; 773/1; 853/2; 894/2; 932/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transposable element Txlc protein 2 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 21-Jul-2000
C;Accession: B32494
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A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-1308 <GAR>
A,Cross-references: GB:M26915; NID:g214844; PIDN:AAA49976.1; PID:g214846
C,Superfamily: pol polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Garrett, J.E.; Knutzon, D.S.; Carroll, D. Mol. Cell. Biol. 9, 3018-3027, 1989
A;Title: Composite transposable elements in the Xenopus laevis genome. A;Reference number: A32494; MuID:89384562; PMID:2550791
A;Accession: B32494
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44.2%; Score 38; DB 2; Length 1426;
Best Local Similarity 72.7%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         Length 1051;
                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1051 <JOR>
A;Experimental source: cultivar Columbia; BAC clone F14L2.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
submitted to the Frotein Sequence Database, April 2000
A;Reference number: Z25008
A;Accession: T48933
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44.2%; Score 38; DB 2;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches
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Matches 7; Conservative
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A;Gene: ATSP:F14L2.80
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A;Genetic code: SGC3
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APPLICANT: Itch, No. US20020082205Aluyuki APPLICANT: Kavanaugh, W. Michael
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_MBW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_MBW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-27-884-78

US-10-230-163-78

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Gapop 10.0 , Gapext 0.5
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US-10-219-466-78

US-10-219-461-78

US-10-219-481-78

US-10-219-481-78

US-10-218-25-78

US-10-218-25-78

US-10-218-956-78

US-10-219-468-78

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US-10-219-468-78

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ALIGNMENTS

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Gaps
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                                                    APPLICANT: LAVALAGE, W. US20020164713Aluyuki
APPLICANT: Kavanaugh, W. Michael
APPLICANT: Kavanaugh, W. Michael
TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: PP-16758 001/201130 408
CURRENT APPLICATION NUMBER: US/10/060,765
CURRENT APPLICATION NUMBER: US/09/715,805
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 17-16
NUMBER OF SEQ ID NOS: 17-16
SEQ ID NO 8
LENGTH: 15
TYPE: RETSEEQ for Windows Version 4.0
TYPE: RETSEE RETSEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 89; DB 13; Length 15; 100.0%; Pred. No. 9.4e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/09801968
; Sequence 8, Application US/10060765; Publication No. US20020164713A1; GENERAL INFORMATION:
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US-10-060-765-8
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: BCOMIS, Michael
APPLICANT: WHITE, Kenneth
APPLICANT: WHITE, Kenneth
APPLICANT: WHITE, Kenneth
APPLICANT: WIRD STROW, Tim
APPLICANT: WITTINGER, Thomas
TITLE OF INVENTION: NOVEL FIEROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
TITLE OF INVENTION: NOVEL FIEROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
CURRENT APPLICATION NUMBER: US/09/901,938
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 34
SOFTWARER: PARENTIN Version 3.0
SEQ ID NO 33
LENGTH: 136
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; Sequence 36, Application US/09802154
; Publication No. US20030105302A1
; GENERAL INFORMATION:
    APPLICANT: ILCh, No. US20030105302Aluyuki
    APPLICANT: Kavanaugh, W. Michael
    TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
    TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE
    TITLE OF INVENTION: HUMAN FGF-23 GENE AND
    TITLE OF INVENTION: HUMAN FGF-369/802,154
    CURRENT APPLICATION NUMBER: US/09/802,154
    CURRENT FILING DATE: 2001-03-07
    NUMBER OF SEQ ID NOS: 46
    SEQ ID NOS: 46
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                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 89; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: PP-17150,001/201130,40901
CURRENT PAPLICATION NUMBER: US/09/801,968
CURRENT FILING DATE: 2011-03-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0
Matches 15; Conservative
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CORGANISM: Homo Sapiens
US-09-901-938-33
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-801-968-36
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US-09-901-938-33
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US-09-802-154-36
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Sequence 33, Application US/10379334

| Sequence 33, Application US/10379334
| Sequence 33, Application US/10379334
| Sequence 33, Application No. US20030181379A1
| Sequence 100 No. US20030181379A1
| Application No. US20030181379A1
| APPLICANT: ECONS, Michael APPLICANT: STROM, Tim APPLICANT: MHITE, Kenneth APPLICANT: MHITE, Tim APPLICANT: MHITE, Tim APPLICANT: MHITE, Tim HITHGER, Thomas APPLICANT: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE FILE REFERENCE: 0530-03-03-04
| CURRENT FILING DATE: 2003-03-04
| PRIOR FILING DATE: 2000-07-19
| PRIOR FILING DATE: 2000-07-19
| PRIOR FILING DATE: 2000-07-19
| PRIOR FILING DATE: 2000-07-19
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| SEQ ID NO 33
| EBNGTH: 136
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    Length 136;
                                               Indels
100.0%; Score 89; DB 9; ; ilarity 100.0%; Pred. No. 7.9e-05; Conservative 0; Mismatches 0;
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; Sequence 2. Application US/09755695
; Patent No. US20020081663A1
; GENERAL INFORMATION:
    APPLICANT: Conklin, En
    TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGF11
; TITLE PEFERENCE: 00-03
; CURRENT APPLICATION NUMBER: US/09/755,695
; CURRENT APPLICATION NUMBER: US 60/174,526
; PRIOR APPLICATION NUMBER: US 60/174,526
; RIOR APPLICATION NUMBER: US 60/174,526
; RIOR FILING DATE: 2001-05-11
; SOFTWARE: FastSEQ ID NOS: 6
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 208
; WINDER OF SEQ ID NOS: 6
; SEQ ID NO 2
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                                                                                                                                          107 HLPGNKSPHRDPAPR 121
                                                                                                1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.1
Matches 15; Conservative
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Matches 15; Conservative
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ORGANISM: Homo sapiens
US-09-755-695-2
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ORGANISM: Homo Sapiens
         Query Match
Best Local Similarity
Matches 15; Conserva
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US-09-755-695-2
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105-101-27-684-78
Sequence 78, Application US/10227844
Publication N- U22003027988A1
Sequence 78, Application US/10227844
SEQUENCE CONTROL UZ2003027988A1
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-08-04
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Length 208;
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R APPLICATION NUMBER: 60/115733
R FILING DATE: 1999-01-12
R APPLICATION NUMBER: 60/119549
R FILING DATE: 1999-02-10
R APPLICATION NUMBER: 60/123618
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PRIOR APPLICATION NUMBER: 60/169835
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RESULT 8
US-10-230-163-78
Sequence 78, Application US/10230163
; Publication No. US20030036635A1
; Publication Revent Revin P.

144 HLPGNKSPHRDPAPR 158

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Gaps
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PRIOR FILING DATE: 1999-03-10
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Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 15; Conservative
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US-10-230-338-78
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APPLICANT:

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PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 66/064103
PRIOR PILING DATE: 1997-10-31
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PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1999-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PILING DATE: 1998-03-25
PRIOR PILING DATE: 1998-03-25
PRIOR PRILING DATE: 1998-03-25
PRIOR PRILING DATE: 1998-03-26
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Publication No. US20030050448A1
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) ORGANISM: Homo Sapien

US-10-218-631-78
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APPLICANT: Gerriteen, Mary
APPLICANT: Gerriteen, Mary
APPLICANT: Geddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victorial
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APPLICANT: Watanabe, Colin L.
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                                                                   APPLICANT: Watenabe, Colin L.
APPLICANT: Watenabe, Colin L.
APPLICANT: Watenabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ADDRESS 105/020.338
FILE REFERENCE: B3530P1C92
CURRENT PILLING DATE: 2002-08-28
PRIOR PELLING DATE: 2002-08-28
PRIOR PELLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/065813
PRIOR APPLICATION NUMBER: 60/065287
PRIOR APPLICATION NUMBER: 60/063549
PRIOR PILLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-10-28
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                                                   Stephan, Jean-Philippe F.
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Publication No. US20030045687A1
GENERAL INFORMATION:
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Matches 15; Conservative
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                                                              APPLICANT:
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GENERAL INFORMATION:

APPLICANT: BAKET, Kevin P.
APPLICANT: Gedard, Audrey
APPLICANT: Gedard, Audrey
APPLICANT: Gedard, Audrey
APPLICANT: Gedreki, Paul J.
APPLICANT: Gedreki, Paul J.
APPLICANT: Gerriten, Vactoria
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Vactoria
APPLICANT: Stephan, Vactoria
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APPLICANT: Stephan, Vactoria
APPLICANT: Stephan, Vactoria
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APPLICANT: Stephan, Vactoria
APPLICANT: Stephan, Vactoria
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANTON: ACIDS ENCODING THE SAME
FILE REFERENCE: P350PLG98
FRIOR FILING DATE: 2002-04-09
RRIOR FILING DATE: 2002-04-09
RRIOR FILING DATE: 1997-09-17
RRIOR FILING DATE: 1997-09-17
RRIOR FILING DATE: 1997-10-13
RRIOR FILING DATE: 1997-10-31
RRIOR FILING DATE: 1997-10-31
RRIOR FILING DATE: 1998-03-20
RRIOR FILING DATE: 1998-03-20
RRIOR PAPLICATION NUMBER: 60/079294
RRIOR RILING DATE: 1998-03-26
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 89; DB 14; Length 208; 100.0%; Pred. No. 0.00012;
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RESULT 14
US-10-227-873-78
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APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geritlesn, Mary
APPLICANT: Geddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: PSJORPIC
CURRENT APPLICATION NUMBER: US/10/119,480
PRIOR APPLICATION NUMBER: US/01/19,480
PRIOR APPLICATION NUMBER: 00/062287
PRIOR APPLICATION NUMBER: 60/06313
PRIOR APPLICATION NUMBER: 60/063287
PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063287
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-21
PRIOR FLING DATE: 1997-10-21
PRIOR FLING DATE: 1997-10-21
PRIOR FLING DATE: 1997-10-22
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PRIOR APPLICATION NUMBER: 60/079910
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100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                          Length 208;
                                                                                                                                               Score 89; DB 14; Lengtn 2v
Pred. No. 0.00012;
...--roheg 0; Indels
                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 78, Application US/10216159A publication No. US20030069397A1 GENERAL INFORMATION:
                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                        1 HLPGNKSPHRDPAPR 15
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ORGANISM: Homo Sapien
                                                     TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-78
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SEQ ID NO 78
LENGTH: 208
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144 HLPGNKSPHRDPAPR 158

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APPLICANT: Gerritsen, mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Goddard, Austin L.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wadanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PL72
CURRENT APPLICATION NUMBER: US/10/22,873
CURRENT APPLICATION NUMBER: G0/069113
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
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PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: G0/06349
PRIOR PILING DATE: 1997-10-31
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PRIOR APPLICATION NUMBER: G0/069873
PRIOR APPLICATION NUMBER: G0/069873
PRIOR APPLICATION NUMBER: G0/069873
PRIOR APPLICATION NUMBER: G0/069873
PRIOR APPLICATION NUMBER: G0/069873
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLIFEFTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLIFEFTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3530PIC11
CURRENT APPLICATION NUMBER: US/10/218,849
CURRENT FILING DATE: 2002-08-12
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 89; DB 14; Length 208; 100.0%; Pred. No. 0.00012; ive 0; Mismatches 0; Indels 0
                                                                                                                   Desnoyers, Inc.
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 78, Application US/10227873
Publication No. US20030073816A1
GENERAL INFORMATION:
Sequence 78, Application US/10218849
Publication No. US20030073814A1
GENERAL INFORMATION:
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Gerritsen, Mary
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                                                                                               APPLICANT: Baker, Kevin P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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APPLICATION NUMBER: 60/100919

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FILING DATE: 1998-05-13
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FILING DATE: 1998-04-15
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FILING DATE: 1998-05-06
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APPLICANT: Geddard, Audrey
APPLICANT: Geddard, Paul J.
APPLICANT: Grandld, J. Christopher
APPLICANT: Grandld, J. Christopher
APPLICANT: Grandld, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBRUCE: P3530PLC78
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100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels (
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Publication No. US20030073817A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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APPLICATION NUMBER: 60/149320
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APPLICANT Goddard, Audrey
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APPLICANT Gurney, Austin L.
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APPLICANT Stephan, Jean-Hilppe F.
APPLICANT Watanabe, Colin L.
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APPLICANT WATANABE, Colin L.
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimald, J. Christopher
APPLICANT: Grimald, J. Christopher
APPLICANT: Sath, Victoria
APPLICANT: Sath, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Matanabe, Colin L.
APPLICANT: Mood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C82
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deenoyers, Luc
APPLICANT: Gerritgen, Mary
                                                                                                                                                                                                       144 HLPGNKSPHRDPAPR 158
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Sequence 78, Application US/10219003

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APPLICANT: Gerriteen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Gormaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: MACANDIN SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLG7
CURRENT APPLICATION NUMBER: US/10/219,464
              APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WOOD AND ACIDS BROODING THE SAME
TITLE OF INVENTION: ACIDS BROODING THE SAME
TITLE OF INVENTION NUMBER: US/10/219,075
CURRENT FILING DATE: 1997-109-14
PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06297
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063849
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063873
PRIOR APPLICATION NUMBER: 60/063873
PRIOR APPLICATION NUMBER: 60/07394
PRIOR FILING DATE: 1997-10-20
PRIOR FILING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/07924
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-26
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PRIOR APPLICATION NUMBER: 60/07924
PRIOR PRIING DATE: 1998-03-26
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PRIOR PRIING DATE: 1998-03-26
PRIOR PRIEME OF SEQ ID NOS: 246
PRIOR PRIEME DATE: 1998-03-26
PRIOR PRIEME OF SEQ ID NOS: 246
PRIOR PRIEME OF SEQ ID NOS: 246
PRIOR PRIEME OF SEQ ID NOS: 246
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Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 78, Application US/10219464 Publication No. US20030088065A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 HLPGNKSPHRDPAPR 158
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Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
) ORGANISM: Homo Sapien
US-10-219-075-78
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US-10-219-464-78
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APPLICANT: Baker, Kevin P.
APPLICANT: Besoryers, Luc
APPLICANT: Besoryers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Godawaki, Paul J.
APPLICANT: Godawaki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victorin I.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: ARTHON: SECRETED AND TRANSMEWBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBNUE: P3530PLG47
CURRENT FILING DATE: 2002-08-13
CURRENT FILING DATE: 2002-08-13
CURRENT FILING DATE: 2002-08-14

PRIOR PELICATION NUMBER: 10/119,480

PRIOR PELICATION NUMBER: 10/119,480

PRIOR PELING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/06287

PRIOR APPLICATION NUMBER: 60/06287

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17

PRIOR PLING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/064103

PRIOR APPLICATION NUMBER: 60/068913

PRIOR APPLICATION NUMBER: 60/068913

PRIOR APPLICATION NUMBER: 60/078910

PRIOR PILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-27

NUMBER: 60/079728

NUMBER: 60/079728

NUMBER: 60/079728

NUMBER: 60/079728
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PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR PELING DATE: 2002-04-09
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR APPLICATION NUMBER: 60/069103
PRIOR APPLICATION NUMBER: 60/069103
PRIOR APPLICATION NUMBER: 60/069103
PRIOR APPLICATION NUMBER: 60/069103
PRIOR APPLICATION NUMBER: 60/069103
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Publication No. US20030088066A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
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CORGANISM: Homo Sapien
US-10-219-464-78
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Best Local Similarity 100.
Matches 15; Conservative
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US-10-230-260-78
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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SEQUENCE 18, APPLICATION US/10219479

PUBLICATION NO. DIS20030088067A1

SEGRERAL INFORMATION

APPLICANT: BEARLY, Kevin P.

APPLICANT: Goodwar, Mary

APPLICANT: Goodwar, Audray

APPLICANT: Goodwar, Audray

APPLICANT: Goodwar, Audray

APPLICANT: Goodwar, Audray

APPLICANT: Goodwar, Deal-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Wood, Milliam I.

TITLE OF INVENTION: SECRETE AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: SCOOT-09-13

FILE OF INVENTION WOMBER: 105/10/19/40

PRIOR APPLICANTON NUMBER: 60/05913

PRIOR APPLICANTON NUMBER: 60/05913

PRIOR APPLICANTON NUMBER: 60/069873

PRIOR PLING DATE: 1997-10-21

PRIOR PLING DATE: 1997-10-12

PRIOR PLING DATE: 1997-10-21

PRIOR PLING DATE: 1999-03-25

PRIOR PLING DATE: 1999-03-25

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PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
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Best Local Similarity 100.0
Matches 15; Conservative
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; ORGANISM: Homo Sapien
US-10-219-479-78
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; ORGANISM: Homo Sapien
US-10-219-466-78
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US-10-219-479-78
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Query Match

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERRACE: P3530P1C28
CURRENT APPLICATION NUMBER: US/10/219,481
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 0/059113
PRIOR APPLICATION NUMBER: 60/062287
PRIOR APPLICATION NUMBER: 60/063287
PRIOR APPLICATION NUMBER: 60/063287
PRIOR APPLICATION NUMBER: 60/063287
PRIOR PLING DATE: 1997-10-17
PRIOR PLING DATE: 1997-10-18
PRIOR PLING DATE: 1997-10-18
PRIOR FILING DATE: 1997-10-31
PRIOR PLING DATE: 1997-10-31
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PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-20
PRIOR PLING DATE: 1998-03-25
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100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels (
                                                          Indels
                       Pred. No. 0.00012; Mismatches 0;
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Godowski, Paul J.
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Jean-Philippe F.
Watanabe, Colin L.
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                                                                                                                                                                                                                                                                                                                                                               US-10-219-481-78
; Sequence 78, Application US/10219481
; Fublication No. US20030088068A1
; GENERAL INFORMATION:
100.001
100.001
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Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo Sapien
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144 HLPGNKSPHRDPAPR 158
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Matches 15; Conservative
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, ORGANISM: Homo Sapien
US-10-232-231-78
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                                                                                                               APPLICANT: GIRINGLAY, OLITISTODINET
APPLICANT: GURLEA, VICTORIA
APPLICANT: SMATCH, VICTORIA
APPLICANT: SMATCH, VICTORIA
APPLICANT: SMATCH, VICTORIA
APPLICANT: Watenabe, Colin L.
APPLICANT: Watenabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETE AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P$3:0P10633
CURRENT APPLICATION NUMBER: 10/119,480
PRIOR PELICATION NUMBER: 10/109-109-17
PRIOR APPLICATION NUMBER: 60/0659113
PRIOR APPLICATION NUMBER: 60/0659113
PRIOR APPLICATION NUMBER: 60/06369
PRIOR FILING DATE: 1997-10-21
PRIOR PELING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/06389
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/069913
PRIOR PELING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/069919
PRIOR PELING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/069919
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079266
PRIOR FILING DATE: 1998-03-27
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APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION WUMBER: US/10/232,231
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 10/119,480
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 HLPGNKSPHRDPAPR 158
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRGANISM: Homo Sapien US-10-230-260-78
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APPLICANT: Desnoyers, Mary
APPLICANT: Geraftsen, Mary
APPLICANT: Godward, Audrey
APPLICANT: Godward, Audrey
APPLICANT: Godward, Austin L.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Swith, Victorian L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PS30PLICAN
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US/10/132,233
PRIOR FILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 2002-04-09
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PEDILOATION NUMBER: 60/062287
PRIOR PEDILOATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR APPLICATION NUMBER: 60/064103
PRIOR APPLICATION NUMBER: 60/06973
PRIOR PILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
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APPLICATION NUMBER: 60/079294
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Publication No. US20030088072A1
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PL77
CURRENT APPLICATION NUMBER: US/10/216,165
CURRENT FILING DATE: 2002-08-09
PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/06287
PRIOR PELICATION NUMBER: 60/06287
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-18
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PRIOR PELING DATE: 1997-10-31
PRIOR PELING DATE: 1997-20-32
PRIOR APPLICATION NUMBER: 60/079910
PRIOR APPLICATION NUMBER: 60/079910
PRIOR PELING DATE: 1998-03-26
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PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
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Best Local Similarity 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerritsen, Mary
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
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CRGANISM: Homo Sapien
US-10-216-165-78
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CORGANISM: Homo Sapien
US-10-232-233-78
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PRIOR FILING NATE: 1999-12-23

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PRIOR PLILANG NATE: 1900-12

PRIOR PLILANG NATE: 1900-12

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PLC30
CURRENT APPLICATION NUMBER: US/10/219,478
CURRENT PILING DATE: 2002-04-09
PRIOR PILING DATE: 2002-04-09
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-01-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062387
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-31
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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Granaldi, J. Christopher
APPLICANT: Granaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Gean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: ALORENTON: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PLC67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 208;
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CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05287
PRIOR FILING DATE: 1997-00-17
PRIOR APPLICATION NUMBER: 60/06287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063849
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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Best Local Similarity 100.
Matches 15; Conservative
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APPLICANT: Goddwaki, Paul J.
APPLICANT: Godcwaki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin I.
APPLICANT: Wood, William I.
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerritsen, Mary
APPLICANT: Godward, Audrey
APPLICANT: Godward, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
                                                           Sequence 78, Application US/10219468
Publication No. US200300928881
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/064103
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PRIOR APPLICATION NUMBER: 60/069873
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Matches 15; Conservative
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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CORGANISM: Homo Sapien
US-10-219-468-78
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US-10-219-478-78
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; ORGANISM: Homo Sapien
US-10-233-205-78
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APPLICANT: Goldowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurnaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wetanabe, Colin L.
APPLICANT: Wetanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION: ACIDS ENCODING THE SAME
TILE OF INVENTION: ACIDS ENCODING THE SAME
TILE REPERENCE: 2002-08-29
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
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PRIOR APPLICATION NUMBER: 60/069873
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
PRIOR PRIOR APPLICATION NUMBER: 60/079566
PRIOR APPLICATION NUMBER: 60/07958
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
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NUMBER OF SEQ ID NOS: 246
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Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels
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Gerritsen, Mary
Goddard, Audrey
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ORGANISM: Homo Sapien
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LENGTH: 208
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LENGTH: 208
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Goddowski, Paul J.
APPLICANT: Gurnay, Austin L.
APPLICANT: Gurnay, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
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APPLICANT: Wood, William I.
APPLICANT: Worder: 1002-04-09
PRIOR FILING DATE: 1002-04-09
PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06387
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100.0%; Score 89; DB 14; Length 208; 100.0%; Pred. No. 0.00012; ive 0; Mismatches 0; Indels (
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Best Local Similarity 100.0%;
Matches 15; Conservative 0.
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               Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                             1 HLPGNKSPHRDPAPR
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US-10-219-072-78
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US-10-219-474-78
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LENGTH: 208
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CURRENT FILING DATE: 2002-08-14

PRIOR FILING DATE: 2002-04-09

PRIOR PELICATION NUMBER: US/10/51313

PRIOR PELICATION NUMBER: 60/065113

PRIOR PELING DATE: 1997-09-17

PRIOR PELING DATE: 1997-10-17

PRIOR PELING DATE: 1997-10-28

PRIOR PELING DATE: 1997-10-28

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PRIOR PELING DATE: 1997-12-17

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APPLICANT: Godweki, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guney, Austin L.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
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APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACLIOS ENCODING THE SAME
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Pred. No. 0.00012;
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Smith, Victoria
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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No. US20030096960A1
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
                                                                                                                                                                Desnoyers, Luc
Gerritsen, Mary
                                                       GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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US-10-219-470-78
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: PS330PLG37 CURRENT PILIDM DATE: 2002-08-13 CURRENT FILING DATE: 2002-08-13 PRIOR PILING DATE: 2002-04-09 PRIOR PILING DATE: 2002-04-09 PRIOR PILING DATE: 1997-09-17 PRIOR FILING DATE: 1997-09-17 PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-10-28 PRIOR FILING DATE: 1997-10-28 PRIOR FILING DATE: 1997-10-28 PRIOR FILING DATE: 1997-10-28 PRIOR FILING DATE: 1997-10-28 PRIOR FILING DATE: 1997-10-28 PRIOR FILING DATE: 1997-10-28
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NUMBER OF SEQ ID NOS: 246
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FILE KEFERENCE: 19350FLC39, 474
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PRIOR PILING DATE: 2002-04-09
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PRIOR PLILING DATE: 1997-01-17
PRIOR APPLICATION NUMBER: 60/06287
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Publication No. US20030096962A1
GENERAL INFORMATION:
APPLICANT: Baker, Navin P.
APPLICANT: Gestoyers, Luc
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Viccoria
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ORGANISM: Homo Sapien
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APPLICANT BAKET, KAVID P.
APPLICANT BAKET, KAVID P.
APPLICANT DESNOYERS, LUC
APPLICANT GENTAGEN, MAY
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APPLICANT GENTAGEN, PAIN TO CHISTOPHER
APPLICANT GONDAEN, PAUL IN.
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APPLICANT GONDAEN, PAUL IN.
APPLICANT SEEPING COLUIL LAPPLINDE F.
APPLICANT MODEL GONDAEN, JOHN DE SNAE
APPLICANT WOOD WILLIAM I.
APPLICANT WOOD WILLIAM I.
APPLICANT WOOD WILLIAM I.
APPLICANT WOOD WILLIAM I.
APPLICANT WOOD SECRETED AND TRANSMERRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMERRANE FOR THE APPLICANT NUMBER: US/10/219,528
CURRENT FILING DATE: 2002-08-19
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PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1998-03-12-17
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR PAPLICATION WUMBER: 60/079294
PRIOR PILING DATE: 1998-03-25
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PRIOR APPLICATION WUMBER: 60/079728
PRIOR APPLICATION DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
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Best Local Similarity 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels C
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US-10-219-524-78
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PRIOR FILING DATE: 1998-05-06

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R FILING DATE: 1999-02-10
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Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C80
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
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Gerritsen, Mary
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March 2, 2004, 15:50:07 ; Search time 9 Seconds
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| | Query Match Length | 15 | 124 | 181 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 208 | 0 |
| ď | Query | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | |
| | Score | 89 | 6 | 68 | 68 | 89 | 8 | 68 | 8 | 89 | 6 | 68 | 68 | 89 | 89 | 8 | 8 | 89 | 8 | 88 | 68 | 68 | 88 | 68 | 8 | : : |
| | Result No. | | 10 | l (r) | 4 | ı LCT | 4 | 7 | - 60 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 119 | 20 | 2.1 | 22 | 23 | 24 | |

| Novel | Human | Adc21797 Human PRO | Adc49828 Novel hum | Adc49027 Novel hum | Adc49544 Novel hum | Novel 1 | Novel | _ | Add06260 Novel hum | | Add50742 Novel hum | Add50988 Novel hum | Add50469 Human PRO | Add50223 Human PRO | Add51234 Novel hum | Adc48781 Novel hum | Ade20952 Novel hum | Ade05796 Human PRO | Add75025 Human PRO | |
|----------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|
| ADB72969 | ADC36807 | ADC21797 | ADC49828 | ADC49027 | ADC49544 | ADC47405 | ADC47150 | ADC78025 | ADD06260 | ADC77779 | ADD50742 | ADD50988 | ADD50469 | ADD50223 | ADD51234 | ADC48781 | ADE20952 | ADE05796 | 3002000 | ADD 13023 |
| 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 7 | 208 B | 208 8 | 208 B | 0 | 0 007 |
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| 26 | 27 | ď | 0 0 |) C | 3 7 | 3.5 | 7 6 | 9 6 | י ע | ייי | 2 6 | ה מ מ | 0 0 | 2 4 | 7 7 | 42 | 43 | 44 | * 1 | 4 4 |

ALIGNMENTS

Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation; hepatic cell; cirrhosis; infertility; impotence; testicular cancer; leukemia; lymphoma; autoimmune disease; thymus proliferative disorder. Epitope-bearing portion of human fibroblast growth factor-21 (FGF-21). AAB68419 standard; peptide; 15 AA. 18-NOV-1999; 99US-0166540P. 11-MAY-2000; 2000US-0203633P. 16-NOV-2000; 2000WO-US031745. 23-JUL-2001 (first entry) Itoh N, Kavanaugh WM; (CHIR) CHIRON CORP. (KYOU) UNIV KYOTO. WPI; 2001-343823/36. WO200136640-A2. Ното варіепв. 25-MAY-2001. AAB68419; RESULT 1 AAB68419 ID AAB6

New nucleic acid molecule useful for treating disease, e.g. infertility, impotence, or testicular cancer.

Claim 17; Page 40; 61pp; English.

The present sequence represents an epitope-bearing portion of human fibroblast growth factor-21 (FGF-21). FGF proteins regulate growth and differentiation of a variety of cell types. FGF-21 nucleic acids and polypeptides are useful for treating diseases and disorders characterised by inadequate numbers of hepatic cells, preferably cirrhosis of the liver. They may also be used in the treatment of infertility, impotence, and testicular cancer, as well as leukemia, lymphoma, autoimmune disease, or proliferative disorders of the thymus

Sequence 15 AA;

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, DB 4; her,
       Length 15;
                      Mismatches
       Score 89;
Pred. No.
                      .
       100.08;
                      Conservative
              Similarity
       Query Match
Best Local Simi
Matches 15;
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ABB81312 standard; protein; 124 AA. ABB81312;

21-AUG-2002 (first entry)

Fibroblast growth factor 9; FGF-9; cytostatic; vulnerary; osteopathic; antiarthritic; vasculogenesis; angiogenesis; FGFR; skeletal disorder; fibroblast growth factor receptor; cancer; bone fracture healing; bone growth; wound healing; achondroplasia; hypochondroplasia; osteoporosis; cartilage defect; multiple myeloma. Human FGF21 core structure amino acid sequence.

Homo sapiens

WO200236732-A2

10-MAY-2002.

18-OCT-2001; 2001WO-IL000962.

31-OCT-2000; 2000IL-00139380

(PROC-) PROCHON BIOTECH

Yayon A; Bogin O, Adar R,

WPI; 2002-479754/51.

New variants of fibroblast growth factor, useful for treating skeletal disorders including osteoporosis, malignancies and to enhance wound and fracture healing.

Disclosure; Fig 1; 74pp; English.

The present invention describes an active variant (I) of a fibroblast growth factor (FGF) having at least one mutation in the beta-8-beta-9 crowth factor (FGF) having at least one meutation in the beta-8-beta-9 crowd and an an activative statements of the corresponding wild type FGF, by decreasing the biological activity mediated by at least one receptor subtype. (I) has cytostatic, vulnerary, osteopathic and antianthritic activities. (I) can be used as a regulator of vasculogenesis or angiogenesis. (I) is useful for preparing a medicament and for treating a disease or disorder related to normal or abnormal FGF receptors FGFRs), especially skeletal disorders, cancer, to enhance bone fracture healing or bone growth processes and wound healing processes. (I) is useful in detection and treatment of various FGFR related disorders including skeletal disorders e.g. achondroplasia, and osteoporosis, and cartilage defects, multiple myploma, epithelial cancers such as transitional cell carcinoma of the bladder and cervical carcinoma. The novel mutants are useful in high carpies of FGFRs in various disorders such as transitional cell carcinoma of the captesion systems unitable for pharmaceutical production, targeting of and serve as template for the formation of improved agonists and carcinoma manner cancer as a processer of any sor other agents to tissues and cells having specific FGFR subtypes, antagonists of FGFRs in various disorders such as switch as skeletal disorders and manner cancer as the contamer as the contament of a skeletal disorders and manner cancer as and cells as skeletal disorders and manner cancer as the contament of a skeletal disorders and manner cancer as the contament of a skeletal disorders and cancer meet an extended to contame and cells as skeletal disorders and cancer as the contament of any contament of the contament of a skeletal disorders and cancer meet and cells and cells and cells and cells and cells and cells and cells and cells and cells and cells and cells and cells and cells and cell cancer. The present sequence represents a FGF core structure amino acid sequence which is given in the exemplification of the present invention

Sequence 124 AA;

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DB 5; Length 124;
 100.0%; Score 89;
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         Gaps
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         Indels
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 Pred. No. 5.6e-05;
Mismatches 0;
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100.0%;
           15; Conservative
 Best Local Similarity
Matches 15; Conserva
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1 HLPGNKSPHRDPAPR 15 ð

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Gaps ; 0 101 HLPGNKSPHRDPAPR 115

AAU00965 standard; protein; 181 AA. AAU00965 ID AAU0

AAU00965;

(first entry) 24-MAY-2001 Human Fibroblast Growth Factor-like (FGF-like) polypeptide fragment.

inflammatory bowel disease; Crohn's disease; Obesity; tubular necrosis; renal tubule damage; gastrointestinal abnormality; wasting syndrome; neurodegenerative disease; haematopoietic cell reconstitution; cachaxia; chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy; multiple sclerosis; short stature; delayed maturation; excessive growth; accomegaly; premature maturation; alopecia; bronchopulmonary dysplasia; androgen target organ abnormality; respiratory distress syndrome; stroke; cancer; atherosclerosis; hypercholesterolaemia; osteoporosis; baldness; decreased stamina; decreased artophy; sarcopenia; increased fatigue; decreased stamina; decreased cardiac function; immune system dysfunction; parkinson's disease; Alzheimer's disease; decreased cognitive function; treatment; cirrhogis; mucositis; diabetes; Fibroblast Growth Factor; FGF; senile dementia; human

WO200118172-A2.

15-MAR-2001.

05-SEP-2000; 2000WO-US024373.

07-SEP-1999; 99US-00391861. 23-AUG-2000; 2000US-00644052.

(AMGE-) AMGEN INC.

WPI; 2001-226743/23.

Thomason AR,

Novel isolated fibroblast growth factor-like polypeptide useful for treating, preventing or ameliorating cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease, diabetes, obesity, stroke and osteoporosis.

Claim 14; Page 116-117; 138pp; English.

The sequence represents a fragment of a fibroblast growth factor-like (FGF-like) polypeptide. FGF-like protein and its associated nucleic acid play a role in modulating body growth, maturation or life-span. They are play a role in modulating by growth, maturation or life-span. They are consultable in the consultable in ameliorating disorders such as circhosis, inflammatory bowel disease, mucositis, Crohn's disease, circhosis, inflammatory bowel disease, mucositis, contexting astrointestinal abnormalities, neurodegenerative confiseases, damage to renal tubules as a result of acute tubular necrosis, haematopoietic cell reconstitution following chemotherapy, wasting syndromes (e.g., cancer associated cachexia), damage to the corneal cyndromes (e.g., cancer associated cachexia), damage to the corneal cyndromes (e.g., cancer associated cachexia), damage to the corneal cyndromes (e.g., cancer associated cachexia), damage to the corneal cyndromes, multiple sofelerosis, myopathies, short staturation, alopecia, abnormalities of androgen target organs, premature maturation, alopecia, abnormalities of androgen target organs, conchopulmonary dysplasia, acute respiratory distress syndrome, tumours of the eye or other tissues, arberosclerosis, hypercholesterolemia, stroke, osteoporosis, osteoarbritis, muscle atrophy, sarcopenia, cardiac function, immune system dysfunction, cancer, Parkinson's disease,

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The present sequence is human fibroblast growth factor (FGF) homologue, zFGF11 protein. zFGF11 gene is located on chromosome 19. zFGF11 is useful for stimulating proliferation of mesenchymal cells, osteoblastic lineage cells. zFGF11 is useful for identifying chromosomal disorders associated with abnormal expression of zFGF11 protein. zFGF11 is also useful for stimulation, inhibition or proliferation of myocytes, smooth muscle cells, adjocytes, chondrocytes, neural tube-derived stem cells, neural crest stem cells and neuronal progenitors, pancreatic cells, prostatederived cells and endothelial cells and inhibiting chondrosarcomas,
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                                                                                                                                                                                                                                                                                                                                 Human, fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis; proliferation; mesenchymal cell; osteoblastic lineage cell; osteoporosis; chromosomal disorder; chondrosarcoma; atherosclerosis; obesity; fracture; bone formation; diabetes mellitus; neural cell development; angiogenesis; amyotrophic lateral sclerosis; cerebrovascular stroke; neuropathy; ulcer; congenital disorder; wound healing; cardiac function; glomerulonephritis; surfactant production; anorectic; ischaemia; neogenesis; hyperplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth factor family, for stimulating proliferation of mesenchymal, osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,
 senile dementia, Alzheimer's disease, and decreased cognitive function
                                                                                     Gape
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                                                          Length 181;
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/label= Human_mature_zFGF11_protein
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                                                            DB 4;
8e-05;
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                                                                                     Mismatches
                                                          Score 89;
Pred. No. 8
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/label= Signal_peptide
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                                                                                                                                                                                                                     AAE05078 standard; protein; 208 AA.
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                                                            100.0%;
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                                                                                                                                                                                                                                                                               (first entry)
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                                                                        Local Similarity 100.
nes 15; Conservative
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                                  Sequence 181 AA;
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tresults in bone formation useful for treating bone defects, fractures, cesults in bone formation useful for treating bone defects, fractures, oteoporosis and other deficiencies in bone structure and formation.

ZEGETI is useful for treating disorders associated with diabetes mellitus, neural cell development or degeneration, amyotrophic lateral escherosis, certebrovascular stroke, neuropathy associated with lack of maintenance of neuronal differentiation and congenital disorders of the maintenance of neuronal differentiation and congenital disorders of the neurous system or lack of neuronal development, promoting angiogenesis and wound healing, for revascularisation in eye, complications related to poor circulation such as diabetic food ulcers, improving cardiac poor circularly in the heart or brain and for inducing skeletal ceremins, particularly in the heart or brain and for inducing skeletal muscle neogenesis and/or hyperplasia, kidney regeneration and/or for treating of systemic and pulmonary hypertension. Antagonists of zFGFII are useful for inhibiting disorders associated with kidney epithelium
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2001WO-US006666
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2000US-0220664P.
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                                                                                                                                                                                                                                                                                            such as glomerulonephritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                  Sequence 208 AA;
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24-AUG-2000;
10-NOV-2000;
28-NOV-2000;
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US2002081663-A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, sepecially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human blood, fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AU83592-AAU83713 represent human PRO protein sequences of the invention
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/note= "Mature fibroblast growth factor homologue,
zFGF11. This sequence is specifically claimed in claim 4"
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                                                                                                                                                                                                                                           One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumors such as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
                                                                                                                                                                                                                                                                                                                                                                                The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polypucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder.
                                                                                                                               Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/label=_Signal_sequence
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            10-MAY-2001; 2001US-00854208
10-MAY-2001; 2001US-00854280
25-MAY-2001; 2001WO-US017092
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22-MAR-2001; 2001US-00816744
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Matches 15; Conservative
                                                                                                                                   Desnoyers L,
C, Gurney AL,
                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                          WPI; 2002-172001/22.
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                                                                                                                                                      Grimaldi JC,
                                                                                                                                   Baker KP,
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Human; extracellular messenger; neurological disorder; epilepsy; XWES-3; Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke; acquired immune deficience; AlDS; Addison's disease; cytostatic; developmental disorder; anaemia; Cushing's syndrome; endocrine disorder; vascular malformation; cell proliferative disorder; gene therapy; cancer; hypertycictive; trauma; hypopicultarism; hypothycidism; antibelminthic; hypertycidism; gonadal steroid hormone; panoreatic disorder; nootropic; diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial; antiviral; antifungal; parasitic; protozoal; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated human polypeptide (1) for zFGF11 (a fibroblast growth factor), and the encoding polynucleotide (II). (I) and (II) are used in methods of the invention stimulating proliferation of mesenchymal cells, detecting the presence of zFGF11 in a biological sample, detecting the presence of FGFRII in a biological stimulating proliferation of scheoblastic lineage cells. The polypeptides, nucleic acid and/or antibodies of the invention may be used in treatment of disorders associated with diabetes mellius, neural cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         development or degeneration, amyotrophic lateral sclerosis, cerebrovascular stroke, neuropathy associated with lack of maintenance of neuronal differentiation, and congenital disorders of the nervous system or lack of neuronal development. Molecules of the invention may also be useful for improving cardiac function and for promoting wound healing of the epidermis. The present sequence represents the amino acid sequence of
                                                                                                                                                                                                                                                                                      Isolated polypeptide for zFGF11 (fibroblast growth factor) useful in treatment of disorders associated with diabetes mellitus, neural cell development or degeneration, amyotrophic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 9.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human extracellular messenger (XMES)-3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 1; 35pp; English.
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                                                                      05-JAN-2001; 2001US-00755695.
                                                                                                           05-JAN-2000; 2000US-0174526P.
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                                                                                                                                                                                                                                                                                                                                                       cerebrovascular stroke.
                                                                                                                                           (CONK/) CONKLIN D C. (CHEN/) CHEN Z.
                                                                                                                                                                                                      Chen Z;
                                                                                                                                                                                                                                         WPI; 2002-626540/67.
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Best Local Similarity
                                                                                                                                                                                                                                                           N-PSDB; ABK91310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 208 AA;
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                                                                                                                                                                                                    Conklin DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human zFGF11
                                     27-JUN-2002.
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WO200194587-A2

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The present invention relates to new extracellular messenger polypeptides and polynuclectides encoding them. XMES is useful in the diagnosis, treatment and prevention of neurological disorders (e.g. epilepsy, stroke, or Alzheimer's disease), autoimmune/inflammatory disorders (e.g. educined immune deficiency syndrome, AIDS, Addison's disease, or allergies), developmental disorders (e.g. renal tubular acidosis, anaemia allergies), asyndrome), endocrine disorders (e.g. hypophysectomy, aneurysm or vascular malformation), and cell proliferative disorders (e.g. cancer), and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of extracellular messengers. XMES may also be used in the treatment of viral, bacterial, fungal, parasitic, protozoal and helminthic, hypothyroidism, hyperthyroidism or gonadal steroid hormones, and panacreatic disorders such as type II diabetes mellitus. The XMES may be used for somatic or germline gene therapy. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
                                                                                                                                                                          Nguyen DB, Walia N, Gandhi AR, Azimzai Y; Iu Y, Baughn MR, Duggan BM, Lee S, Hafalia A;
                                                                                                                                                                                                                                                                                             New extracellular messenger polypeptides and polynucleotides encoding them, useful for diagnosing, treating or preventing e.g. neurological, autoimmune, inflammatory, developmental and endocrine disorders.
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                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 111; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is human XMES-3 protein
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                                                                           06-JUN-2000; 2000US-0210233P.
23-JUN-2000; 2000US-0213465P.
14-NOV-2000; 2000US-0249019P.
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                                             36-JUN-2001; 2001WO-US018476
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                                                                                                                                                  (INCY-) INCYTE GENOMICS INC
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Best Local Similarity 100.v
                                                                                                                                                                                  Yue H, He A,
O, Tang YT,
                                                                                                                                                                                                                                                     WPI; 2002-154573/20.
                                                                                                                                                                                                                                                                      N-PSDB; AAD28493.
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                                                                                                                                                                                                                     Policky JL;
               13-DEC-2001
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the diagnosts and treatment of tumours. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABU80739-ABU80860 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted and transmembrane protein; PRO; cytostatic; antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; pericyte stimulator; fibroblast modulator; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour; oclon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; bone disorder; cartilage disorder; sports injury;
                                                                                                        Godowski PJ;
                                                                                                                                                                                                                  One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                    Gerritsen ME, Goddard A, Godowski P
Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 89; DB 6; I
100.0%; Pred. No. 9.2e-05;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                  Claim 11; Fig 78; 314pp; English
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-AUG-2002; 2002US-00218631
          25-JUL-2000; 2000US-0220638P.
01-JUN-2001; 2001MO-US017800.
29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Conservative
                                                                                                                         Desnoyers L,
                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                          WPI; 2003-342045/32.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 208 AA;
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                                                                                                                          Baker KP, De
Grimaldi JC,
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01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

25-JUL-2000; 01-JUN-2001;

(GETH) GENENTECH INC.

12-AUG-2002; 2002US-00219003

US2003088063-A1

08-MAY-2003

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI;

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The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide are useful sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polymucleotides are useful as pharmaceuticals, diagnostice, biosensors or bioreactors. These are particularly useful for detecting tumour, colon tumour, breast tumour, prostate tumour, ectal lumour, or liver tumour, in a mammal, for stimulating the release of TNP-alpha from human blood, or of stimulating proliferation or differentiation of chondrocyte cells, for stimulating proliferation or differentiation of chondrocyte cells, for stimulating proliferation of pericyte cells, or for modulating normal human dermal fibroblast proliferation. The PRO nucleic acid or polypeptide is also useful for treating tumours or various bone and/or cartilage disorders (e.g. sports injuries or arthritis), or wounds. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic actenination of the presence of those diseases. The PRO polypeptides are useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective served and or also be used and acid sequence of a novel human secreted and transmembrane PRO polypeptide sequence of a novel human secreted and
                                                                                                                                                                                                             New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or
                                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig 78; 314pp; English.
                                                      Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
(GETH ) GENENTECH INC
                                                                                                                                     WPI; 2003-512315/48.
                                                                                                                                                                                                                                                                                                       wounds in a mammal.
                                                                                                                                                                 N-PSDB; ACD68631.
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100.0%; Score 89; DB 6; Length 208; 100.0%; Pred. No. 9.2e-05; Live 0; Mismatches 0; Indels 1 HLPGNKSPHRDPAPR 15 15; Conservative Sest Local Similarity Sequence 208 AA;

셤 ABU82086 standard; protein; 208 AA ABU82086;

25-JUN-2003 (first entry)

Novel human secreted and transmembrane protein PRO10196.

Human; secreted and transmembrane protein; PRO; cardiant; cytostatic; antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; arterial restenosis; rheumatoid arthritis; angina; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping RESULT 10
ABUB2086
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Ното варіепв

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and attagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, agerelated macular degeneration, atherosclerosis, hypertension, arterial restenoisis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
                                                                                                                                                                                                                                    Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                              One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Fig 78; 314pp; English
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                          Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
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N-PSDB; ACA68535.
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144 HLPGNKSPHRDPAPR 158 셤

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Gaps

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RESULT 11

ABP96156 standard; protein; 208 AA. ABP96156; ABP96156

12-MAY-2003 (first entry)

Human fibroblast growth factor 21 protein SEQ ID NO:2.

Human, fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter; diabetes; obesity; antidiabetic; anoxectic; type 2 diabetes; type 1 diabetes.

Homo sapiens.

WO2003011213-A2.

13-FEB-2003.

22-JUL-2002; 2002WO-US021290.

30-JUL-2001; 2001US-0308702P. 10-JAN-2002; 2002US-0347991P.

us-10-060-765-8.rag

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ABJ72266 standard; protein; 208 AA.
                                                                        Claim 3; Fig 1; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001; 2001MO-US017800.
29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                          144 HLPGNKSPHRDPAPR 158
                                                                                                                                                                                                                                  1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                 Human PRO10196 protein.
     (ELIL ) LILLY & CO ELI
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                                                                                                                                                                                                                Local Similarity
                              WPI; 2003-248106/24
                                    N-PSDB; ABZ79797
                                                                                                                                                                                              Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                             US2003050448-A1
                  Glasebrook AL,
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Matches
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The invention relates to a novel isolated nucleic acid encoding a fully defined PRO polypeptide. The molecules of the invention may be useful for stimulating proliferation or gene expression in periorte cells or the release of TNF-alpha from human blood. Other possible uses include the atimulation or inhibition of chondrocyte proliferation or inhibition of chondrocyte proliferation or proliferation of mammal adexmal fibroblast cell proliferation and the detection of the presence of a tumour within a mammal. Purthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or for measuring or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO protein of the invention
                                      New nucleic acid encoding for a PRO protein, useful for the manufacture of a medicament for diagnosing or treating tumors or for measuring or detecting expression of an associated gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rno; μισοα; proliferation; pericyte cell; TNF alpha; chondrocyte; tumour necrosis factor; proliferation; differentiation; gene therapy; dermal fibroblast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen ME, Goddard A, Godowski
Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 100.0%; Score 89; DB 6; Length 208; Local Similarity 100.0%; Pred. No. 9.2e-05; les 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ72394 standard; protein; 208 AA.
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                                                                                                                                               Claim 11; Fig 78; 315pp; English
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO10196 protein
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N-PSDB; ABT44264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 208 AA;
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ID ABJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                  The present sequence represents human fibroblast growth factor 21 (FGF-21). FGF-21 is located to chromosome 19, more specifically to 19q13.1-cathology present invention describes a method for treating a mammal exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal for obesity which comprises administering to the mammal a composition comprising FGF-21 which has at least 95% amino acid sequence identity to the 200 amino acid sequence given in ABP96156. Also described: (1) inducing an increase in glucose uptake in adipocyte cells by administering FGF-21 to induce an increase in glucose uptake in adipocyte cells by administering a medicament for treating type 1 diabetes, type 2 diabetes or obesity in a mammal using FGF-21 having 95% amino acid sequence identity to ABP96156. FGF-21 has antidiabetic and anorectic activities. The method is useful for treating a mammal exhibiting type 2 or 1 diabetes or for treating a mammal exhibiting type 2 or 1 useful for treating a mammal for obesity. The method is preferably useful for treating type 1 or type 2 diabetes, and for treating domestic animals for obesity type 1 or type 2 diabetes, and for treating animals for obesity type 1 or type 2 diabetes, and for treating animals for obesity type 1 or type 2 diabetes, and for
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                                                                                                                                                                                             Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or obesity, by administering composition comprising fibroblast growth factor
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
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100.0%; Pred. No. 9.2e-05;
.ive 0; Mismatches 0; Indels
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                                                                          Hammond LJ,
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Gaps

tissue typing, Anti-PRO antibodies are useful in diagnostic assays for PRO and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence represents the amino acid sequence of a human secreted/transmembrane PRO polypeptide

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The invention relates to an isolated nucleic acid encoding a PRO polypeptide. Nucleic acids that encode PRO can be used to generate either transgenic animals or knock-out animals useful in developing and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy for replacing defective gene, in chromosome identification, as chromosome markers, or in generating probes to isolate full length PRO cDNA. The PRO Polypeptides are useful for chondrocyte stimulation, TNR-alpha stimulation, human dermal fibroblasts stimulation and for detecting the presence of tumour in an mammal. The PRO polypeptides are useful as molecular markers for protein electrophoresis and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in
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acid. The nucleic acid of the invention may be useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a tummour in a mammal. Furthermore, the molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells, the release of tummour necrosis factor (TNF) alpha from human blood, the proliferation or differentiation of fondrocyte cells and inhibiting the proliferation of normal human dermal fibroblast cells. Finally, the molecules may be utilised during gene therapy. The current sequence is that of the human PRO protein of the invention
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                       100.0%; Score 89; DB 6; Length 208; 100.0%; Pred. No. 9.2e-05;
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted/transmembrane polypeptide PRO 10196.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-2003 (first entry)
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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Grimaldi JC, Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              affinity purification
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                                                                                                                                                                                                      Sequence 208 AA;
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09-APR-2002;
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The present invention describes a method for the reduction of mortality and morbidity in critically ill patients, which involves the administration of fibroblast growth factor 21 (FGF-21) (1). (1) has cartificated or fibroblast growth factor 21 (FGF-21) (1). (1) has cartificated to an elementary, respiratory, antibacterial, immunosuppressive, vasotropic, haemostatic and nephrotropic activities, and can be used as a glucose level regulator, a glucose uptake stimulator, and an insulin can the reduction of morbidity and mortality in critically ill patients infering from systemic inflammatory response syndrome (SIRS), respiratory distress, acute lung injury, acute respiratory distress acute lung injury, acute respiratory distress acute lung injury, acute respiratory distress constituction syndrome, sepsis and chronic obstructive pulmonary disease (e.g. emphysema and chronic bronchies pancreatitis, ischaemia, multiple trauma and tissue injury, haemorrhagic shock, immune-mediated organ injury, shock and renal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or reduction of mortality and e.g. systemic inflammatory response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mortality; morbidity; fibroblast growth factor 21; FGF-21; antinflammatory; respiratory; antibacterial; immunosuppressive; vasotropic; haemostatic; nephrotropic; glucose level regulator; glucose uptake stimulator; insulin is septivity enhancer; respiratory systemic inflammatory response syndrome; respiratory distress; acute lung injury; acute respiratory distress syndrome; multiple organ dysfunction syndrome; sepais; chronic obstructive pulmonary disease; emphysema; chronic bronchitis; pancreatitis; ischaemia; multiple trauma; tissue injury; haemorrhagic shock; immune-mediated organ injury; shock; renal failure.
                                                                                                                                                                   Gaps
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                                                                                                                               Length 208;
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                                                                                                                               100.0%; Score 89; DB 6; I
100.0%; Pred. No. 9.2e-05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                ADA37038 standard; protein; 208 AA.
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                                                                                                                                                                      15; Conservative
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                                                                                                                                                   Best Local Similarity
                                                                                              Sequence 208 AA;
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                                                                                                                                   Query Match
                                                                                                                                                                      Matches
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This invention relates to one hundred and twenty two novel nucleic acids encoding human PRO membrane bound proteins or receptors. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are
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failure. FGF-12 regulates glucose levels in response to nutrient digestion; affects the overall metabolic state and counter-acts negative side effects that occur during the body's stress response to sepsis, reduces morbidity and mortality that occurs in critically ill patients; and stimulates glucose uptake and enhances insulin sensitivity. The present sequence represents the human FGF-21 amino acid sequence, which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
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                                                                                                                                                                                                               Gaps
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                                                                                                                                                                           Length 208;
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                                                                                                                                                                             100.0%; Score 89; DB 7; I 100.0%; Pred. No. 9.2e-05;
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Smith V, Stephan JF,
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
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                                                                                                                                                                                                                 15; Conservative
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Grimaldi JC, Gurney AL,
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                                                                                                                                                                                                 Similarity
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                                                                                                                                              Sequence 208 AA;
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09-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                               Query Match
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proteined and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human, secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF) -alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated PRO (secreted and transmembrane) polypeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in
                                                                                                                                                                                                                                                                                                                    Gaps
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Smith V, Stephan JF, Watanabe CK, Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                              Length 208;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                                100.0%; Score 89; DB 7; I 100.0%; Pred. No. 9.2e-05;
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB83568 standard; protein; 208 AA.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                           144 HLPGNKSPHRDPAPR 158
                                                                                                                                                                                                                                                                                                                                                         1 HLPGNKSPHRDPAPR 15
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                                                                                                                                                                                                                                                                                                                         Conservative
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N-PSDB; ADB83567.
                                                                                                                                                                                                                                                                                                     Local Similarity
ses 15; Conserv
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                                                                                                                                                                                                                                                  Sequence 208 AA;
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Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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perioque cells. PRO357, PRO259, PRO1172 or Pro4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO357, PRO357, PRO155, PRO1155, PRO11419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNRF)-
are useful for stimulating the release of tumour necrosis factor (TNRF)-
pro247, PRO337, PRO526, PRO363, PRO361, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, PRO1081, P
pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of Alfferentiation 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane PRO polypeptide
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Sequence 208 AA;

ö Gape ; 0 100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; ive 0; Mismatches 0; Indels 100.08; Query Match Best Local Similarity 100.0 Matches 15, Conservative

ADB80674 standard; protein; 208 AA ADB80674; RESULT 18 ADB80674

04-DEC-2003 (first entry)

Novel human secreted and transmembrane protein PRO10196.

Human, secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping; gene therapy.

Homo sapiens.

08-MAY-2003.

US2003088068-A1

13-AUG-2002; 2002US-00219481

01-JUN-2001; 2001WO-US017800

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The invention describes an isolated PRO (secreted and transmembrane)

CC Useful for stimulating the proliferation of or gene expression in periopte cells. PRO382, PRO1829. PRO1839 polypeptide are useful for stimulating the proliferation of conductocyte cells. PRO317, PRO229, PRO1820 or PRO4405 polypeptide are useful cor stimulating the proliferation of differentiation of chondrocyte cells. PRO317, PRO725, PRO1836, PRO1816, PRO1816, PRO1816, PRO1816, PRO1816, PRO1816, PRO1816, PRO1816, PRO1817, PRO1809, PRO317, PRO725, PRO18106, PRO1816, PRO1817, PRO1801, PRO1817, PRO1801, PRO1817, PRO1801, PRO1817, PRO1801, PRO1817, PRO1801, PRO1817, PRO1801, PRO1817, PRO1801, PRO1817, PRO1801, PRO1817, PRO1801, PRO1817, PRO1801, PRO1817, PRO1801, PRO1817, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, 
                                                                                                                                                                                                                                                     One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                      Wood WI;
                                                                                                               Goddard A, Godowski PJ;
phan JF, Watanabe CK, W
                                                                                                               Gerritsen ME, Goddard Smith V, Stephan JF,
                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 78; 305pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane PRO polypeptide.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                  Desnoyers L,
                                                                     (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                N-PSDB; ADB80673
                                                                                                                                             Grimaldi JC,
                                                                                                                  Baker KP,
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Gaps 0 100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; 0; Indels 0; Mismatches 144 HLPGNKSPHRDPAPR 158 1 HLPGNKSPHRDPAPR 15 Query Match 100. Best Local Similarity 100. Matches 15; Conservative g ð

ADB73215 standard; protein; 208 AA. ADB73215; RESULT 19 ADB73215 田城站城市城田

Novel human secreted and transmembrane protein PRO10196. 04-DEC-2003 (first entry)

Sequence 208 AA

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22-MAY-2003
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human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiatrhritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNP)-alpha release; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; oclon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                         release;
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Homo sapiens.

US2003096968-A1

29-AUG-2002; 2002US-00232223

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Desnoyers L, 2, Gurney AL, Grimaldi JC, Baker KP,

WPI; 2003-765525/72. N-PSDB; ADB73214.

New isolated PRO polypeptides useful as molecular weight markers in protein electrophoresis, useful for tissue typing, and for treating arthritis and tumors.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

Cypyptide (I) PRO982, PRO1160, PRO1197 or PRO1329 polypeptide are

useful for stimulating the proliferation of or gene expression in

periove cells. PRO357, PRO212, PRO1272 or PRO4405 polypeptide are useful

Cor stimulating the proliferation of differentiation of chondrocyte

cells. PRO357, PRO502, PRO3130, PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TMF)
alpha from human blood. PRO982, PRO317, PRO175, PRO1306, PRO1419,

PRO147, PRO337, PRO5125, PRO1195, PRO1197, PRO1197, PRO1191,

PRO124, PRO1337, PRO5126, PRO1195, PRO1197, PRO1197, PRO1191,

PRO125, PRO1181, PRO1367, PRO1186, PRO1187, PRO1197, PRO1197,

PRO1286, PRO1391, PRO1386, PRO1186, PRO1197, PRO1197, PRO1197,

PRO1286, PRO1392, PRO9183 or PRO11005 pRO149Pptide are useful for

ERO1286, PRO51928, PRO4341, PRO1801, PRO1197, PRO1197, PRO1197,

PRO1341, PRO529, PRO9186, PRO1186, PRO1197, PRO1197, PRO1197,

PRO1341, PRO529, PRO9186, PRO1186, PRO1197, PRO1197, PRO1197,

PRO1341, PRO529, PRO9186, PRO1186, PRO1197, PRO1197, PRO1197,

PRO1341, PRO529, PRO9186, PRO1194, PRO1273, PRO1486, PRO432, PRO432,

CR PRO5181, PRO529, PRO9186, PRO1186, PRO1197, PRO1197, PRO1186,

PRO5184, PRO529, PRO9186, PRO1186, PRO1197, PRO1186, PRO432,

CR PRO5184, PRO529, PRO9186, PRO1186, PRO1197, PRO1187, PRO4408,

PRO5184, PRO529, PRO9186, PRO1186, PRO1197, PRO1186, PRO4408,

PRO5184, PRO529, PRO9186, PRO1186, PRO1197, PRO1187, PRO4408,

PRO5184, PRO529, PRO9186, PRO1186, PRO5178, PRO5778, PRO4408,

PRO5184, PRO529, PRO9186, PRO1186, PRO5778, PRO5778, PRO5778,

PRO5184, PRO529, PRO5084, PRO5084, PRO5778, PRO5778, PRO5778,

PRO5184, PRO5184, PRO5084, PRO5084, PRO5778, PRO5778, PRO5778,

PRO5184, PRO5184, PRO5084, PRO5084, PRO5778, PRO5778, PRO5778,

PRO5184, PRO5184, PRO5084, PRO5778, P ransmembrane PRO polypeptide

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The Intellation describes an insulated FRO Secreted and Limination describes and transfer are periods (1). PROS92, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in periody-e cells. PRO357, PRO229, PRO125 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO351, PRO357, PRO155, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrossis factor (TNE)- alpha from human blood. PRO982, PRO155, PRO155, PRO1419, PRO1419, PRO247, PRO37, PRO566, PRO180, PRO180, PRO140, PRO1006, PRO1144, PRO1104, PRO1106, PRO1195, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1197, PRO1993, PRO9940, PRO9984, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, PRO1993, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; perioyte cell proliferation; chondrocyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necroais factor alpha release; (TNR)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated PRO polypeptide useful for tissue typing, gene therapy, amplecular weight markers in protein electrophoresis, and for treating arthritis and tumors.
                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an isolated PRO (secreted and transmembrane)
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Smith V, Stephan JF, Watanabe CK, W
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  Length 208;
                                                       Indels
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100.0%; Score 89; DB 7; 1
100.0%; Pred. No. 9.2e-05;
                                                          Mismatches
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     100.0%; F.
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                                                                                                                                                                                                                                                                                                     ADB78297 standard; protein; 208
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                  144 HLPGNKSPHRDPAPR 158
                                                                                                              1 HLPGNKSPHRDPAPR 15
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                          Best Local Similarity 100.
Matches 15; Conservative
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N-PSDB; ADB78296.
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Grimaldi JC,
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  Query Match
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PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO604, PRO4981, PRO7774, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for careaing transgenic animals or knock-out animals which are useful cor treating transgenic animals or knock-out animals which are useful secentic injuries). This is the amino acid sequence of a human secreted and
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Sequence 208 AA;

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Gaps
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0
100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; Live 0; Mismatches 0; Indel8
                                                                                          144 HLPGNKSPHRDPAPR 158
                                                                  1 HLPGNKSPHRDPAPR 15
                                   15; Conservative
                  Local Similarity
   Query Match
                                   Matches
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RESULT 21 ADB84945

ADB84945 standard; protein; 208 AA. 04-DEC-2003 (first entry) Human PRO polypeptide #39. ADB84945;

Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.

ното варіепв.

US2003073817-A1.

17-APR-2003.

26-AUG-2002; 2002US-00227883.

01-AUG-2000; 2000US-0222425P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Goddard A, Godowski PJ; sphan JF, Watanabe CK, Wood WI; Gerritsen ME, Goddard Smith V, Stephan JF, Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

2003-730024/69 N-PSDB; ADB84944

New PRO polypeptides and nucleic acids encoding the polypeptides, useful e.g. in gene therapy, disease diagnosis, chromosome identification and tissue typing.

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Claim 11; Fig 78; 314pp; English
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Godowski PJ;

Goddard A,

Gerritsen ME,

Desnoyers L,

Baker KP,

(GETH) GENENTECH INC.

transmembrane polypeptides) and the PRO polymucleotides encoding them.
The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, protat tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TRP) alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene chondrocyte cells, for stimulating the proliferation of or gene choraction in pericyte cells or for stimulating the proliferation of or gene confaront planch of the proliferation of the series of the proliferation of the companies of the companies of the proliferation of the companies of the proliferation of the proliferation of the proliferation of the proliferation of the proliferation of the proliferation of the proliferation of the proposition of the proliferation as chromosome condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartiage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartiage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention. ô Human; secreted and transmembrane protein, PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping; Gaps ; 0 The invention relates to human PRO polypeptides (secreted and Length 208; 0; Indels Novel human secreted and transmembrane protein PRO10196. 100.0%; Score 89; DB 7; I 100.0%; Pred. No. 9.2e-05; 0; Mismatches ADB78051 standard; protein; 208 AA 25-JUL-2000; 2000US-0220607P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480. 09-AUG-2002; 2002US-00216165. 144 HLPGNKSPHRDPAPR 158 1 HLPGNKSPHRDPAPR 15 (first entry) Conservative Local Similarity Los 15; Conserv Sequence 208 AA; US2003092886-A1. Homo sapiens gene therapy 04-DEC-2003 L5-MAY-2003. ADB78051; Query Match Matches RESULT 22 ADB78051 PART OF THE PART O ¥88888888888888888888888888888888 à g

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The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

CC useful for stimulating the proliferation of or gene expression in

Dericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are

CC cells. PRO31, PRO357, PRO229, PRO1275 PRO4405 polypeptide are useful

for stimulating the proliferation or differentiation of chondrocyte

CC cells. PRO31, PRO357, PRO325, PRO1155, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNF)-

alpha from human blood. PRO982, PRO337, PRO125, PRO1306, PRO1419, PRO1419,

CC PRO1025, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1130,

CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1274, PRO1412,

CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1444, PRO1274, PRO1306,

CC PRO1286, PRO1337, PRO330, PRO1331, PRO1431, PRO1331,

CC PRO1887, PRO337, PRO330, PRO1301, PRO1431, PRO1316,

CC PRO1887, PRO1328, PRO4341, PRO1801, PRO1431, PRO1324,

CC PRO1887, PRO5239, PRO4341, PRO1801, PRO4331, PRO1327,

CC PRO1887, PRO5239, PRO7184, PRO1873, PRO1484, PRO4322,

CC PRO1887, PRO5239, PRO7184, or PRO1404, PRO5738, PRO4408,

CC PRO1881, PRO5229, PRO7184, or PRO1425 POlypeptide are useful for detecting the presence of tumour in a mammal which

CC Inhibiting the proliferation of normal human dermal fibroblast cells. PRO

CC Inhibiting the proliferation of normal human dermal fibroblast cells.

CC PRO5723, PRO5725, PRO7184, or PRO4981, PRO1374, PRO5773, PRO4408,

CC Inhibiting the proliferation of normal human dermal fibroblast

CC Inhibiting the proliferation of normal human dermal fibroblast

CC Inhibiting the proliferation of normal human dermal fibroblast

CC Inhibiting the proliferation of normal human dermal fibroblast

CC Inhibiting the proliferation of normal human dermal fibroblast

CC Inhibiting the proliferation of normal human dermal fibroblast

CC Inhibiting the proliferation of normal human dermal fibroblast

CC Inhibiting the proliferation of normal 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO259, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
                                                                                                                         Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers in protein electrophoresis, for treating
  Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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  Watanabe CK,
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  Stephan JF,
Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB87117 standard; protein; 208 AA.
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Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
                                                  2003-765494/72
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Matches 15; Conserv
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                                                                         N-PSDB; ADB78050
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ADB87117
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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polypeptides encoding them.

The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, colon tumour, breast tumour, colon tumour, breast tumour, colon tumour or liver tumour) in a mammal, for stimulating the proliferation or differentiation of condrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells or for stimulating the proliferation of condrocyte cells, for stimulating the proliferation of condrocyte cells, for stimulating the proliferation of condrocyte cells, for stimulating the proliferation of condrocyte cells, for stimulating the proliferation of condrocyte cells, for stimulating the proliferation of condrocyte in percenting transpendence and gene mapping, in generating transpendence and gene mapping, in generating transpendence and gene mapping, in generating probes. The PRO polypeptides by recombinant condrocytes, and in generating probes. The PRO polypeptides, or anti-PRO markers and in generating probes. The PRO polypeptides or anti-PRO antibodies, are useful for preparing a medicament for treating and condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving and euseful as condition which is responsive electrophoresis, and in tissue typing. This condition and propertides or anti-PRO antibodies, are protein electrophoresis, and in tissue typing. This condition where the proposition electrophoresis, and in tissue typing. This condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                            Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB84699 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Fig 78; 314pp; English.
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                                                                                                                                                                                         01-JUN-2001; 2001MO-US017800.
29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                   13-AUG-2002; 2002US-00219479
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Best Local Similarity luv...
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                                                                                                                                                                                                                                                                                                                            Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-657981/62.
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                                                               US2003088067-A1.
                      Homo sapiens.
                                                                                                          08-MAY-2003
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Claim 11; Fig 78; 308pp; English.
                                                                      24-FEB-2000; 2000WO-US005004.

02-WAR-2000; 2000WO-US00541.

01-JUN-2001; 2001WO-US017800.

29-JUN-2001; 2001WO-US017860.

09-APR-2002; 2002US-00119480.
                                                         14-AUG-2002; 2002US-00219536.
                                                                   99US-0146222P
                                                                                                               Desnoyers L,
C, Gurney AL,
                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                              2003-777259/73.
                                                                                                                                   N-PSDB; ADB84698.
                                      US2003092890-A1.
                                                                                                              Baker KP, Der
Grimaldi JC,
                            Homo sapiens
                                                                   28-JUL-1999;
                                                15-MAY-2003
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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polypeotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumnours (e.g. lung tumnour, colon tumnour, breast tumnour, classificate tumnour, rectal tumnour or liver tumnour) in a mammal, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene chondrocyte cells, for stimulating the proliferation of corgene expression in pericyte cells or for stimulating the proliferation of corgene expression in pericyte cells or for stimulating the proliferation of corganization probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides or anti-PRO condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumnours and bone and/or cartilage condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumnours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.

Sequence 208 AA;

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Gaps
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0
100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; ive 0; Mismatches 0; Indels
  100.0%; +-
                           15; Conservative
             Local Similarity
  Query Match
                           Matches
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RESULT 25 ADB83814

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; New isolated PRO polypeptides, useful for tissue typing, gene therapy, molecular weight markers in protein electrophoresis, and for treating arthritis and tumors. Human, PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;

Novel human secreted and transmembrane protein PRO10196

(first entry)

04-DEC-2003

ADB83814 standard; protein; 208 AA

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL, (GETH) GENENTECH INC.

WPI; 2003-657584/62.

25-JUL-2000; 2000US-0220607P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

as

09-AUG-2002; 2002US-00216159.

US2003069397-A1 Homo sapiens. gene therapy

10-APR-2003.

New isolated polypeptides designated PRO polypeptides including polypeptides useful for stimulating the proliferation or differentiation of specific cell types, and for diagnosing cancer. N-PSDB; ADB83813.

Claim 11; Fig 78; 314pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

Co polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

Co useful for stimulating the proliferation of or gene expression in

Co pericyte cells. PRO357, PRO229, PRO1127 or PRO4405 polypeptide are useful

Co for stimulating the proliferation or differentiation of chondrocyte

Co for stimulating the proliferation or differentiation of chondrocyte

CC for stimulating the proliferation or differentiation of chondrocyte

CC for stimulating the proliferation or differentiation of chondrocyte

CC for stimulating the proliferation or differentiation of chondrocyte

CC stls. PRO313, PRO326, PRO363, PRO3157, PRO126, PRO1419, PRO1419, PRO1416,

CC PRO125, PRO1181, PRO326, PRO1065, PRO1192, PRO1244, PRO1411, PRO1412,

CC PRO1256, PRO1367, PRO1367, PRO1373, PRO1274, PRO1374, PRO1376,

CC PRO1286, PRO1376, PRO1405, PRO1405, PRO1474, PRO1377, PRO1376,

CC PRO1887, PRO1376, PRO4341, PRO1405, PRO1474, PRO1377, PRO1376, PRO1386,

CRO3404, PRO6105, PRO9836 or PRO10096 polypeptide are useful for

Stimulating the proliferation of normal human dermal fibroblasts cells.

CR STIMULATING the proliferation of normal human dermal fibroblasts

CC STIMULATION THE proliferation of normal human dermal fibroblast cells. PRO

CC Inhibiting the proliferation of normal human dermal fibroblast cells. PRO

CC Inhibiting the proliferation of normal human dermal fibroblast cells. PRO

CC Inhibiting the proliferation of normal human dermal fibroblast cells. PRO

CC Inhibiting the proliferation of formal human dermal fibroblast cells. PRO

CC Oplypeptides such as PRO6004, PRO491, PRO7174, PRO5778, PRO4332, etc.,

are useful for detecting the presence of tumour in a mammal which

CC Involves comparing the level of expression of the above PRO polypeptides

CC Involves Comparing the level of expression of the prosence of tumour, not the mammal. The tumour of the prosence of tumour, prosente tumour, rectal tumour or liver liver tumour. (I) is useful as molecular weight

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typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                  human, secreted and transmembrane protein; PRO; cytostatic; vulnezary; antiathritic; perioyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated PRO polypeptide useful for tissue typing, gene therapy, molecular weight markers, for treating arthritis, tumor.
                                                                                                                                                          Gaps
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                                                                                                                              Score 89; DB 7; Length 208; Pred. No. 9.2e-05; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                            Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                              ADB72969 standard; protein; 208 AA.
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                                                                                                                                 100.0%;
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09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                             144 HLPGNKSPHRDPAPR 158
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                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desnoyers L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-777258/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-777258,
N-PSDB; ADB72968
                                                                                                        Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003092887-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baker KP, Der
Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy
                                                                                                                                                                                                                                                                                                                                   04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L5-MAY-2003
                                                                                                                                                                                                                                                                                                         ADB72969;
                                                                                                                                                                                                                                                       RESULT 26
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PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1212, PRO11286, PRO1330, PRO1347, PRO1367, PRO1367, PRO1367, PRO1367, PRO1367, PRO1367, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO1378, PRO4321, PRO1378, PRO4323, PRO529, PRO4381, PRO1379, PRO1379, PRO1378, PRO1372, PRO1378, PRO1372, PRO1378, PRO1372, PRO1378, PRO1372, PRO1378, PRO1372, PRO1373, PRO5725, PRO1144, Or PRO1372, PRO1372, PRO1373, PRO5725, PRO1374, Or PRO1372, PRO1374, PRO1374, PRO1372, PRO4382, PRO4382, PRO1374, OR PRO1373, PRO5725, PRO1374, OR PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, PRO1374, 
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane PRO polypeptide.
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 HLPGNKSPHRDPAPR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2002; 2002US-00219464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HLPGNKSPHRDPAPR 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
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C, Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-657979/62.
N-PSDB; ADC36806.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003088065-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC36807;
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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them.

Cransmembrane polypeptides) and the PRO polymucleotides encoding them.

Cransmembrane polypeptides and polymucleotides are useful as pharmaccuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours fe.g. lung tumour, colon tumour, breast tumour, colon tumour or liver tumour) in a mammal, for stimulating the proliferation or differentiation of condrocyte cells, for stimulating the proliferation of or gene chordrocyte cells, for stimulating the proliferation of or gene captression in pericyte cells or for stimulating the proliferation of condrocyte cells, for stimulating the proliferation of or gene captression in pericyte cells or for stimulating the proliferation of condrising the proliferation of the proliferation of condrising transpension and gene mapping, in generating transpension and gene mapping, in generating transpension and gene mapping, in generating probes. The PRO polypeptides by recombinant reagents, in gene therapy, in chromosome identification, as chromosome condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage condition which is responsive to the PRO polypeptides or anti-PRO disorders (e.g. arthritis, sports injuries), involving inducing the redisorders (e.g. arthritis, sports injuries), involving inducing the redisorders (e.g. arthritis, sports injuries), involving inducing the redisorders (e.g. arthritis, sports injuries), involving inducing the redisorders (e.g. arthritis, sports injuries), involving inducing the redisorders (e.g. arthritis, sports injuries), involving inducing the redisorders (e.g. arthritis, sports injuries), and in tissue typing. This condition and the properties of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, or for preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC21797 standard; protein; 208 AA.
                                                                                            Claim 11; Fig 78; 315pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000005-0209832P.
200005-0212901P.
200005-0213807P.
200005-0219556P.
200005-02205085P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 208 AA;
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20-JUL-2000;
25-JUL-2000;
25-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2003
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Gaps

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polymucleotides encoding them.

The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours rectal tumour colon tumour, breast tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF) alpha from human blood, for stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the proliferation of or gene chondrocyte cells, for stimulating the proliferation of chondrocyte cells, for stimulating the proliferation of chordrocyte cells, for stimulating the proliferation of chordrocyte cells, for stimulating the proliferation of chordrocyte cells, in chromosome and gene mapping, in generating transpanic animals which technology, in generating transpanic animals or knock-out animals which reagents, in gene therapy, in chromosome independent or antimals which reagents, in gene therapy, in chromosome independent for treating a condition which is responsive to the PRO polypeptides, or anti-PRO antibodies, such as perioyre-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injures), involving inducing the recombination of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated PRO polypeptide useful for tissue typing, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard A, Godowski PJ;
phan JF, Watanabe CK, W
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Pred. No. 9.2e-05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           Gerritsen ME, Goddard
Smith V, Stephan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Fig 78; 308pp; English.
                                                                     2000US-0220666P.
2000US-0220893P.
2000US-0222425P.
                                                                                                                                                                2000WO-US023328.
                                                                                                                                                                                    2000WO-US030873
                                                                                                                                                                                                       2000US-0253646P
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                                                                                                                                                                                                                                                                                               2001WO-US017092
                                                                                                                                                                                                                                                                                                                2001WO-US017800
                                                                                                                                                                                                                                                                                                                                                       2002US-00119480
                                                                                                                                                                                                                                                                                                                                                                                                                              Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                          (GETH.) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-765526/72.
N-PSDB; ADC21796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 208 AA;
                                                                     25-JUL-2000; 26-JUL-2000; 201-AUG-2000; 2
                                                                                                                                                                                                                                                                                                                                                         09-APR-2002;
                                                                                                                            22-AUG-2000;
23-AUG-2000;
                                                                                                                                                                24-AUG-2000;
10-NOV-2000;
                                                                                                                                                                                                       28-NOV-2000;
                                                                                                                                                                                                                       01-DEC-2000;
                                                                                                                                                                                                                                          20-DEC-2000;
                                                                                                                                                                                                                                                            20-DEC-2000;
                                                                                                                                                                                                                                                                             28-FEB-2001;
                                                                                                                                                                                                                                                                                                25-MAY-2001;
                                                                                                                                                                                                                                                                                                                    01-JUN-2001;
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. 0

Gaps

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Indels

, 0

Local Similarity 100.

Matches

8

Query Match

1 HLPGNKSPHRDPAPR 15

144 HLPGNKSPHRDPAPR

100.08; 100.0%; ADC49828 standard; protein; 208 AA.

RESULT 29 ADC49828 ID ADC498

(first entry)

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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

cuseful for stimulating the proliferation of or gene expression in

pericyte cells. PRO357, PRO225, PRO1155, or PRO4405 polypeptide are useful

for stimulating the proliferation or differentiation of chondrocyte

cells. PRO231, PRO357, PRO353, PRO1155, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TRNP)

alpha from human blood. PRO982, PRO1155, PRO1306, PRO1419, PRO1411,

PRO247, PRO337, PRO526, PRO363, PRO537, PRO1305, PRO1419, PRO1411, PRO1160,

PRO1025, PRO1181, PRO126, PRO1186, PRO1192, PRO1274, PRO1411, PRO1309,

PRO1026, PRO130, PRO1347, PRO1305, PRO1927, PRO1274, PRO1309,

PRO10286, PRO1330, PRO1347, PRO1305, PRO1373, PRO1374, PRO1376, PRO1338,

PRO1987, PRO1987, PRO1387, PRO1305, PRO1373, PRO1374, PRO1360, PRO1367,

PRO1987, PRO1983, PRO4341, PRO1801, PRO4333, PRO3444, PRO4322,

PRO1987, PRO529, PRO7983, PRO1194, PRO1373, PRO3432, PRO3484, PRO5725, PRO1184, PRO1378, PRO1387, PRO1360, PRO4382,

PRO1987, PRO5725, PRO7184, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO1987, PRO5725, PRO778, or PRO778, PRO378, PRO4302, PRO4302, PRO5725, PRO1184, PRO5725, PRO1184, PRO5725, PRO1184, PRO5725, PRO1184, PRO5725, PRO1184, PRO5725, PRO1184, PRO5725, PRO1184, PRO5778, PRO3738, PRO4302, etc.,

are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides

c in a test sample of cells taken from the mammal, and a control sample of the PRO polypeptides in the test sample as compared to the control sample

c in indicative of the pase tender of tumour in the temmal. The tumour is lump. Functive rumour, reperal tumour, remember 1000 propriet rumour, remember 1000 propriet rumour, remember 1000 propriet rumour. Properate rumour is lump.
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                                                                                                                                                                human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; prostate tumour; rectal tumour; liver tumour; prostate tumour; horast tumour; prostate tumour; prostate tumour; second tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New secreted and transmembrane PRO polypeptide useful for preparing medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody, e.g. cancer.
                                                                                                                        Novel human secreted and transmembrane protein PRO10196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 78; 314pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUL-2000; 2000US-0220605P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
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N-PSDB; ADC49827.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                       gene therapy
                                                                        18-DEC-2003
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                        ADC49828;
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useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO127 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                              human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
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                                                                                                                                                                      Gaps
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Stephan JF, Watanabe CK, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;
                                                                                                                                     100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05;
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted and transmembrane protein PRO10196
                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen ME,
                                                                                                                                                                                                                                                                                                               ADC49027 standard; protein; 208 AA.
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                       1 HLPGNKSPHRDPAPR 15
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N-PSDB; ADC49026.
                                                                                                                                                       Best Local Similarity
                                                                                                           Sequence 208 AA;
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Grimaldi JC,
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                                                                                                                                         Query Match
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Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood WI;

Gerritsen ME, Goddard 1 Smith V, Stephan JF,

2002US-00119480

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polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the pro11feration or differentiation of chondrocyte cells. PRO331, PRO357, PRO725, PRO1155, PRO136 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO247, PRO337, PRO526, PRO3631, PRO683, PRO8400, PRO1080,

The invention describes an isolated PRO (secreted and transmembrane)

Wood WI;

Stephan JF, Watanabe CK,

Smith V,

Grimaldi JC, Gurney AL,

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FRO1925, PRO1181, PRO1126, PRO1105, FRO1921, PRO1214, PRO1214, PRO1126, PRO1126, PRO1131, PRO1126, PRO1136, PRO1136, PRO1136, PRO1330, PRO1330, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1340, PRO1341, PRO1360, PRO1341, PRO1360, PRO1343, PRO1371, PRO1360, PRO1321, PRO1361, PRO1341, PRO1361, PRO1321, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO4321, PRO4361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO1361, PRO
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PRO1411, PRO1309
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PRO809, PRO1071,
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PRO1005,
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Best Local Similarity 100.1
Matches 15; Conservative
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88699999999999999999998888
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ADC49544 standard; protein; 208 AA. 18-DEC-2003 (first entry) ADC49544; ADC49544

human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; Novel human secreted and transmembrane protein PRO10196.

antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell differentiation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; broast tumour; prostate tumour; rectal tumour; lung tumour; liver tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping; gene therapy

Homo sapiens

US2003088071-A1.

29-AUG-2002; 2002US-00232231 08-MAY-2003

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Godowski PJ; Goddard A, Gerritsen ME, Desnoyers L, Baker KP,

The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (1): PRO982, PRO1160, PRO1197 or PRO1329 polypeptide are useful for stimulating the proliferation of of one expression in periotyte cells. PRO397, PRO2129, PRO1292 or PRO4405 polypeptide are useful for stimulating the proliferation of differentiation of chondrocyte cells. PRO397, PRO352, PRO1155, PRO11306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TMF)- alpha from human blood. PRO992, PRO351, PRO1306, PRO1419, PRO214, PRO2147, PRO337, PRO352, PRO351, PRO1306, PRO1190, PRO1419, PRO1419, PRO1414, PRO1414, PRO1417, PRO1417, PRO1417, PRO1417, PRO1417, PRO1417, PRO1417, PRO1406, PRO1306, PRO1265, PRO1926, PRO1926, PRO1065, PRO1192, PRO1192, PRO1406, PRO1326, PRO1926, PR Human, secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; Gaps New PRO polypeptides and nucleic acids encoding the polypeptides, in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping. ; Length 208; Novel human secreted and transmembrane protein PRO10196. Claim 11; SEQ ID NO 78; 315pp; English. ADC47405 standard; protein; 208 AA. transmembrane PRO polypeptide. 144 HLPGNKSPHRDPAPR 158 15 (first entry) Local Similarity 100. 1 HLPGNKSPHRDPAPR 2003-801156/75. N-PSDB; ADC49543 Sequence 208 AA; 18-DEC-2003 ADC47405; Query Match Matches RESULT 32 ADC47405 ð g

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Claim 11; Fig 78; 314pp; English.
                                                                                                                                                                                                                                                                                                  transmembrane PRO polypeptide
                                                            01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                29-AUG-2002; 2002US-00232233.
                                                         25-JUL-2000; 2000US-0220605P.
                                                                                        Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                               (GETH ) GENENTECH INC.
                                                                                                     WPI; 2003-801157/75.
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                      Ното варіепв
              gene therapy
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RESULT 33
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polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
useful for stimulating the pro21sferation of or gene expression in
pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
for stimulating the pro11sferation or differentiation of chondrocyte
cells. PRO231, PRO357, PRO1155, PRO1136 or PRO1419 polypeptide
are useful for stimulating the release of tumour necrosis factor (INF)-
alpha from human blood. PRO982, PRO357, PRO136, PRO1419, PRO1419,
PRO127, PRO337, PRO526, PRO363, PRO537, PRO1035, PRO1419, PRO1419,
PRO1025, PRO1181, PRO1136, PRO1057, PRO1017, PRO1419, PRO1412,
PRO1026, PRO1330, PRO1347, PRO1305, PRO1279, PRO1274, PRO1432,
PRO1386, PRO1330, PRO4341, PRO1801, PRO4331, PRO1373, PRO1356,
PRO1897, PRO1928, PRO4341, PRO1801, PRO4331, PRO1351,
PRO18940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
CR stimulating the pro11sferation of normal human dermal fibroblasts cells.
PRO5723, PRO5725, PRO7184, Or PRO7425 polypeptide are useful for
inhibiting the pro11sferation of normal human dermal fibroblasts cells.
CR inhibiting the pro11sferation of normal human dermal fibroblasts cells.
CR inhibiting the pro11sferation of normal human dermal fibroblasts cells.
CR inhibiting the pro11sferation of normal human dermal fibroblasts cells.
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CR Inhibiting the pro11sferation of normal human dermal fibroblasts cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard A, Godowski PJ;
phan JF, Watanabe CK, Wood WI;
dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New PRO polypeptide for use as molecular weight markers for protein electrophoresis purposes and for detecting the presence of tumor in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen ME, Goddard Smith V, Stephan JF,
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Gaps

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Length 208; Indels

/ Match 100.0%; Score 89; DB 7; L Local Similarity 100.0%; Pred. No. 9.2e-05; Les 15; Conservative 0; Mismatches 0;

Query Match

Best Loca Matches

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The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
useful for stimulating the proliferation of or gene expression in

pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful

for stimulating the proliferation or differentiation of chondrocyte

cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNP)-

alpha from human blood. PRO982, PRO357, PRO125, PRO1306, PRO1419, PRO214,

PRO247, PRO337, PRO526, PRO363, PRO531, PRO1081, PRO1419, PRO1412,

PRO1028, PRO1181, PRO826, PRO1106, PRO1092, PRO1419, PRO1412,

PRO10286, PRO1134, PRO126, PRO1106, PRO1192, PRO1274, PRO1412,

PRO10286, PRO1330, PRO1347, PRO1306, PRO1474, PRO1279, PRO1340, PRO1320,

PRO1987, PRO1928, PRO4341, PRO1801, PRO1474, PRO1412,

PRO198940, PRO66079, PRO9836 or PRO10096 polypeptide are useful for

stimulating the proliferation of normal human dermal fibroblasts cells.

PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for

inhibiting the proliferation of normal human dermal fibroblast cells.

PRO5723, PRO5725, PRO7154, or PRO7428 polypeptide are useful for

inhibiting the proliferation of normal human dermal fibroblast cells.

PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for

chibiting the proliferation of normal human dermal fibroblast cells.

PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for

chibiting the proliferation of normal human dermal fibroblast cells.

PRO5723, PRO5725, PRO7164, PRO4981, PRO7174, PRO5778, PRO5732, etc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.
                                                                                                                                                                                                                                                                                                                      Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; periote cell proliferation; chondrocyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNR)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;
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Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                                                                 ADC47150 standard; protein; 208
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01-JUN-2001; 2010WO-US017800.
29-JUN-2001; 2001WO-US011066.
09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-2002; 2002US-00219070.
144 HLPGNKSPHRDPAPR 158
                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grimaldi JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy
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                                                                                                                                                                                  ADC47150;
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are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lump tumour, colon tumour, breast tumour, prostate tumour, rectal tumour is luyent tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful creating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and
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Sequence 208 AA;

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100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; ive 0; Mismatches 0; Indels
                                                                                                      144 HLPGNKSPHRDPAPR 158
                                                                             1 HLPGNKSPHRDPAPR 15
Query Match
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Gaps

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ADC78025 standard; protein; 208 AA. ADC78025;

01-JAN-2004 (first entry)

Novel human secreted and transmembrane protein PRO10196.

Human, secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping; gene therapy

Homo sapiens.

US2003096972-A1.

22-MAY-2003.

29-AUG-2002; 2002US-00232234.

01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-765529/72. N-PSDB; ADC78024 Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers, for treating arthritis and tumor.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1275 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO351, PRO357, PRO155, PRO1306 or PRO1419 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte care useful for stimulating the PRO9357, PRO9357, PRO1356, PRO1306, PRO1419, PRO214, PRO1364, PRO1306, PRO1419, PRO214, PRO1365, PRO1305, PRO1305, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO1306, PRO1307, PRO13 o, Gaps .. 0 Length 208; 0; Indels Score 89; DB 7; 1 Pred. No. 9.2e-05; Mismatches 0 100.0%; transmembrane PRO polypeptide. 1 HLPGNKSPHRDPAPR 15 Query Match
Best Local Similarity 10v...
For 15; Conservative Sequence 208 AA; RESULT 35 g à

ADD06260

ADD06260 standard; protein; 208 AA. ADD06260;

01-JAN-2004 (first entry)

Novel human secreted and transmembrane protein PRO10196.

release; human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; lissue typing; chromosome mapping; gene mapping;

therapy gene

Homo sapiens

US2003073816-A1.

17-APR-2003.

26-AUG-2002; 2002US-00227873.

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The invertion describes an isolated pro | Secreted and transmemorane)

polypeptide (I). PRO982, PRO1166, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in constitution that proliferation of or gene expression in pericyte cells. PRO357, PRO125, PRO1136 or PRO1419 polypeptide are useful for stimulating the proliferation of dicementation of chondrocyte cells. PRO331, PRO357, PRO1357, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TME)-alpha from human blood. PRO982, PRO1357, PRO1305, PRO1419, PRO141, PRO1419, PRO141, PRO1419, PRO1419, PRO1419, PRO1419, PRO1419, PRO1347, PRO1347, PRO1347, PRO1347, PRO1347, PRO1347, PRO1347, PRO1347, PRO1347, PRO1347, PRO1347, PRO1347, PRO1348, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO1349, PRO
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                                                                                                                                                                                                                                                                                                                                                                                   New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
                                                                                                                                                                                                           Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention describes an isolated PRO (secreted and transmembrane)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID NO 78; 314pp; English.
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                                                            2001WO-US021066.
                            01-JUN-2001; 2001WO-US017800.
                                                                                  09-APR-2002; 2002US-00119480.
                                                                                                                                                                                                           Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                              (GETH ) GENENTECH INC
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Sequence 208 AA;

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Gaps
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100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05;
                            0; Indels
                            0; Mismatches
                            15; Conservative
             Local Similarity
   Query Match
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Matches
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HIPGNKSPHRDPAPR 158 1 HLPGNKSPHRDPAPR 15

à 셤

ADC77779 standard; protein; 208 AA. 01-JAN-2004 (first entry) ADC77779; RESULT 36
ADC77779
ID ADC77
XX
AC ADC77
XX
DT 01-JA

Human, secreted and transmembrane protein, PRO, cytostatic, vulnerary, antiarthritic, pericyte cell proliferation, pericyte cell differentiation, chondrocyte cell proliferation, Novel human secreted and transmembrane protein PRO10196.

release; tumour; choidrocyte cell differentiation; tumour necrosis factor alpha choidrocyte cell differentiation; tumour necrosis factor alpha dermal fibroblast cell differentiation inhibitor; tumour; lung colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping;

gene therapy.

Homo sapiens

US2003088066-A1.

08-MAY-2003.

13-AUG-2002; 2002US-00219466

01-JUN-2001; 2001WO-US017800

29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,

WPI; 2003-657980/62. N-PSDB; ADC77778

useful in gene therapy, or for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody, One hundred and twenty two nucleic acids encoding PRO polypeptides, e.g. cancer.

Claim 11; Fig 78; 314pp; English.

The invention describes an isolated PRO (secreted and transmembrane)

polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

useful for stimulating the proliferation of or gene expression in

pericyte cells. PRO357, PRO229, PRO1152, or PRO4405 polypeptide are useful

for stimulating the proliferation or differentiation of chondrocyte

cells. PRO337, PRO357, PRO155, PRO1155, PRO1196 or PRO1419 polypeptide

are useful for stimulating the release of tumour necrosis factor (TNP)
alpha from human blood. PRO982, PRO357, PRO125, PRO1149, PRO1419, PRO114,

PRO1025, PRO1137, PRO526, PRO363, PRO357, PRO1083, PRO1419, PRO1144, PRO1134,

PRO1025, PRO1134, PRO1065, PRO1195, PRO1192, PRO1411, PRO1401,

PRO1026, PRO1330, PRO1409, PRO1194, PRO1144, PRO144, PRO1441, PRO14657,

PRO1887, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1446, PRO4322,

PRO1987, PRO1928, PRO4441, PRO11095, PRO4444, PRO1944, PRO4444, PRO1957,

PRO1987, PRO529, PRO788, PRO1194, PRO11943, PRO3444, PRO4322,

PRO1987, PRO529, PRO788, PRO1194, PRO1197, PRO1488, PRO4408,

PRO5723, PRO5725, PRO7154, or PRO7425 POlypeptide are useful for chemel human dermal fibroblasts cells. PRO 1019; PRO5725, PRO7154, or PRO7425 POlypeptide are useful for checkting the proliferation of normal human dermal fibroblast cells. PRO 2019; PRO5725, PRO5726, PRO5728, in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polymucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO329, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis,

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This is the amino acid sequence of a human secreted and
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Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell proliferation; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; prostate tumour; rectal tumour; liver tumour; chondrocyte cumour; chondrocyte colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tumour; colon tum
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                                                                                                                                            Score 89; DB 7; Length 208;
Pred. No. 9.2e-05;
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                                transmembrane PRO polypeptide.
                                                                                                                                                      100.0%;
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09-APR-2002; 2002US-00119480.
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                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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Grimaldi JC, Gurney
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   sport injuries).
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EXENSIBLY, EXCORD, FACULOUS DELYPEDLICE STEUSELIES.

EXENSIBLY, EXCORD, FACULOUS, EXCOLDES EXCOLDES EXECUTED SET STEUSELY, EXCOLDES EXECUTED SET STEUSELY.

EXECUTED, PRO152, PRO718, OF PRO122, PRO1488, PRO432, PRO4408, PRO5181, PRO525, PRO7184, or PRO7425 POLYPEDLICE are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO 1919 peptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., collypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., collypeptides such as presence of tumour in a mammal which in a test sample of cells taken from the mammal, and a control sample of in a test sample of cells taken from the mammal, and a control sample of the presence of tumour in the mammal. The tumour is lung the PRO polypeptides in the test sample as compared to the control sample of is indicative of the presence of tumour in the mammal. The tumour is lung the tumour, colon tumour. Present tumour, prostate tumour, rectal tumour is lung typing, or as therapeutic agents. A polymucleotide [II) encoding [I] is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polymucleotide [II] encoding [I] is useful for thromsome and gene mapping or gene therapy. (II) is useful secreting transgenic animals or knock-out animals which are useful screening useful for transmender and man animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control as animal secreted and control a
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Smith V, Stephan JF, Watanabe CK, Wood WI;
PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells.
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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Best Local Similarity 100.
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N-PSDB; ADD50987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003105290-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD50988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 38
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Page 23

22-MAY-2003

The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
useful for stimulating the proliferation of or gene expression in
pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
Cc ells. PRO211, PRO357, PRO1255, PRO1165, PRO1405 polypeptide are useful
CC ells. PRO213, PRO357, PRO1255, PRO1166 or PRO1419 polypeptide
are useful for stimulating the release of tumour necrosis factor (TMP)alpha from human blood. PRO982, PRO357, PRO125, PRO11080,
CC PRO4478, PRO1317, PRO625, PRO1005, PRO10191, PRO1411, PRO1419,
CC PRO4478, PRO1314, PRO826, PRO1065, PRO1092, PRO1025, PRO1130, PRO1313,
CC PRO1478, PRO1314, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO13108,
CC PRO1478, PRO1377, PRO1379, PRO1379, PRO1370, PRO1370,
CC PRO1478, PRO1377, PRO1379, PRO1474, PRO1370, PRO1370,
CC STIMULATING the PRO1164, PRO1191, PRO1191, PRO11670, PRO1387,
CC STIMULATING the PRO1164, PRO1194, PRO1174, PRO1301, PRO4181,
CC STIMULATING the PRO1164-A PRO1194, PRO1174, PRO1301, PRO4181,
CC STIMULATING the PRO1164-A PRO1194, PRO1174, PRO1301, PRO4182,
CC STIMULATING the PRO1164-A PRO1174, PRO1770, PRO4186,
CC Inhibiting the Pro1164-A PRO1174, PRO1779, PRO4132, etc.,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4324,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4324,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4304,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4304,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4304,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4304,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4704,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4705,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4705,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4705,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4705,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4705,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4705,
CC Inhibiting the Pro1164-A PRO1174, PRO5778, PRO4705,
CC Inhibiting the P the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents, A polynuclectide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful screening useful reagents. PROJS7, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and new isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy. Claim 11; Fig 78; 309pp; English. ransmembrane PRO polypeptide.

Sequence 208 AA;

Gaps ö 100.0%; Score 89; DB 7; Length 208; 100.0%; Pred. No. 9.2e-05; Live 0; Mismatches 0; Indels Query Match 100.0 Best Local Similarity 100.0 Matches 15; Conservative

; 0

RESULT 39 ADD50469

ADD50469 standard; protein; 208 AA.

ADD50469;

15-JAN-2004 (first entry)

Human PRO polypeptide #39.

Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNP-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic

Homo sapiens.

US2003096971-A1

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polypucleotides encoding them.

CT The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, for stimulating the release of tumour necrosis factor (TMF) -alpha from human blood, for stimulating the proliferation of differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in perioyte cells or for stimulating the proliferation of or gene copression in perioyte cells or for stimulating the proliferation of or gene copression in perioyte cells or for stimulating the proliferation of chondrocyte cells, in chromosome and gene mapping, in generating thy pridisation probes, in chromosome and gene mapping, in generating cut technology, in generating properties by recombinant technology, in generating probes. The PRO polypeptides by recombinant technology, in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a machine condition which is responsive to the PRO polypeptides or anti-PRO antibodies, are useful for preparing a medicament for treating as condition which is responsive to the PRO polypeptides or anti-PRO antibodies, are useful separation electrophoresis, involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as condition and a markers for protein electrophoresis, and in tissue typing. This process and an electrophoresis, involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein electrophoresis, and in tissue typing. This human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated PRO polypeptide useful for tissue typing, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.
                                                                                                                                                                                                                                                                             Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                 Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Fig 78; 308pp; English.
                                                                                               01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                29-AUG-2002; 2002US-00232229.
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                                                                                                                                                                                                                                                    Baker KP, Desnoyers L, Grimaldi JC, Gurney AL,
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Matches 15; Conservative
                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                         WPI; 2003-765528/72.
                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADD50468.
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                                                                                                                                                                                                                                                 Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD50223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 40
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Human PRO polypeptide #39.

Human, PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.

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The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polypucleotides encoding them. The PRO polypeptides and polymucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene comman in periotyce cells or for stimulating the proliferation of normal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating transgenic animals which may be used in the development and screening of therapeutically useful reagents, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibodies, such as pericyte-associated timours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the redifferentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated PRO polypeptides useful as molecular weight markers in protein electrophoresis, and useful for tissue typing, for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Fig 78; 308pp; English.
                                                                                                                                                                                  26-JUL-2000; 2000US-0220893P.
01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
                                                                                                                                         29-AUG-2002; 2002US-0023227.
                                                                                                                                                                                                                                                                                                                                                  Baker KP, Desnoyers L,
Grimaldi JC, Gurney AL,
                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-765527/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis, tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADD50222.
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                                              US2003096970-A1.
    Homo sapiens.
                                                                                          22-MAY-2003
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Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI;

Gaps ٥; Query Match 100.0%; Score 89; DB 7; Length 208; Best Local Similarity 100.0%; Pred. No. 9.2e-05; Matches 15; Conservative 0; Mismatches 0; Indels

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Search completed: March 2, 2004, 16:04:51 Job time : 9 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2004, 15:51:17; Search time 1.4375 Seconds (without alignments) 543.341 Million cell updates/sec March Run on:

US-10-060-765-8

Perfect score: ritle:

1 HLPGNKSPHRDPAPR 15 Sequence:

BLOSUM62

Scoring table:

141681 segs, 52070155 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB B

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRAMADIES

| SUMMARIES | 4 | Description | | | | PAVPN P18546 porcine par | HUMAN Q14055 homo sapien | P38346 | 3E Q91xr9 1 | Q91xr8 | N 08ng57 | P07141 | P53529 | Q8ni27 | 002062 | Q24106 | | P25371 | Q99687 | Q8ci61 | P29776 | P03559 | Q05651 | P03557 | P13218 | 062893 | Q9es18 | 5ppp60 | | | | homo sa | P25058 | |
|-----------|--------|--------------|------------|---------|---------|--------------------------|--------------------------|---------|-------------|----------|----------|---------|------------|---------|------------|-----------|------------|------------|---------|------------|------------|------------|---------|---------|---------|----------|------------|--------|---------|---------|---------|---------|-----------|-------|
| SINAM | í | A . | FGFL HUMAN | COA1 PA | COA1 PA | COA1 PA | CA29 HD | YB90 YE | GX42 MO | GX42 RAT | ELA3_HU | CSF1 MO | PYRG MYCLE | THO2 HU | KASB STRCO | HID DROME | AMHZ HUMAN | ADP1_YEAST | MEI3 HU | BAG4 MOUSE | ETS6 DROME | IBMP_CAMVS | IBMP CA | IBMP CP | IBMP CA | AMH2 RAT | FXJ2 MOUSE | NBEACE | AXN2 BF | K852 HL | NBEA MC | NBEA HT | GAG BLVAU | 11111 |
| | | 8 | - | | | | Н | | Н | Н | Н | Н | Н | Н | Н | Н | Н | Ч | Н | ч | ٦ | Н | Н | н | | | | | | ۲ | | | | |
| | | Match Length | 209 | 729 | 729 | 729 | 689 | 545 | 253 | 253 | 546 | 552 | 590 | 1478 | 407 | 410 | 573 | 1049 | 382 | 457 | 475 | 520 | 520 | 522 | 522 | 557 | 565 | 793 | 812 | 970 | 2936 | 2946 | 392 | |
| | Query | Match | 100.0 | 51.7 | 51.7 | 51.7 | 50.6 | 50.0 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 48.3 | 48.3 | 48.3 | 48.3 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | • | |
| | | Score | 89 | 46 | 46 | 46 | 45 | 44.5 | 44 | 44 | 44 | 44 | 44 | 44 | 43 | 43 | 43 | 43 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42 | 41.5 | |
| | Result | No. | 1 | 7 | m | 4 | ß | 9 | 7 | 60 | σ, | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | c |

| 094425 ciona intes P22547 cauliflower P02558 cauliflower 002954 cauliflower 000957 cauliflower 08445 buchnera ap 039088 homo sapien 013444 homo sapien 049859 glycine max P30365 medicago tr P16329 pisum sativ |
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The secretical protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."; Genome Res. 13:2265-2270 (2003).
-: SUBCELITAR LOCATION: Secreted (Potential).
-: SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22887296; PubMed=12975309; MEDLINE=22887296; PubMed=12975309; MEDLINE=22887296; PubMed=12975309; Clark H.F., Gurney A.L., Abaya E., Cark W. Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Haung A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Kie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDINE-20461777; PubMed=10858549;
Nishlimura T., Nakatake Y., Konishi M., Itoh N.;
"Identification of a novel FGF, FGF-21, preferentially expressed in
                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Fibroblast growth factor-21 precursor (FGF-21) (UNQ3115/PRO10196).
                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007165; P:signal transduction; TAS.
                                209 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the liver.";
Biochim. Biophys. Acta 1492:203-206(2000).
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                                PRT;
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                                STANDARD;
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Q9NSA1;
FGFL_HUMAN
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729 AA

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A SEQUENCE ### SEQUENCE ### SEQUENCE ### SEQUENCE ### SEQUENCE ### SEQUENCE ### SEQUENCE OF CAPACITY ### SEQUENCE OF CAPACITY ### SEQUENCE OF CAPACITY ### SEQUENCE OF CAPACITY ### SEQUENCE OF CAPACITY ### SEQUENCE OF CAPACITY ### SECTION NS-1.

-1- SUBJULY: AND VP3 AND A NONCAPRID PROTEIN NS-1.

-1- MISCELLANBOUS: VP3 MICHT BE A POSTTRANSLATIONAL CLEAVAGE PRODUCT OF VP2 IN SEVERAL AUTONOMOUS PARVOVIRUSES.

-1- SIMILARITY: BELONGS to the parvoviruses coat protein family.

R HSSP; PAD129; ADPV.

R HSSP; PAD129; ADPV.

R INTERPRO; IPRO01403; Parvo_coat.

R INTERPRO; IPRO01403; Viral_cap_coat.

R Pfam; PF00740; Parvo_coat.

R Pfam; PF00740; Parvo_coat.

R Pfam; PF00740; Parvo_coat.
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                                                                                                                                                                                                                                                                                  Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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(POTENTIAL)
                                                                                                            100.0%; Score 89; DB 1; Length 209; 100.0%; Pred. No. 3.8e-06; Live 0; Mismatches 0; Indels
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                                                                POTENTIAL.
FIBROBLAST GROWTH FACTOR-21.
MISSING (IN REF. 2).
27925C52A0023823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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01-FEB-1994 (Rel. 28, Last sequence update)
16-0CT-2001 (Rel. 40, Last amotation update)
Cost protein VPI (Contains: Cost protein VP2]
Porcine parvovirus (strain 90HS) (PPV)
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          ProDom; PD000831; ILLHBGF.
SMART; SM00442; FGF; T.
PROSITE; P800247; HBGF_FGF; FALSE_NEG.
Growth factor; Signal.
                                                                        29 209 E
23 23 M
209 AA; 22300 MW;
  InterPro; IPR002348; IL1_HBGF
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CHAIN 1 729
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      Pfam; PF00167; FGF; J. PRINTS; PR00262; IL1HBGF. ProDom; PD000831; IL1 HRG
                                                                                                                       Local Similarity 100.
1es 15; Conservative
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P33484;
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COAL_PAVPK

RESULT 3

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                                                                                                                                                                                                                                                                                                                                                                    J. Virol. 70:2508-2515(1996).
-!- SUBUNIT: MATURE VIRION CONTAINS THREE CAPSID PROTEINS DESIGNATED VPI, VPI, VP2, AND VP3 AND A NONCAPSID PROTEIN NS-1.
-!- MISCELLANBOUS: VP3 MIGHT BE A POSTTRANSLATIONAL CLEAVAGE PRODUCT OF VP2 IN SEVERAL AUTONOMOUS PARVOVIRUSES.
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ID COAL PAVPN

STANDAL,

AC P18546; P22964; Q89816;

AC D18546; P22964; Q89816;

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 02-RFBE-2003 (Rel. 41, Last annotation update)

DE Coat protein VPI [Contains: Coat protein VP2].

OS Porcine parvovirus (strain NADL-2) (PPV).

OC Viruses; seDNA viruses; Parvoviridae; Parvovirus.
                                                                                                                                                                                                                                   MEDLINE=96183900; PubMed=8642680;
Bergeron J., Hebert B., Tijssen P.;
"Genome organization of the Kresse strain of porcine parvovirus:
identification of the allotropic determinant and comparison with
those of NADL-2 and field isolates.";
J. virol. 70:2508-2515(1996).

    !- SIMILARITY: Belongs to the parvoviruses coat protein family.

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                                                                                                                                   ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus
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Pred. No. 26;
2; Mismatches 3; Indels
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01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
16-0cT-2010 (Rel. 40, Last annotation update)
16-0ct protein VPI (Contains: Coat protein VP2)
Porcine parvovirus (strain Kresse) (PPV)
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InterPro; IPR01403; Parvo_coat.
InterPro; IPR0040375; Viral_cap_coat.
Pfam; PF00740; Parvo_coat; 1.
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61.5%;
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729 AA;
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Best Local Similarity
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                                                                                                                                                      NCBI_TaxID=73487;
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MEDLINE=90085785; PubMed=2596019;

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                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                          Ranz A.I., Manclus J.J., Diaz-Aroca E., Casal J.I.;
"Porcine parvovirus. DNA sequence and genome organization.";
J. Gen. Virol. 70:2541-2553 (1989).
I. SUBGUIT: MATREE VIRON CONTAINS THREE CAPSID PROTEINS DESIGNATED
                                                                                                                                                                                                                                                                VP1, VP2, AND VP3 AND A NONCAPSID PROTEIN NS-1.
-!- MISCELLANEOUS: VP3 MIGHT BE A POSTTRANSLATIONAL CLEAVAGE PRODUCT OF VP2 IN SEVERAL AUTONOMOUS PARVOVIRUSES.
        Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.; "Nucleotide sequence analysis of the capsid genes and the right-hand terminal palindrome of porcine parvovirus, strain NADL-2."; Virology 173:368-377(1989).
                                                                                            MEDLINE=91021005; PubMed=2219713;
Vasudevacharya J., Basak S., Srinivas R.V., Compans R.W.;
"The complete nucleotide sequence of an infectious clone of porcine parvovirus, strain NADL-2";
Virology 178:611-616(1990).
                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the parvoviruses coat protein family.
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G -> A (IN REF. 3).

T -> S (IN REF. 3).

V -> S (IN REF. 3).

E -> A (IN REF. 3).

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InterPro; IPR008975; Viral cap coat.
Pfam; PF00740; Parvo coat; 1.
                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=90010964; PubMed=2794971;
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EMBL; M38367; AAA46519.1; --
EMBL; M38367; AAA46921.1; --
EMBL; D00623; BAA00502.1; --
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PIR; B33743; VCPVNA.
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DB 1; Length 729;
                       3; Indels
              Pred. No. 26;
2; Mismatches
              61.5%;
             Local Similarity 61.5
nes 8; Conservative
                Best Loc
Matches
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Science 285:409-412(1999).
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MEDLINE=98370844; PubMed=9707347;
Pihlajamaa T., Vuoristo M.M., Annunen S., Peraelae M., Frockop D.J.,
Ala-Kokko L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           VARLANT IDD TRP-326, AND VARIANT ARG-326.
MEDLINE=99340300; PubMed=10411504;
Annunen S., Paassilta P., Lohiniva J., Peraelae M., Pihlajamaa T.,
Karppinen J., Tervonen O., Kroeger H., Laehde S., Vanharanta H.,
Karppinen J., Goering H.H.H., Ott J., Prockop D.J., Ala-Kokko L.;
"An allele of COL9A2 associated with intervertebral disc disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Heterotrimer of an alpha 1(IX), an alpha 2(IX) and an
                                                                                                                                                                                                                                                     "Human COL9A1 and COL9A2 genes. Two genes of 90 and 15 kb code for similar polypeptides of the same collagen molecule.";
Matrix Biol. 17:237-241(1998).
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                    Peraelae M., Hanninen M., Hastbacka J., Elima K., Vuorio E., "Molecular cloning of the human alpha 2(IX) collagen cDNA and assignment of the human COL9A2 gene to chromosome 1."; FEBS Lett. 319:177-180(1993).
                                                                                                                                                                                                                                                                                                                      Donnelly S.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
COLJAGEN àlpha 2(IX) chain precursor.
                                                         689 AA
                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Cartilage;
MEDLINE=93202262; PubMed=8454052;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 50-668 FROM N.A.
117 PGSKPPGKRPAPR 129
                                                        STANDARD;
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                                                                                                                                                                                                 SEQUENCE FROM N.A.
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GX42_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aigle M., Baclet M.C., Barthe C., Biteau N., Crouzet M., Doignon F., Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                        Q -> W (in IDD; requires 2 nucleotide substitutions).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Pungi; Aecomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 61.3 kDa protein in MRPL37-RIF1 intergenic region.
YBR270C OR YBR1738.
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                 Pfan, PF01391; Collagen; 9.
ProDom; PD000007; Clg_helix; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                             Collagen; Signal; Glycoprotein; Proteoglycan; Disease mutation;
                                                                                                                                                                                                                                               INTERCHAIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (BY
                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 1; Length 689;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                    EB6106E02F6FA862 CRC64;
                                                                                                                                                                            NON-HELICAL REGION 1.
TRIPLE-HELICAL REGION 2.
NON-HELICAL REGION 2.
                                                                                                                                                        COLLAGEN ALPHA 2 (IX) CHA TRIPLE-HELICAL REGION 1.
                                                                                                                                                                                                          TRIPLE-HELICAL REGION 3.
                                                                                                                                                                                                                 NONHELICAL REGION 3.
TRIPLE-HELICAL REGION 4.
NONHELICAL REGION 4.
                                                                                                                                                                                                                                                                                         ) -> R. //FTId=VAR_012659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545 AA.
                                                MIM; 603992; -. Gollagen type IX; TAS. GO; GO:0005594; C:collagen type IX; TAS. GO; GO:00101501; P:skeletal development; TAS. InterPro; IPR008161; Clg helix. InterPro; IPR008160; Collagen.
                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                              /FTId=VAR
EMBL; ALO50341; CAB81611.1; -.
EMBL; M95610; AAA80977.1; -.
Genew; HGNC:2218; COL9A2.
MIM; 120260; -.
                                                                                                                                                                                                                                                                                                                                       689 AA; 65131 MW;
                                                                                                                                                                                                                                                                                                                                                         50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                  567 PGKQGPHGHPGPR 579
                                                                                                                                                                                                                                                                                                                                                                                               PGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 53.8
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                 23
689
1163
1180
519
519
632
632
634
689
                                                                                                                                                                                                                                                                                        326
                                                                                                                                                                                                                                                                                                           326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                 24
24
27
27
1164
1181
181
520
550
633
663
665
174
178
                                                                                                                                                                                                                                                                                       326
                                                                                                                                                                                                                                                                                                           326
                                                                                                                                        Polymorphism.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YEAST
                                                                                                                                                                                                                                                                                                                                                                                                ٣
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YB90 YEP
P38346;
                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
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Yant L.J., Ran Q., Rao L., Van Remmen H., Shibatani T., Belter J.G.,
Notta L., Richardson A., Prolla T.A.;

Motta L., Richardson A., Prolla T.A.;

"The selenoprotein GPX4 is essential for mouse development and
protects from radiation and oxidative damage insults.";

"Free Radic. Biol. Med. 34:496-502(2003)

"I Free Radic. Biol. Med. 34:496-502(2003)

"I Free Radic. Biol. Med. 24:496-502(2003)

"I Caralymic Acrivity. 2 glutathione + H(2)0(2) = oxidized

"I Caralymic Acrivity. 2 glutathione + H(2)0(2) = oxidized

"I Caralymin Proceeding Codon, UGA.

"I SINGELLULAR LOCATION: Nuclear.

"I ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21242617; PubMed-11344089; Pfeifer H., Conrad M., Roethlein D., Kyriakopoulos A., Brielmeier M., Pfeifer H., Conrad M., Roethlein D., Kyriakopoulos A., Brielmeier M., Bornkamm G.W., Behne D.; "Identification of a specific sperm nuclei selencenzyme necessary for proteamine thiol cross-linking during sperm maturation."; FASEB J. 15:1236-1238(2001).
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- TISSUE SPECIFICITY: Expressed exclusively in sperm.
                                                                                                                                                                                                                        Score 44.5; DB 1; Length 545; Pred. No. 31; 1; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91XE9; Q8K4U8;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Phospholipid hydroperoxide glutathione peroxidase, nuclear
(EC 1.11.1.12) (GPX-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=129/SVJ; TISSUB=Liver;
Imai H. Nakagawa Y.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Z36139; CAA85233.1; -.
PIR; S46151; S46151.
GermCnline; 138813; -.
SGD; S0000474; YER270C.
HYPOCHETICAL protein.
SEQUENCE 545 AA; 61301 MW; 5655D51206EF728B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q91XR9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Mitochondrial;
IBoId=070325-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22453509; PubMed=12566075;
                                                                                                                                                                                                                              50.0%;
                                                                                                                                                                                                                                                                                                                                                                  1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                               53 HLKTSKSPH-DAAPR 66
                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GX42 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                                                                  GO; GO:0005829; C:cytosol; IDA.
GO; GO:0005739; C:mitochondrion; IDA.
GO; GO:0005635; C:miclear membrane; IDA.
GO; GO:0004602; F:glutathione.peroxidase activity; IDA.
GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; IDA.
GO; GO:0007283; P:spermatogenesis; IDA.
InterPro; IPR000889; Glut peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maiorino M., Scapin M., Ursini F., Biasolo M., Bosello V., Flohe L., "Distinct promoters determine alternative transcription of gpx-4 into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2019id hydroperoxide glutathione peroxidase, nuclear
(EC 1.11.1.12) (GPX-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.4%; Score 44; DB 1; Length 253; 53.8%; Pred. No. 17; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear procein; Alternative splicing.
ACT SITE 129 129 BY SIMILARITY.
SECUS 129 BY SIMILARITY.
SECUS 253 AA; 29204 MW; C55E36875B830053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-250 FROM N.A., AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Developmental protein; Selenium; Selenocysteine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS00460, GLUTATHIONE PEROXID_1; 1. PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                  EMBL; AF274027; AAK74112.1; -. EMBL; AB030643; BAC06509.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00255; GSHPx; 1.
PRINTS; PR01011; GLUTPROXDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; Peroxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : | | : | ||
27 PGRQSPRKRPGPR 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                          MGD; MGI:104767; Gpx4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHGPx variants."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GX42 RAT
Q91XR8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ537598; CAD61278.1; -.
EMBL; AF774028; AAK74113.1; -.
EMBL; AF774028; AAK74113.1; -.
GO; GO:0000551; C:nucleus; ISS.
GO; GO:0006325; F:Gutachinome peroxidase activity; ISS.
GO; GO:0007325; P:establishment and/or maintenance of chromat. . .; ISS.
GO; GO:0007283; P:spermatcgenesis; ISS.
InterPro; IPR000889; Glut_peroxidase.
Pfam; PF00255; GSHPx; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription elongation factor, elongin A3.";
J. Biol. Chem. 277:26444-26451 (2002)
-!- FUNCTION: SIII, also known as elongin, is a general transcription elongation factor that increases the RNA polymerase II transcription elongation past template-encoded arresting sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RNA polymerase II transcription factor SIII subunit A3 (Elongin A3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 14 RGRCRQ -> PGRQCAGIRPYGP (IN REF. 2).
101 101 S -> A (IN REF. 2).
253 AA; 29304 MW; FSAECICFIB7AD7BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., FUNCTION, AND SUBUNIT.
MEDLINE=22113023; PubMed=11994304;
Yamazari K., Gvo L., Sugahara K., Zhang C., Enzan H., Nakabeppu
Kitajima S., Aso T.;
"Identification and biochemical characterization of a novel
-!- COFACTOR: Selenocysteine. The active-site selenocysteine is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the glutathione peroxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.4%; Score 44; DB 1; Length 253; 53.8%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO1011; GLUTPROXDASE.
PROSITE; PS00466; GLUTATHIONE PEROXID 1; 1.
PROSITE; PS00765; GLUTATHIONE_PEROXID 2; 1.
Oxidoreductaes; Peroxidase;
Developmental protein; Selenium; Selenocysteine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             546 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                 IsoId=Q91XR8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                 IsoId=P36970-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein; Alternative splicing ACT SITE 129 129 SE CYS 129 129
                           encoded by the opil codon, UGA.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.8%;
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27 PGRQSPRKRPGPR 39
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                                                                                                                                                                                                                                   Name=Mitochondrial;
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                                                                                                                                                                      Name=Nuclear;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                   -:- SUBUNIT: Heterotrimer of an A (A1, A2 or A3), B and C subunit.
-:- SUBCELDULAR LOCATION: Nuclear.
-:- TISSUE SPECIPICITY: Widely expressed.
-:- DOMAIN: The elongin BC complex binding domain is also known as BC-box with the consensus [APST]-L-x(3)-C-x(3)-[AILV].
-:- SIMILARITY: Contains 1 TFS2-N domain.
Subunit A3 is transcriptionally active but its transcription activity is not enhanced by binding to the dimeric complex of the SIII regulatory subunits B and C (elongin BC complex). SUBUNIT: Heterotrimer of an A (A1, A2 or A3), B and C subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "CDNA cloning and expression of murine macrophage colony-stimulating factor from L929 cells.";
Proc. Natl. Acad. Sci. U.S.A. 85:6706-6710(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borycki A.G., Lenormund J., Guillier M., Leibovitch S.A., "Isolation and characterization of a cDNA clone encoding for rat CSF-1 gene. Post-transcriptional repression occurs in myogenic differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSF1 MOUSE STANDARD; PRT; 552 AA.
P07141; QBR3C8;
01-APR-1988 (Rel. 07, Created)
01-FEB-1996 (Rel. 31, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Macrophage colony stimulating factor-1 precursor (CSF-1) (MCSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88320507; PubMed=2457916;
Ladner M.B., Martin G.A., Noble J.A., Wittman V.P., Warren M.K.,
McGrogan M., Stanley E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delamarter J.F., Hession C., Semon D., Gough N.M., Rothenbuhler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVATION DOMAIN (BY SIMILARITY) INTERACTING WITH ELONGIN BC (BY
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Pred. No. 37;
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59760 MW; E98AE3DD548C5492 CRC64;
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Nucleic Acids Res. 15:2389-2390(1987)
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MEDLINE=93363632; Pubmed=8357831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87174763; PubMed=3494232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB076840; BAC01113.1; -. InterPro; IPR003617; TFS2_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.48;
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162 PADSGPHRDPPTR 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003617; TFS
SMART; SM00509; TFS2N; 1
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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MISCARL S. Colling P.S., Wagner L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L., Brownetein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownetein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J., Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mriting M., Madan A., Young A.C., Shevchenko Y., Bouffaxd G.G., Mriting M., Madan A., Young A.C., Shevchenko Y., Bouffaxd G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

Muterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerchion and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manual Marker Description of the Marker S.C. Jr., D'Angelo M., Safadi F.F., Van Wesenbeeck L., Odgren D.R., Marker S.C. Jr., Popoff S.N., Van Hul W., Marker S.C. Jr., "The osteopetrotic mutation trochless (tl) is a loss-of-function setteopetrotic mutation in the rat Csfl gene: evidence of a crucial role for CSF-1 in osteoclastogenesis and endochondral ossification.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-100 FROM N.A.
MEDIATURE-8714721; PubMed=3493488;
REJAVASA; PubMed=3493488;
Shively J.E., Lusis A.J.;
Shively J.E., Lusis A.J.;
"Cloning and tissue-specific expression of mouse macrophage colony-stimulating factor mRNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:1157-1161(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and characterization of the murine promoter for the colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ď
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MEDLINE=91340149; PubMed=1874443;
Harrington M.A., Edenberg H.J., Saxman S.M., Pedigo L.M., Daub R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino-terminal amino acid sequence of murine colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dobbins D.E., Sood R., Hashiramoto A., Hansen C.T., Wilder R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mutation of macrophage colony stimulating factor (Csfl) causes osteopetrosis in the tl rat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 33-57.
MEDILINE=85242705; PubMed=3925458;
Ben-Avram C.M., Shively J.E., Shadduck R.K., Waheed A.,
Rajavashisth T.B., Lusis A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:14303-14308(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lochem. Blophys. Res. Commun. 294:1114-1120(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 82:4486-4489(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHOWS THAT REF. 3 SEQUENCE ORIGINATES FROM MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHOWS THAT REF.3 SEQUENCE ORIGINATES FROM MOUSE.
Biochim. Biophys. Acta 1174:143-152(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stimulating factor-1-encoding gene.";
Gene 102:165-170(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Biol. Chem. 267:2190-2199(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22294966; PubMed=12379742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92129287; PubMed=1733926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=12074592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22069908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteoglycan.";
    BETTERK RRETTERRK RRETTERRK BRETTERK RRETTER BRETTER BRETTERREKETTER BREKETTER BREKERFERRE BREKERFERRERE
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STRAIN=TN;
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                     Note-No experimental confirmation available;
Note-No experimental confirmation available;
Note-No experimental confirmation available;
Note-No experimental The predominant soluble form is a chondroitin sulfate-confaining proteoglycan.
-!- DISEASE: A defect in CSF1 is the cause of osteopetrosis.
Osteopetrotic mice (op/op) are severely deficient in mature macrophages and osteoclasts, display failed tooth eruption, and have a restricted capacity for bone remodelling.
-!- CAUTION: Ref. 3 sequence was originally thought to originate from rat, but was later shown (Ref. 8 and Ref. 9) to be derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MACROPHAGE COLONY STIMULATING FACTOR-1.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Missing (in isoform 2).
/FIId-VSP_001189.
D -> G.
S -> P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X05510; CAA28660.1; -.

REMBL; M21952; AAA37481.1; -.

REMBL; M21149; AAA37482.1; -.

REMBL; M31149; AAA37482.1; -.

REMBL; M31592; AAA37480.1; -.

REMBL; M31316; AAA37480.1; -.

REMBL; M31316; AAA19866.1; -.

REMBL; M31319; AAA19866.1; -.

RIR; A31401; A31401. -.

RIR; A31401; A31401, M31401. -.

RIR; PF05337; CSF1.

R Pfam; PF05337; CSF-1. 2.

R Cytokine; Growth factor; Glycoprotein; Proteoglycan; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P07141-2; Sequence=VSP_001189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P07141-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Alternative splicing.
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CARBOHYD
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21128732; PubMed=11234002;

Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Srom D., Chillingworth T., Connor R.,
Davier R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).

--- FUNCTION: Catalyzes the ATP-dependent amination of UTP to CTP with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          either Lightamine or ammonia as the source of nitrogen (By similarity).

-!-CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CTP.

-!-ENZYME REGULATION: Allosterically activated by GTP, when glutamine is the substrate. Inhibited by CTP (By similarity).

-!- PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP; third
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBDNIT: Homotetramer (By similarity).
-1- SIMILARITY: Belongs to the CTP synthase family.
-1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) (CTP synthetase).
PYRG OR ML1363 OR MLC1351.09C.
                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinomycetales; Corymebacteridae; Actinomycetales; Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                 49.4%; Score 44; DB 1; Length 552; 58.3%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Smith D.R., Robison K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
3 3 MISSING (IN REF. 5).
6 6 A -> R (IN REF. 5).
7 8 AG -> PR (IN REF. 5).
246 246 P -> A (IN REF. 1).
552 AA; 60648 MW; 3886D72D70B770AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 590 AA
                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U00021; AAA50916.1; -.
EMBL; Z95117; CAB08284.1; -.
EMBL; AL583921; CAC31744.1; -.
PIR; S72961; S72961.
Leproma; Mil363; -; HAWARP; MF_01277; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                    | : |||: |||
202 PASASPHQPPAP 213
                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                 3 PGNKSPHRDPAP 14
                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRG MYCLE
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IsoId=Q8NI27-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KASB STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
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-- FUNCTION: The THO/TREX complex is recruited to transcribed genes and travels with the RNA polymerase during elongation. It may physically link proteins that function in transcription and in RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBGNIT: Part of the heteromultimeric THO/TREX complex containing THOC1, THOC2, THOC3, THOC4 and NEX1/UAP56.
SUBCENLUAR LOCATION: Nuclear (Probable).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogai T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninoniya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     furt E.; The substitution of the messenger of the substitution with messenger of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of the substitution of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Straesser K., Masuda S., Mason P., Pfannstiel J., Oppizzi M.,
Rodriguez-Navarro S., Rondon A.G., Aguilera A., Struhl K., Reed R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                              PROSITE; PS00442; GATASE_TYPE_I; 1.
Pyrimidine biosynthesis; Ligase; Glutamine amidotransferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 1; Length 590; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                      GLUTANINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GALOGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1151-1478 FROM N.A. (ISOFORM 2).
TISSUE-Salivary gland;
                                                                                                                                                                                                                   AMINATOR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 444-1162 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22010388; PubMed=11979277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| : : |||
567 HLPNSSNQHRDGVERSFPAP 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HLPGNKSPHRD-----PAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THOS HUMAN STANDARD; PR. QBN127; Q9H816; 10-OCT-2003 (Rel. 42, Last seque 10-OCT-2003 (Rel. 42, Last seque 10-OCT-2003 (Rel. 42, Last annot THO complex subunit 2 (Tho2).
                                  InterPro; IPR004468; PyrG_synth.
Pfam; PF00117; GATase; 1.
TIGRFAMB; TIGR00337; PyrG; 1.
                                                                                                                                                                                                                                                                                                                                                                       64081 MW;
   InterPro; IPR000991; GATase_1
                                                                                                                                                                                                                                                                                                                                                                                                                                49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 45.0 tes 9, Conservative
                                                                                                                                                                                                                   312
590
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                                                                                                                                                                                                                                                                                                                                                                       590 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA export."
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DSLI -> VSIA (in isoform 2).

/FILGL=VSP 008587.

Missing (in isoform 2).

/FILGL=VSP 008588.

F -> S (IN REF. 2).

E -> K (IN REF. 3).
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Actinorhodin polyketide putative beta-ketoacyl synthase 2 (EC 2.3.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cotranscribed
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STRAIN=A312) / M145;
MEDLINE=21396410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequence and deduced functions of a set of cotranson genes of Streptomyces coelicolor A3(2) including the polyketide synthase for the antibiotic actinorhodin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 1; Length 1478; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2) / M145;
MEDLINE=92406871; PubMed=1527048;
Fernandez-Moreno M.A., Martinez E., Boto L., Hopwood D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport; mRNA transport; mRNA processing; mRNA splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1478 AA; 169580 MW; FEICBCE28C560BCF CRC64;
                                     008588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear protein; RNA-binding; Alternative splicing
                                                                      Note=No experimental confirmation available; --- SIMILARITY: Belongs to the THOC2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomycineae; Streptomycetaceae; Streptomyces
Name=2;
IsoId=Q8NI27-2; Sequence=VSP_008587; VSP_IsoId=Q8NI27-2; Sequence=VSP_008587; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8NI27-2; IsoId=Q8
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EMBL; AK023659; BAB14630.1; ALT_INIT.
EMBL; BX648654; CAE46196.1; -.
Genew; HGNC:19073; THOC2.
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1066 IPENEFHHKDPPPR 1079
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1161
1241
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Best Local Similarity
7; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 300395;
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Seabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seanders D., Sharp S., Squares R., Squares S., Taylor K., Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.;
                                                                                                                                                                    Nature 417:141-147(2002).
-!- MISCELLANEOUS: This putative ketoacyl synthase lacks the active

    -!- SIMILARITY: Belongs to the beta-ketoacyl-ACP synthases family.

                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor {\rm A3}\,(2)\,.\,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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MEDLINE=95347579; PubMed=7622034;
Grether M.E., Abrams J.M., Agapite J., White K., Steller H.;
"The head involution defective gene of Drosophila melanogaster functions in programmed cell death.";
Genes Dev. 9:1694-1708(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.3%; Score 43; DB 1; Length 407; 46.7%; Pred. No. 38; tive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF00109; ketoacyl-synt; l.
Pfam, PF02801; ketoacyl-synt_C; l.
Antibiotic biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 AA; 42549 MW; 59FC75A5A0D94632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HID_DROME STANDARD; PRT; 410 AA. 024106; QSVVD1; 01-NOV-1997 (Rel. 35, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 110-OCT-2003 (Rel. 42, Last annotation update) Head involution defective protein (Wrinkled protein).
                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AL939122; CAC44201.1; -.
PIR; S25841; S25841.
HSSP; P73283; IE5M.
InterPro; IPR000794; Ketoacyl_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X63449; CAA45044.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 HIPGRLLPQTÖPSTR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 46.7 hes 7; Conservative
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A BAIL 1 J. F., Aglayari A., M. H.-J., Andreas Ffamnor C., Baldwin D., Baller R.W., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno P.V., Benno
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7; Conservative 4 GNKSPHRDPAP 14

Matches

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Score 43; DB 1; Length 410; Pred. No. 38;

48.3%;

Query Match Best Local Similarity

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EMBL;
MEDLINE=21434063; PubMed=11549681;

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MEDLINE=21434063; PubMed=11549681;

MEDLINE=21434063; PubMed=11549681;

MEDLINE=21434063; PubMed=11549681;

MEDLINE=21434063; PubMed=1.6., Picard J.-Y., Josso N., di Clemente N.;

Matcosomal recessive segregation of a truncating mutation of a nti-Mullerian type II receptor in a family affected by the persistent Mullerian duct syndrome contrasts with its dominant negative activity in vitro.";

J. Clin. Endocrinol. Metab. 86:4390-4397(2001).

C. I. FUNCTION: Receptor for anti-Mullerian hormone.

I. CATALVITC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

C. I. SUBCELLULAR LOCATION: Type I membrane protein.

C. I. DISEASE: Defects in AMHR2 are the cause of persistent Mullerian duct syndrome type II (PMDS-2) [MMM:261550]; a form of male gued obsermabhroditism characterized by a failure of Mullerian duct regression in otherwise normal males.

C. I. SIMILARITY: Belongs to the Ser/Thr family of protein kinases. TGFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
MEDLINE=96028015; PubWed=7488027;
WISSET J.A., McLuskey A., van Beers T., Weghuis D.O., van Kessel A.G.,
Grootegoed J.A., Themmen A.P.N.;
"Structure and chromosomal localization of the human anti-mullerian
hormone type II receptor gene.";
Biochem. Biophys. Res. Commun. 215:1029-1036 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Masiakos P.T., Maclaughlin D.T., Maheswaran S., Teixeira J., Fuller A.F. Jr., Shah P.C., Kehas D.J., Kenneally M.K., Dombkowski D.M., Ha T.U., Preffer F.I., Donahoe P.K., "Human ovarian cancer, cell lines, and primary ascites cells express the human Mullerian inhibiting substance (MIS) type II receptor, bind, and are responsive to MIS.", Clin. Cancer Res. 5:3488-3499(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE 97026287; PubMed=8872466; Imbeaud S., Belville C., Messika-Zeitoun L., Rey R., di Clemente N., Josso N., Picard J.-Y.;
"A 27 base-pair deletion of the anti-Mullerian type II receptor gene is the most common cause of the persistent Mullerian duct syndrome."; Hum. Mol. Genet. 5:1269-1277(1996).
                                                                                                                 AMH2 HUMAN STANDARD; PRT; 573 AA.

Q16671, Q13762,

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2003 (Rel. 42, Last annotation update)

Anti-Mullerian hormone type II receptor precursor (BC 2.7.1.37) (AMH type II receptor) (MIS type II receptor)

AMHR2 OR AMHR2 OR AMHR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS PMDS-2 CYS-54; VAL-142; GLN-282; GLY-426; ALA-458; HIS-491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cate R.L., Picard J.-Y.;
"Insensityity to anti-mullerian hormone due to a mutation in the human anti-mullerian hormone receptor.";
Nat. Genet. 11:382-388(1995).
                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=96083884; PubMed=7493017; Imbeaud S., Faure E., Lamarre I., Mattei M.-G., di Clemente N. Tizard R., Carre-Eusebe D., Belville C., Tragethon L., Tonkin Nelson J., McAuliffe M., Bidart J.-M., Lababidi A., Josso N.,
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MEDLINE=20055680; PubMed=10589763;
24 GNSSPHNHPLP 34
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R MIM; 261550; -

R MIM; 261550; -

R GO; GO:0004872; F:receptor activity; TAS.

GO; GO:0007165; P:signal transduction; TAS.

R GO; GO:0007165; P:st Drukinae.

R InterPro; IPR0080719; Proc Kinae.

R InterPro; IPR008271; Ser thr. pkin.AS.

R Ffam; PR00069; pkinae; 1.

R PFAM; PR000601; Prot kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.

R PROSITE; PS0011; PROTEIN KINASE ST; RALSE NEG.

R Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding; Transmembrane; Glycoprotein; Signal; Pseudohermaphroditism;
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EXTRACELLULAR (POTENTIAL).
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V -> A (in PWDS-2).

FTIG=VAR 015530.

D -> H (in PWDS-2).

/FTIG=VAR 015531.

R -> C (in PWDS-2).

/FTIG=VAR 015532.

L -> V (IN REF 2; CAA62593).

M; 1347C10C2942FDBA CRC64;
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BY SIMILARITY.

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R -> C (in PMDS-2).
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G -> V (in PMDS-2).

H -> Q (in PMDS-2).

/FTId=VAR 015526.

FTID=VAR 015527.

R -> Q (in PMDS-2).

/FTID=VAR 015528.

D -> G (in PMDS-2).

/FTID=VAR 015529.
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EMBL: U29700; AAC50328.1; -.
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          ·.
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                              MEDIINE=92160395; PubMed=1789009; Brinaile B., Skala J., Goffeau A.; "The product of the YCR105 gene located on the chromosome III from Saccharomyces cerevisiae presents homologies to ATP-dependent
                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE ATP-DEPENDENT PERMEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
ATP-binding; Transmembrane; Glycoprotein; Transport; Signal.
          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X59720; CAA42328.1; -.
PIR; 919421; S19421.
PIRS, 919421.
S19421; S19421.
SGD; S0000604; ADP1.
GO; GO: 0005793; C: ndoplasmic reticulum; IDA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transporter.
                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
61.5%; Pred. No. 55; tive 2; Mismatches
                                                                                                                                      Probable ATP-dependent permease precursor.
ADP1 OR YCR011C OR YCR105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. POTENTIAL.
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ProDom; PD000006; ABC transporter; 1.
SWART; SM00382; AAA; 1.
                           3 PGNKSPHRDPAPR 15
                                      85 PGCESLHCDPSPR 97
         8; Conservative
                                                                                           STANDARD;
                                                                                                                                                                                                                                                           [east 7:867-872(1991)
Best Local Similarity
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                           ADP1 YEAST
P25371;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97202105, PubMed=9049632; Steelman S., Moskow J.J., Muzynski K., North C., Druck T., Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.; "Identification of a conserved family of Meisl-related homeobox
                                                                                                                                                                                                                                                                                      .<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0996B'; QONDW2;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homeobox protein Meis3 (Meis1-related protein 2) (Fragment).
MBIS3 OR MRG2.
                                                                                                                                                                                                                               Score 43; DB 1; Length 1049;
Pred. No. 1e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 7:142-156(1997).
--- SUBCELLULAR LOCATION: Nuclear (Probable).
--- SIMILARITY: Belongs to the TALE/MEIS homeobox family.
--- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                        MW; ABC9CE54BCFDF6A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blum H., Bauersachs S., Mewes H.-W., Weil B., Wiemann S. Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                           (GLCNAC. . .)
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EMBL; U68385; AAB19195.1; -.
HSSP; P40424; 1B72.
TRANSFAC; T03412; -.
Genew; HGNC:7002; MEIS3.
GO; GO:0005634; C:runcleus; ISS.
GO; GO:0008287; F:DNA binding; ISS.
GO; GO:0008283; P:cell proliferation; ISS.
InterPro; IPR091356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; FALSE_NEG.
PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Nuclear protein; Homeobox.
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                                                                                                                                                                                                                                            48.3%;
                                                                                                                                                                                                                                                                63.68;
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                                                                                                                                                                                                                                                                Sest Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   307 IPGYKSPSKOP 317
                                                                                                                                                                                                                                                                                                                                     2 LPGNKSPHRDP 12
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                                                                                                                                                                                             1049 AA;
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1114
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Convenue From N. N. Stath State Embryonic stem cells;

KARAN=CSTSBL/60; TISSUE=Embryonic stem cells;

KARAN=CSTSBL/60; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arakawa T., Sarawa M., Nishi K., Kyosawa H., Kondo S., Yamanaka I.,

A Adota K., Matsuda H.A., Ashburner M., Barlov S., Casavant T.,

A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

A Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

A Robin P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Byons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Saaki H., Sato K., Schoenbach C., Seya T., Shibate Y., Storch K.-F.,

M. Wynshaw-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Havashizaki V.;

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STRAIN=BALB/C; TISSUE=Testis; MEDLINE=21907217; PubMed=11909948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miki K., Eddy E.M.;
"Tumor necrosis factor receptor 1 is an ATPase regulated by silencer
of death domain.";
Mol. Cell. Biol. 22:2536-2543 (2002).
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                        ö
                ASP/GLU-RICH (ACIDIC).
HOMEOBOX (TALE-TYPE).
KM -> RP (IN REF. 2).
M -> I (IN REF. 2).
D -> V (IN REF. 2).
R -> P (IN REF. 2).
R -> P (IN REF. 2).
VAPPG -> FRAPA (IN REF. 2).
VARPG -> PERAPA (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAG4_MOUSE STANDARD; rri; r., .....
Q8C161, Q91VTF; Q9CMC2.
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
BAG-family molecular chaperone regulator-4 (Silencer of death
                                                                                                                                                                                                                                                          47.2%; Score 42; DB 1; Length 382; 53.8%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRALME-ETUBN, TISSUB-Brain, and Mammary gland;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                              41821 MW; A2C11BE8061FB718 CRC64;
                                                                                                                                                                                                                                                                                   Pred. No. 50;
1; Mismatches
SER/THR-RICH.
                                                                                                                                                                                                                                                                                   milarity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                    2 LPGNKSPHRDPAP 14
                                                                                                                                                                                                                                                                                                                                                                                             38 VPGPYGPHRPPOP 50
  256
266
331
176
209
245
245
358
367
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Mus musculus (Mouse).
                                                                                                                                                                                                                   382 AA;
                                                                                                                                                                                                                                                                               Local Similarity
hes 7; Conserv
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  217
259
269
175
209
245
DOMAIN
DOMAIN
DNA BIND
CONFLICT
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CONFLICT
SEQUENCE
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Matches
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hableh F.,
Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muxny D.M., Sodergren B.J., Lu X., Gibbs R.R.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rhiting M., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Mannar and mouse constance ""
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L->P: ABOLISHES INTERACTION WITH HSP70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A->P: ABOLISHES INTERACTION WITH HSP70 AND INFRSF1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

1- FUNCTION: Inhibits the chaperone activity of HSP70/HSC70 by promoting substrate release. Prevents constitutive TNFRSFIA signaling (By similarity).

1- SUBDNIT: Binds to the ATPase domain of HSP70/HSC chaperones. B to the death domain of TNFRSFI2 (By similarity). Binds to the ATPase domain of TNFRSFIA in the absence of TNF and thereby prevents binding of adapter molecules such as TRADD or TRAF2.

1- SUBCELLULAR LOCATION: Cytoplasmic.

1- SIMILARITY: Contains 1 BAG domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 60;
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Pfam; PF02179; BAG; 1.
SMART; SM00264; BAG; 1.
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es 7; Conservative
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387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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Matches
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                      S TITITITITIES SHEET BELL SOURCE COURT TO THE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SE
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Addams W.D., Celniker S.E., Holf R.A., Evens C.A., Gocayne J.D.,
Addams W.D., Celniker S.E., Holf R.A., Edshins R.A., Galle R.F.,
CGCTGE R.A., Echies S.E., Holf G., Milson C.R., Miklos G.L.G.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,
Admintides P.G., Edsker E.G., Helf G., Nelson C.R., Miklos G.L.G.,
Adrian K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayari A., A H.-J., Addrews-Ffannkoch C., Basaley B.M.,
Beeson K.H., Bencs P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beris K.C., Edsam D.A., Bulter H., Cadieu E., Ecoter A., Chandra I.,
Ra Cherry J.M., Cawley S., Dalnike C., Davenpour L.B., Davies P.,
RA Cherry J.M., Cawley S., Dalnike C., Bayamari D., Bow I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dalnike C., Rerriera S., Fleischmann W.,
RA Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Galbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Galbar W.M., Glasser K.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Kechum K.A.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kanjon J.A., Kechum K.A.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liux Y., Matter B., McAntcoh T.C., McLeod M.P., Norberson D.,
Merkulov G., Milshina N.V., Wobarriy J., Muzny D.M., Nelson D.L.,
Relazzolo M., Pittman G.S., Pan S., Pollard J., Puri, V. Saich T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith H.O.,
K. Mang C.-Y., Wassamman D.A., Weinsecheler F., Wang X.,
Wang Z.-Y., Wassamman D.A., Weinsecheler F., Was Sanich T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Sanich H.O.,
K. Matter G. M., Worley K.C., Wu D., Yang S., Yao Q.A.,
Wang Z.-Y., Wassamman D.A., Weinsecheler F., Span G.,
Steince Sequence of Drosophila melanogaster.",
Spier E., Shong E.C., Stapleton M., Shupser S.,
St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Chen T., Bunting M., Karim F.D., Thummel C.S.;
"Isolation and characterization of five Drosophila genes that encode
an ets-related DNA binding domain.";
Dev. Biol. 151:176-191(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 235-352 FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: EMBRYONIC VENTRAL NERVOUS SYSTEM AND 1 PAIR
NEURONS IN EACH THORACIC SEGMENT.
DNA-binding protein D-ETS-6.
ETS21C OR ETS-6 OR CG2914.
Drosophila melanogater (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoplera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ebhydroida, Drosophilidae, Drosophila.
NGBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DEVELOPMENTAL STACE: Expressed throughout development.
-!- SIMILARITY: Belongs to the ETS family.
-!- CAUTION: Ref.2 sequence differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frameshift in position 242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Canton-S; TISSUE=Larva;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        STRAIN-Berkeley;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutetation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCISTRONIC MRNA'S DERIVED FROM CALLIFLOWER MOSAIC VIRUS.
-i- SUBCELLULAR LOCATION: CYtoplasmic inclusion bodies.
-i- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INPECTED CE.
-i- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.2%; Score 42; DB 1; Length 475; 53.8%; Pred. No. 63; tive 2; Mismatches 4; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 1; Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Franck A., Guilley H., Jonard G., Richards K., Hirth L., "Nucleotide sequence of cauliflower mosaic virus DNA."; Cell 21:285-294(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cauliflower mosaic virus (strain Strasbourg) (CaMV).
Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002609; Caulimo_VI.
InterPro; IPR009027; L9 N like.
Pfam; PF01693; Caulimo_VI; l.
Trans-acting factor; Translation regulation.
SEQUENCE 520 AA; 57992 MW; DD41D89DD2D5E8EI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0D382C41C03B1502 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Inclusion body matrix protein (Viroplasmin).
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETS-DOMAIN
                 EMEL; AE003589; AAF51484.1; -... EMEL; M88475; AAA28452.1; ALT_FRAME. HSSP; Q01543; IFUI. FlyBase; FBG0005660; Ets21C. InterPro; IPR000418; Ets. InterPro; IPR002341; HSP_ETS. InterPro; IPR00118; SAM_PNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00345; ETS_DOMAIN_1; 1. PROSITE; PS00346; ETS_DOMAIN_2; 1. PS0051TE; PS50061; ETS_DOMAIN_3; 1. DNA-Dinding; Nuclear protein.

DNA_BIND 255 335 ETS_DOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=81001865; PubMed=7407912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 AA; 51802 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                      Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
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Best Local Similarity 53.0.
7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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cauliflower mosaic virus.";
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                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A04160;
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P13218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93383405; PubMed-8372449; Wintermantell W.M., Anderson E.J., Schoelz J.E.; ilflower mosaic virus "identification of domains within gene VI of cauliflower mosaic virus that influence systemic infection of Nicotiana bigelovii in a light-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Balazs E., Guilley H., Jonard G., Richards K.; "Nucleotide sequence of DNA from an altered-virulence isolate D/H of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology 196:789-798 (1993).

-!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCISTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
-!- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
-!- MISCELLANBOORS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CEST, SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
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Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; Retroid viruses; Caulimoviridae; Caulimovirus. NCBI _ TaxID=10645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01693; Caulimo \overline{\rm V17} 1. Translation regulation. Translation regulation according factor, Translation regulation SEQUENCE 520 AA; 57976 WW; 4BR110D55BBB9647 CRC64;
                                                                                                                                                                                                                                                                                                                           Cauliflower mosaic virus (strain W260) (CaMV).
Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
01-ANG-1991 (Rel. 19; Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
Inclusion body matrix protein (Viroplasmin).
                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Inclusion body matrix protein (Viroplasmin).
                                                                                                                                                                   520 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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MEDLINE-83106468; PubMed=7152260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L09053; AAA46360.1; -.
InterPro; IPR002609; Caulimo VI.
InterPro; IPR009027; L9 N like.
                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
15-JUL-1999 (Rel. 38, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 58.3
les 7; Conservative
                                                    228 GTKKPSSDPAPK 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
            GNKSPHRDPAPR 15
                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dependent manner."
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=31558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBMP CAMVD
P03557;
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Matches
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                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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Gene 19:239-249(1982).

--- FUNCTION: ENRANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCISTRONIC MRNA'S DERLYDE FROM CAULIFLOWER MOSAIC VIRUS.

---- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.

---- MISCELLAMEQUES: THE INCLUSION BODIES ARE THE SITE OF VIRLE DNA SYNTHESIS, VIRLON ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.

---- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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-!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON

-!- FUNCTIONIC MENA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.

-!- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.

-!- MISCELLANBOUST THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA.

SYNTHESIS, VIRION ASSEMBLY AND ACCUMILATION IN THE INFECTED CE.

-!- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Length 522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cauliflower mosaic virus (strain S-Japan) (CaMV). Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.NCBI_TaxID=10646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002609; Caulimo_VI.
InterPro; IPR009027; L9 N like.
Pfam, PF01693; Caulimo_VI; l.
SEQUENCE 522 AA; 58285 MW; F87CB62C1F30DD57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
115-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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InterPro; IRR002609; Caulimo VI.
InterPro; IPR009027; L9 N like.
Pfam; PF01693; Caulimo VI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X14911; CAA33037.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
7; Conserva
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SIGNAL
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                                                                                                                                            AMPR RAT STANDARD; PRT; 557 AA.

70(2893; 063045; 09R0A7;
16-0CT-2001 (Rel. 40, Last sequence update)
115-0CT-2001 (Rel. 43, Last annotation update)
115-MAR-2004 (Rel. 43, Last annotation update)
Anti-Mullerian hormone type II receptor precursor (EC 2.7.1.37) (AMH type II receptor) (MIS type II receptor) (MIS type II receptor)
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                         MEDLINE=96107132; PubMed=8536608;
Teixeira J., He W.W., Shah P.C., Morikawa N., Lee M.M., Catlin B.A., Hudson P.L., Wing J., Maclaughlin D.T., Donahoe P.K.;
"Developmental expression of a candidate mullerian inhibiting substance type II receptor.";
Endocrinology 137:160-165(1996).
                                                      Gaps
                                                      ö
                           / Match 17.2%; Score 42; DB 1; Length 522; Local Similarity 58.3%; Pred. No. 69; 1; Conservative 1; Mismatches 4; Indels
Trans-acting factor; Translation regulation.
SEQUENCE 522 AA; 58410 MW; 8EB136BB17ED408A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley;
MEDLINE=20040636; PubMed=10570158;
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94163972; PubMed=8119126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-16 FROM N.A.
                                                                                                 228 GTKKPSSDPAPK 239
                                                                            4 GNKSPHRDPAPR 15
                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testis;
                                  Query Match
                                              Best Loca
Matches
                                                                                                                                 RESULT 24
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EMBL; X71916; CAA50731.1; -. EMBL; AF092445; AAC64138.1; -. EMBL; U42427; AAC52343.1; -.

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STRAIN-FVB/N, TISSUE-Salivary gland;

STRAIN-FVB/N, TISSUE-Salivary gland;

XX MEDLINE=2238827; PubMed=12477932;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Learner R.D., Colling F.S., Margner L., Shemmen C.M., Schuler G.D., Rlausner R.D., Colling F.S., Margner L., Shemmen C.M., Schuler G.D., A lischnil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., In Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L., Brownstein M.J., Usdin T.B., Toshhyuki S., Carninci P., Brange S.A., Inquellano N.A., Perters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.A., Wolley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., A Willalon D.K., Macham A., Rodrigues S., Sanchez A., Aniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                              ANTI-MULLERIAN HORMONE TYPE II RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20480369; PubMed-11025217; Granadino B., Arias-de-la-Fuente C., Perez-Sanchez C., Parraga M., Lopez-Fernandez L.A., del Mazo J., Rey-Campos J.; "Fhx (Foxj2) expression is activated during spermatogenesis and very
InterPro; IRR000472; Activin receptor.
InterPro; IRR000471; Prot Kinase.
InterPro; IRR0004271; Ser_thr_pkin_AS.
Pfam; PR01064; Activin recp; 1.
Pfam; PR01069; pkinase; 1.
ProDom; PD000001; Prot Kinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG.
PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG.
RECEPTO; PS50011; PROTEIN KINASE_DOM; 1.
RECEPTO; Transferase; Serine/threonine-protein kinase; ATP-binding; Transmembrane; Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                           PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 1; Length 557;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REDEE9COC32EBDD5 CRC64;
                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Forkhead box protein J2 (Fork head homologous X).
FOXLO OR FHX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               early in embryonic development."; Mech. Dev. 97:157-160(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 PGCESLHCDPVPR 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Mouse)
                                                                                                                                                                                                                                                                                                  166
166
201
201
228
331
66
119
557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FXJ2 MOUSE
Q9ES18;
                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CONFLICT
SEQUENCE
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NON TER
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                                                                                                                                                                                             Membrane.
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                  BRARE
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                  AXN2_
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                 Wang X., Herberg F.W., Laue M.M., Wullner C., Hu B.,
Petrasch-Parwez E., Kilimann M.W.;
"Neurobeachin: a protein kinase A-anchoring, beige/Chediak-Higashi
"Neurobeachin: a protein in neuronal membrane traffic.";
J. Neurosci. 20:8551-8565(2000).
-:- FUNCTION: Binds to type II regulatory subunits of protein kinase A
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes; Phasianidae, Phasianinae;
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                          Score 42; DB 1; Length 565;
Pred. No. 75;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                     POLY-GLN.
9178AFF3F9227AD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                               -!- SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                   793 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                     POLY-SER.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20556611; PubMed=11102458;
                                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, List sequ
10-0CT-2003 (Rel. 42, List amon
Neurobeachin protein (Fragment)
                                                                                                                                                                                                                                                                                                     306 314 PC
565 AA; 61569 MW;
                                                                                                                                                              EMBL; AF253052; AAG30406.1; -.
EMBL; BC040395; AAH40395.1; -.
                                                                                                                                                                                                                                                                                                                              47.2%;
                                                                                                                                                                                                                                                                                                                                     ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                             470 HMPQQGGSHRPPAP 483
                                                                                                                                                                                                                                                                                                                                                              1 HLPGNKSPHRDPAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                               HSSP; Q63245; 2HFH.
                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBL_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                     CHICK
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            090005;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
and anchors/targets them to the membrane. May anchor the kinase cycoskeletal and/or organelle-associated proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                   SUBUNIT: Interacts with RII subunit of PKA (By similarity) SUBCELLUIAR LOCATION: Cytoplasmic and membrane-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 793 AA; 87803 MW; 19F5AC6C49A7F2A2 CRC64;
                                                                                                                                                                                                   SIMILARITY: Belongs to the neurobeachin family.
                                                                                                                                                                   -!- TISSUE SPECIFICITY: Forebrain and cerebellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.2%; Score 42; DB 1; I
58.3%; Pred. No. 1.1e+02;
tive 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P57095;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-WRR-2004 (Rel. 43, Last annotation update)
Axin 2 (Axis inhibition protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PS50197; BEACH; PARTIAL.
PROSITE; PS00678; WD REPEATS 1; PARTIAL.
PROSITE; PS50082; WD REPEATS 2; PARTIAL.
PROSITE; PS50084; WD_REPEATS_REGION; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  812 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (By similarity).
-!- SIMILARITY: Contains 1 RGS domain.
-!- SIMILARITY: Contains 1 DIX domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20171051; PubMed=10704853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, Y18277; CAC18801.1; -.
InterPro; IPR000409; Beige_BEACH.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::||| || :||
621 NVPGNLSPIKDP 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 58.3
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HLPGNKSPHRDP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7955;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P SEQUENCE FROM NA.

YEQUINCE SOUTH A.R., Collins J.E., Bruskiewich R., Beare D.M.,
Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Babage A.K.,
Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Babage A.K.,
Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
Bard C.P., Blakey S.B., Bridgeman A.M., Buck D., Burgess J.,
Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
A Conroy D., Corby N.R., Cole C.G., Collier R.E., Connor R.,
Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Cox J., Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
A Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE—99156230; PubMed=10046485;
Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                 GSK3B BINDING SITE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                         47.2%; Score 42; DB 1; Length 812; 46.7%; Pred. No. 1.1e+02; Live 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                BETA-CATENIN BINDING SITE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46E5ADA6DE2240CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9Y6X9; Q9UP28; Q9Y6V2;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
20-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               970 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-SER.
                                                                                                                                     InterPro; IPR001158; DIX.
InterPro; IPR000342; Regl_Gprotein.
                                                                                                 HSSP; P49799; IAGR.
ZFIN; ZDB-GENE-000403-2; axin2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              730 812 D
812 AA; 91496 MW;
                                                                            EMBL; AB032263; BAA92440.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457 HSPRSRSPEQRPLPR 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HLPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                              Pfam; PF00778; DIX; 1.
Pfam; PF00615; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                               203
415
467
                                                                                                                                                                                                                                                                                                                                                                                                                                                419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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haird G.K., inageced C.F. inverseba M. Matthess I.H., McCorn D.M.,
McMichay J.D. Mugheregold C.P., Willies S.M., McDilance B.J.C.J.,
Codello.K., Pavitt R., Pearce A.V., Pearson D., Phillingce B.J.C.J.,
Codello.K., Pavitt R., Pearce A.V., Pearson D., Phillingce B.J.C.J.,
Codello.K., Pavitt R., Pearce A.V., Pearson D., Phillingce B.J.C.J.,
Codello.K., Pavitt R., Pearce A.V., Pearson D., Phillingce B.J.C.J.,
Scott. C.E., Schra H.K., Skuc C.D., Smalley S., Smith M.L.,
Scott C.E., Schra H.K., Skuc C.D., Smalley S., Smith M.L.,
Scott C.E., Schra H.K., Skuc C.D., Smalley S., Smith M.L.,
Scott C.E., Schra H.K., Skuc C.D., Smalley S., Smith M.L.,
Mandling S., Mandling M. M. Mallis J.M. Millish M.L.,
Minchina S., Mally R., Pavitt R., Skuc C.D., Smalley S., Smith M.L.,
Schramma S., Shindry K., Vorbizaki Y., Acki N., Mitsuyama S., Langer J., Park M. Minchina S., Langer J., Park M. Minchina S., Langer J., Park M. Minchina S., Langer J., Park M. Minchina S., Langer J., Park M. Minchina S., Langer J., Park M. Minchina S., Langer J., Park M. Minchina S., Langer J., Park M. Minchina S., Langer J., Park M. Minchina S., Langer J., Park M. Minchina S., Langer J., Park M. Minchina D., Waller C., Manaley A., Wohldeann D., Werson S., Langer J., Park M. Minchina D., Schoole J., Schoole D., Graves T., Hawkins J.,
School J.A., Shillar M., Woller C., Manaley A., Wohldeann D., Pearle M., Minchina D., Seronesi B., Franson II., Tapia I., Buck C.E.,
School J.A., Shillar M., Waller C., Manaley A., Wohldeann D., Pearle M., Minchina J., School B. J.,

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STRAIN=C57BL/6J; TISSUB=Cerebellum;

MEDINTRE-2534683; Pubmed=1246681;

KASUKARY Y. Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Najai K., Tomaru Y., Haegawa Y., Nogami H., Schombach C., Golbori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

A Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Gaseterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pertea G., Pesole G.,

Nagashima T., Numata K., Pontlus J.U., Qi D., Ramachandran S.,

Nagashima T., Numatus K., Pontlus J.U., Qi D., Ramachandran S.,

Nagashima T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang X., Herberg F.W., Lave M.M., Wullner C., Hu B.,
Perrasch-Parwez E., Kilimann M.W.;
Neurobeachin: a protein kinase A-anchoring, beige/Chediak-Higashi
protein homolog implicated in neuronal membrane traffic.";
J. Neurosci. 20:8551-8565(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEGUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
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                                                                                                                                                                                                                                            47.2%; Score 42; DB 1; Length 970; 50.0%; Pred, No. 1.3e+02; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDEPNI; QBC931; QDEPNO; QDEPNO; QDWVN9; 10-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last sequence update) Neurobeachin protein (Lysosomal trafficking regulator 2) NBEA OR LYST2
                                                                                                                                                                                                        970 AA; 110724 MW; 459161807BBB53F6 CRC64;
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COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
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            EMBL; AB020659; BAA74875.1; -.
EMBL; AC004542; AAC12554.1; AIT_SEQ.
EMBL; BC012257; AAH19257.1; -.
EMBL; AL133637; CAB63760.1; -.
EMBL; T43455; T43455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
MEDLINE=22150869; PubMed=12160729;
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MEDLINE=20556611; PubMed=11102458;
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638 LPNSKSPREVPSPK 651
                                                                                                                                                                                                                                                                                                                        2 LPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                Local Similarity 50.0
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                                                                                                                            220
485
679
904
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                 Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wanger, L., Wahlestedt C., Wang Y., Watenabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Haza A., Hashizume W., Imceni K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Hayashizaki Y., Yoshino M., Waterston R., Lander B.S., Rogers J., Birney E., Hayashizaki Y., Waterston R., Lander B.S., Rogers J., "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tchernev V.T., McMurtrie E.B., Nguyen Q.A., Mishra V.S., Barbosa M.D.F.S., McIndoe R., Kingsmore S.F.; "Identification of LYS72, a brain-specific member of the Chediak-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isoid=09EPN1-2; Sequence=VSP_050540;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9EPN1-3; Sequence=VSP_050541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBOId=Q9EPN1-1; Sequence=Displayed;
                                                                                                                                                                                                   SEQUENCE OF 2220-2936 FROM N.A.
                                                                                                                                                                        Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=4;
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activity; IDA.

MGD; MGI:1147075; Nbea.
GO; GO:0005829; C:cytcsol; IDA.
GO; GO:0005802; C:cytcsol; IDA.
GO; GO:0005802; C:Golgi trans face; IDA.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0005079; F:protein kinase A anchoring a
GO; GO:0019901; F:protein kinase binding; IDA.

EMBL; AK043125; BAC31466.1; -. EMBL; AF072372; AAD41634.1; -. EMBL; Y18276; CAC18811.1; -.
EMBL; Y18276; CAC18812.1; -.
EMBL; Y18276; CAC18813.1; -.

SEQUENCE FROM N.A. (ISOFORM 2)

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TISSUBERTAIN, and Spleen;
MEDLINE=22150869; PubMed=12160729;
Dyomin V.G., Chaganti S.R., Dyomina K., Palanisamy N., Murty V.V.V.S.,
Dalla-Favera R., Chaganti R.S.K.;
Dalla-Faveri R., Chaganti R.S.K.;
probleins with presumptive protein kinase A anchoring function.";
denomics 80:158-165(2002).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NBEA HUMAN STANDARD; PRI; 2946 AA.
QBNFP9; QSHCM8; QSNSUI; QSNW98; Q9xGJI;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Neurobeachin protein (Lysosomal trafficking regulator 2) (BCL8B
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                                                                                                               | Pfam; Frvc. | Pfam; Frvc. | Pfam; Frvc. | Prodom; PD007848; Dec. | R Prodom; PD00720; W040; 4. |
| R PROSITE; PS000320; W040; 4. |
| R PROSITE; PS000420; WD REPEATS 1; FALSE NEG. |
| R PROSITE; PS00042; WD REPEATS 2; FALSE NEG. |
| R PROSITE; PS050294; WD REPEATS REGION; 1. |
| KW Repeat; WD repeat; Membrane; Alternative splicing. |
| FT REPEAT 1316 1358 WD 1. |
| FT REPEAT 2708 2808 WD 3. |
| FT REPEAT 2708 2808 WD 3. |
| FT REPEAT 2708 2808 WD 4. |
| FT REPEAT 2708 2899 WD 4. |
| FT REPEAT 2708 2899 WD 4. |
| FT REPEAT 2708 2899 WD 5. |
| FT REPEAT 2708 2899 WD 5. |
| FT REPEAT 2708 2899 WD 5. |
| FT REPEAT 2708 2899 WD 5. |
| FT REPEAT 2708 2899 WD 6. |
| FT REPEAT 2850 2899 WD 6. |
| FT REPEAT 2850 2899 WD 6. |
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| FT REPEAT 2850 2899 WD 7. |
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| FTId=VSP 050540.
| Missing (in isoform 3).
| FTId=VSP 050541.
| Missing (in isoform 4).
| FTId=VSP 050541.
| FTID=VSP 050542.
| FM -> SR (IN REF. 2).
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| D -> H (IN REF. 2).
GO; GO:0006892; P:post-Golgi transport; NAS.
InterPro; PR008983; ARM.
InterPro; IPR000409; Beige_BEACH.
InterPro; IPR001680; WD40.
Pfam; PF002138; Beach; 1.
Pfam; PF00400; WD40; 5.
Pfam; PF00400; WD40; 5.
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1513 NVPGNLSPIKDP 1524
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note=No experimental confirmation available;
TISSUE SPECIFICITY: Predominant in many brain structures. Also expressed at medium levels in spleen, thymus, prostate, testis and ovary. Low level expression is seen in heart, kidney, pancreas, skeletal muscle and intestine.
DOMAIN: RII-alpha binding site, predicted to form an amphipathic helix, could participate in protein-protein interactions with a complementary surface on the R-subunit dimer (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1919-2946 FROM N.A. (ISOFORM 1).
MEDLINE=20450683; PubMed=10997877;
Nagaee T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 7:273-281(2000).
                                   Duesterhoeft A., Lauber J., Mewes H.-W., Gassenhuber J., Wiemann S.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

similarity).
Similarity).
Similarity: Belongs to the neurobeachin family.
SIMILARITY: Contains 1 BEACH downin.
SIMILARITY: Contains 5 WD repeats.
CAUTION: Ref.3 sequence differs from that shown due to a stop codon in position 762.
CAUTION: Ref.5 sequence differs from that shown due to a frameshift in position 2900.

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TChernev V.T., McMurtrie E.B., Nguyen Q.A., Mishra V.S.,
Barbosa M.D.F.S., McIndoe R., Kingsmore S.F.;
"Identification of LYST2, a brain-specific member of the Chediak-Higashi syndrome gene family.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Interacts with RII subunit of PKA (By similarity).
                                                                                                                                                                                                                   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikkawa T., Magai K., Sugiano S., Takabashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakanatau A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
-!- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                SEQUENCE OF 606-1118 FROM N.A.
                                                                                                                                                                                           TISSUE=Embryonic head;
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TISSUE=Testis;
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GAG_BLVJ
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Coulston J., Naif H., Brandon R., Kumar S., Khan S., Daniel R.C.W.,
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01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ads polyprotein [Contains: Core protein P15 (Matrix protein); Core protein P24; Core protein P12].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00138; Beach; 1.
Pfam; PF00400; WD40; 5.
Probon; PD07484; Beige BEACH; 1.
PROSITE; PS0197; BEACH; 1.
PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
PROSITE; PS0094; WD_REPEATS_2; FALSE_NEG.
RROSITE; PS0094; WD_REPEATS_REGION; 1.
REPEAT; MD_REPEATS_REGION; 1.
REPEAT; MD_REPEATS_REGION; 1.
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 1; Length 2946; Pred. No. 4.3e+02; 3; Mismatches 2; Indels
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S -> N (IN REF. 5).
S -> T (IN REF. 5).
MW; 6CDA70D61F1E255E CRC64;
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WD 3.
WD 4.
WD 5.
Missing (in isoform 2).
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                                         R EMBL; ACKO1059; BAA91485.1; -... EMBL; ABA047485.1; -.. EMBL; ABA047674; BAB13370.1; -.. EMBL; AF072371; AAA41633.1; ALT_FRAME. PDB; 1MI1; 27-SEP-02. Genew; HGNC:7648; NEEA.
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     send an email to license@isb-sib.ch)
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1523 NVPGNLSPIKDP 1534
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Best Local Similarity 58.5-
The 7; Conservative
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                                                                                MEDLINE=96283625; PubMed=8670827;
Matthews S., Mixhailov M., Burny A., Roy P.;
Matthews S., Mixhailov M., Burny A., Roy P.;
"The solution structure of the bovine leukaemia virus matrix protein and similarity with lentiviral matrix proteins.";
EMBO J. 15:3267-3274(1996).
--- SIMILARITY: VERY STRONG, WITH THE BOVINE LEUKEMIA VIRUS GAG POLYPROTEIN FROM OTHER ISOLATES.
--- SIMILARITY: Contains 2 CCHC-type zinc fingers.
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10-OCT-2003 (Rel. 42, Last annotation update)
GAG polyprotein [Contains: Core protein P15 (Matrix protein); Core protein P24; Core protein P12].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R DIR; JO0554; FOLJGA.

R InterPro; IPR001139; Gag_p19.

R InterPro; IPR00121; Gag_p29.

R InterPro; IPR008016; Retrow_capsid_C.

R InterPro; IPR008019; Retrow_capsid_N.

R InterPro; IPR008018; Znf_CCHC.

R Fam; PF00228; Gag_p19; T.

R Pfam; PF00509; Zf_CCHC; 2.

R Pfam; PF00098; zf_CCHC; 2.

R RFINYS; PR00999; Zf_CCHC; 2.

R RRINYS; RR00343; Znf_CCHC; 1.

R RROSITE; PS50158; Znf_CCHC; 1.

R PROSITE; PS50158; Znf_CCHC; 1.
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CORE PROTEIN P24 (BY SIMILARITY).
CORE PROTEIN P24 (GENOME-BINDING PR
WITH REPEATED SEQUENCES).
CCHC-TYPE 1.
CCHC-TYPE 2.
CCHC-TYPE 2.
CCHC-TYPE 2.
CCHC-TYPE 2.
CCHC-TYPE 3.
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Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
VCBI_TaxID=11907;
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MEDLINE=85140159; PubMed=2983308;
Gen. Virol. 71:1737-1746(1990)
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Best Local Similarity 56.2.
Best Local 9; Conservative
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Zinc-finger; Lipoprotein.
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392 AA;
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NCBI_TaxID=7719;
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SEQUENCE
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                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                  "Complete nucleotide sequence of the genome of bovine leukemia virus: its evolutionary relationship to other retroviruses."; Proc. Natl. Acad. Sci. U.S.A. 82:677-681(1985).
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CORE PROTEIN P24.

CORE PROTEIN P12 (GENOME-BINDING PROTEIN P12 (GENOME-BINDING PROTEIN CCHC-TYPE 1.

CCHC-TYPE 1.
                                                                                                                                                                             MEDLINE-83210199; PubMed-6303852;
Copeland T.D., Morgan M.A., Oroszlan S.;
"Complete amino acid sequence of the nucleic acid-binding protein of
bovine leukemia virus.";
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Sagata N., Yasunaga T., Tsuzuku-Kawamura J., Ohishi K., Ogawa Y.,
                                                                                                           "Amino-terminal sequence of bovine leukemia virus major internal protein: homology with mammalian type C virus p30 structural
                                                                                                                                                                                                                       FEBS Lett. 156:37-40(1983).
-!- SIMILARITY: VERY STRONG, WITH THE BOVINE LEUKEMIA VIRUS GAG POLYPROTEIN PROM OTHER ISOLATES.
-!- SIMILARITY: Contains 2 CCHC-cype zinc fingers.
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SMART; SM00343; ZnF C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 1.
Core protein; Polyprotein; Phosphorylation; Repeat; Myristate;
Zinc-finger; Lipoprotein.
                                                                 SEQUENCE OF 110-164.
MEDLINE=79223918; PubMed=223166;
Oroszlan S., Copeland T.D., Henderson L.E., Stephenson J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 392;
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                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 76:2996-3000(1979)
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InterPro; IPR008919; Retroy capsid
InterPro; IPR001878; Znf CCHC.
Pfam, PF02228; Gag_pl9; I.
Pfam, PF00607; Gag_p24; I.
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InterPro; IPR003139; Gag_p19.
InterPro; IPR000721; Gag_p24.
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                                                                                                                                                                  SEQUENCE OF 324-392.
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367
392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                    Gilden R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠.
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P06486;
                                                                                                                                   proteins."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
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ID US10_H8
AC P06486
DT 01-JAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=84169548; PubMed=6324121;

Rixon F.J., McGeoch D.J.;

Rixon F.J., McGeoch D.J.;

Rixon F.J., McGeoch D.J.;

Rixon F.J., McGeoch D.J.;

Rixon F.J., McGeoch D.J.;

Rixon F.J., McGeoch D.J.;

Rixon F.J., McGeoch D.J.;

Rixon F.J., McGeoch D.J.;

Rixon F.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J., McGeoch G.J.,
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Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=85160822; PubMed=2984429;
McGeoch D.J., Dolan A., Donald S., Rixon F.J.;
Sequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1.";
J. Mol. Biol. 181:1-13(1985).
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Bird A.P., Clark V., Jones S.J.M., Leitgeb S., Lennard N.,
Tweedie S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
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12D01B0E7C920EA3 CRC64;
                                                                                                                                                                                                   Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1;
Pred. No. 56;
01-JAN-1988 (Rel. 06, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Virion protein US10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 AA.
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                                                                                                                                                                                                                                                                                                             Alphaherpesvirinae; Simplexvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X14112; CAA32275.1; -. EMBL, X02138; CAA256126.1; -. EMBL, X00428; CAA25126.1; -. EMBL, L00036; AAA96678.1; -. PIR, A05242; QQBE07. InterPro; IPR008160; Collagen. InterPro; IPR009160; Collagen. Pfam; PP02053; Gene66; 1. Prints; PR00957; GENE66.
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312 AA; 34055 MW;
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58.38;
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Guery Match
Best Local Similarity 58.30,
7, Conservative
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                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10299;
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Gaps

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46.1%; Score 41; DB 1; Length 520; 58.3%; Pred. No. 97; tive 1; Mismatches 4; Indels

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InterPro; IPR002609; Caulimo_VI.
InterPro; IPR009027; L9 N like.
Pfam; PF01693; Caulimo_VI; I.
Trans-acting factor; Translation regulation.
SEQUENCE 520 AA; 58140 MW; 6884E2952B6AA5D9 CRC64;
                                                                                                                                                                                                                                                                                        228 GTKRPSSDPAPK 239
                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                           4 GNKSPHRDPAPR 15
                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 IBMP_CAMVC
P03558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Messing J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAMVE
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IBMP_CAMVE
ID_IBMP_C
                                                                                                                                                                                                                                                                                                                                                                    T 36
CAMVC
                                                                                                                                                                         Best Loca
Matches
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       张明珠 $ $
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                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00133; trans. 1; 1.
PRINTS; PR00984; TRNASINTHILE.
PROSITE; PS00178; AA, TRNA, LIGASE I; PARTIAL.
Aminoacyl-trnA synthétase; Protein biosynthesis; Ligase; ATP-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                           -!- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(IIe) = AMP + diphosphate + L-isoleucyl-tRNA(IIe). -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCISTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
-i- SUBCELGULAR LOCATION: CYLOPLASMIC inclusion bodies.
-i- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CE -:- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDIJNE=92216136; PubMed=2134858;
MEDIJNE=92216136; PubMed=2134858;
MEDIJNE=92216136; PubMed=2134858;
Medific symptom oraliflower mosaic virus gene VI confer host-specific symptom changes.";
Mol. Plant Microbe Interact. 3:341-345(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.1%; Score 41; DB 1; Length 413; 70.0%; Pred. No. 76;
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     Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cauliflower mosaic virus (strain D4) (CaMV).
Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
NCBI_TaxID=10642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 301 ATP (BY SIMILARITY).
413 AA; 46895 MW; 69B098FD71CL00CE CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                        INTERPOS IPR002300; TRNA-SYML la.
INTERPOS, IPR001412; TRNA-SYML I.
INTERPOS, IPR002301; TRNA-SYML ile.
INTERPOS, IPR009008; Valks_IleRs_edit.
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01-AUG-1991 (Rel. 19, Last sequ
15-JUL-1999 (Rel. 38, Last arm
                                                                                                                                                                                                                                                                                                                         EMBL; Z80904; CAB02584.1; -. PIR; T31663; T31663.
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Best Local Similarity 70...
7; Conservative
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IBMP C P22847
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                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-82014878; PubMed=6269062;
Gardner R.C., Howarth A.J., Hahn P., Brown-Luedi M., Shepherd R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                       Cauliflower mosaic virus (strain CM-1841) (CaMV).
Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
NCBL_TaxID=10644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 AA; 57907 MW; F02E7885699B2F49 CRC64;
                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
Inclusion body matrix protein (Viroplasmin).
520 AA
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01-UUL-1993 (Rel. 26, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
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1; Mismatches
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PRT;
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Interpro; IPR002609; Caulimo VI.
Interpro; IPR009027; L9 N like.
Pfam; PF01693; Caulimo VI; 1.
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                                                                                                            MEDLINE=93154593; PubMed=8428667;
Chenault K.D., Melcher U.K.;
"The complete nucleotide sequence of cauliflower mosaic virus isolate
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-!- FUNCTION: ENHANDES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCISTRONIC MENA'S DERIVED FROM CAULIFLOWER MOSALC VIRUS.
-!- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
-!- MISCELLAMEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRIOM ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
-!- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
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                                                                                                                                                                              Gene 123:255-257 (1993).

-!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCISTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
-!- SUBCELLULAR LOCATION: CYCOPLASMIC inclusion bodies.
-!- MISCELLANBOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INPECTED CE.
-!- SIMILARITY: Belongs to the caulimoviruses viroplasmin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chenault K.D., Steffens D.L., Melcher U.K.; "Nucleotide sequence of cauliflower mosaic virus isolate NY8153.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.1%; Score 41; DB 1; Length 520; ilarity 58.3%; Pred. No. 97; Conservative 1; Mismatches 4; Indels
                                       Cauliflower mosaic virus (strain BBC) (CaMV).
Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cauliflower mosaic virus (strain NY8153) (CaMV).
Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
NCBI_TaxID=31557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
          inclusion body matrix protein (Viroplasmin).
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InterPro; PR002609; Caulimo VI.
InterPro; IPR009027; L9 N like.
Pfam; PF01693; Caulimo VI; 1.
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                                                                    NCBI_TaxID=31556;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
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Usage by
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InterPro; IPR002609; Caulimo_VI.
InterPro; IRR009027; L9 N like.
Pfam; PF01693; Caulimo_VI; I.
Trans-acting factor; Translation regulation.
SEQUENCE 520 AA; 57799 MW; 3459A028087CB41D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1;
Pred. No. 97;
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-!- SIMILARITY: Belongs to the fliF family.
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46.1%; Score 41; DB
Best Local Similarity 63.6%; Pred. No. 1e+0
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                           entities requires a license agreement (Son send an email to license@isb-sib.ch).
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InterPro; IPR000667; FlgMring FLIF.
InterPro; IPR006182; YscJ_FliF.
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PRINTS; PR01009; FLGMRINGFLIF.
TIGREAMS; TIGR00206; fliF; 1.
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Best Local Similarity 58.3-
Transport 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ansorge W., Wirkner U., Mewes H.-W., Weil B., Wiemann S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Transcriptional activator. Able to bind to two different type of DNA binding sites. Isoform FOXJ2.L behaves as a more potent transactivator than FOXJ2.S.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perez-Sanchez C., Gomez-Ferreria M.A., de la Fuente C.A., Granadino B., Velasco G., Esteban A., Rey-Campos J.;
J. Biol. Chem. 275.12909-12916(2000).

(2)
SEQUENCE FROM N.A. (ISOFORM FOXJZ.S).
MEDLINE=20425082; Pubmed=10966786;
Perez-Sanchez C., de la Fuente C.A., Gomez-Ferreria M.A.,
Granadino B., Rey-Campos J.;
Ferez-Sanchez C., de la Fuente C.A., Gomez-Ferreria M.A.,
FRIX.L and FHX.S, two isoforms of the human fork-head factor FHX (FOXJZ) with differential activity.";
                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing, Named isoforms=2;
Name=FOXJ2.L; Synonyms=FHX.L;
IsoId=Q9P0X8-1; Sequence=Displayed;
Name=FOXJ2.S; Synonyms=FHX.S;
IsoId=Q9P0X8-2; Sequence=VSP 001544;
IsoId=Q9P0X8-2; Sequence=VSP 01544;
-:- TISSUB SPECIFICITY: Widely expressed.
-:- SIMILARITY: Contains 1 fork-head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 458-574 FROM N.A. (ISOFORM FOXJ2.L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF155132; AAF65927.1; -.
EMBL; AF155133; AAK49016.1; -.
EMBL; AL161978; CAB82315.1; -.
EMBL; AL161978; CAB82315.1; -.
HSSP; Q63245; ZHFH.
TRANSFAC; T04109; -.
TRANSFAC; T04171; -.
TRANSFAC; T04171; -.
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TRANSFAC; T04171; -.
TRANSFAC; T04171; -.
TRANSFAC; T04171; -.
TRANSFAC; T04171; -.
TRANSFAC; T04171; -.
TRANSFAC; T04171; -.
TRANSFAC; T04171; -.
FROMOSS; FORKHEAD.
PROBITE; PS00657; FORK_HEAD_1; FALSE_NEG.
                                                                                                                                                                                                                           574 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM FOXJ2.L).
MEDLINE=20239944; PubMed=10777590;
                                                                                                                                                                                                                              STANDARD;
                                                                                  102 HFSENNSPHRD 112
                                   1 HLPGNKSPHRD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Melanoma;
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VINSYGHPQAPHLYPGPSPMYPIPTQDSAGYNRPAHHMVPRP.
SVPPPGANEEIPDDPDWDLIT -> GTAPSQLPWRWRLC
                                                                                                                                                                                                                                                            Gaps
PROSITE; PS00658; FORK HEAD 2; 1.

PROSITE; PS50039; FORK_HEAD 3; 1.

Areamscription regulation; DNA-binding; Nuclear protein; Activator;

Alternative splicing.

BND 66 143 FORK-HEAD.

DOMA.N 266 270 POLY-SER.
                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                              Score 41; DB 1; Length 574;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                     258120EDAE4B11EB CRC64;
                                                                                                                                                                          (in isoform FOXJ2.S). /FTId=VSP_001544.
                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Search completed: March 2, 2004, 16:05:27 Job time: 2.4375 secs
                                                                                                                                                                                                        574 AA; 62394 MW;
                                                                                                                                                                                                                                  46.1%;
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270
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2295
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 2, 2004, 16:00:38 ; Search time 2.125 Seconds
(without alignments)
678.999 Million cell updates/sec Run on:

1 HLPGNKSPHRDPAPR 15 US-10-060-765-8 89 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | C-terminal domain- | hypothetical prote | sugar kinase, FGGY | | coat protein VP1 - | | probable carbohydr | collagen alpha 2(I | EIN2 protein - Ara | н | GH1 protein - soyb | macrophage colony- | colony-stimulating | CTP synthase (EC 6 | hypothetical prote | probable aldehyde | beta-ketoacyl synt | anti-mullerian hor | hypothetical prote | hypothetical prote | collagen alpha 1(V | ATP-dependent perm | hypothetical prote | ඟ | | hypothetical prote | inclusion body mat | probable anti-mull | mullerian-inhibiti |
|-----------|----------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|
| SUMMAKIES | ID | T31421 | G72619 | C72417 | VCPVPP | VCPVNA | A60006 | AG0157 | S32436 | T48349 | S46151 | T05726 | A31401 | 835703 | S72961 | C72631 | T35432 | S25841 | JC4335 | T21021 | T41551 | A45748 | S19421 | T35379 | T31128 | S9CA6S | OOCA6 | 206092 | S41627 | JC5629 |
| | DB | . ~ | 0 | 01 | ⊣. | Н | Н | 7 | 7 | 7 | 7 | 7 | Н | Н | 7 | 7 | 7 | 7 | N | ~ | 7 | • | Н | • | • | Н | Н | N | 7 | 7 |
| | Length | 1173 | 165 | 492 | 723 | 729 | 729 | 517 | 618 | 1294 | 545 | 339 | 552 | 552 | 590 | 105 | 280 | 407 | 573 | 779 | 781 | 920 | 1049 | 278 | 355 | 520 | 522 | 522 | 557 | 568 |
| de | Query Match | 58.4 | 56.2 | 53.9 | 51.7 | 51.7 | 51.7 | 50.6 | 9.05 | 50.6 | 20.0 | 49.4 | 49.4 | 49.4 | 49.4 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 | 47.2 |
| | Score | 52 | 20 | 48 | 46 | 46 | 46 | 45 | 45 | 45 | 44.5 | 44 | 44 | 44 | 44 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 42 | 42 | 42 | 42 | 42 | 42 | 42 |
| | Result No. | - | 7 | m | 4 | Ŋ | ø | 7 | 89 | Ø. | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 |

| proline-rich prote | gag-like protein p | nypornerical profe | lmbI protein - Str | gag polyprotein - | gag polyprotein - | gag protein - bovi | related to suppres | hypothetical prote | hypothetical prote | hypothetical 13.2K | hypothetical prote | US10 protein - hum | isoleucine-tRNA li | hypothetical prote | hypothetical 58K p |
|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
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| T02436 | T13172 | C86194 | 844956 | FOLJGB | FOLJGA | S29356 | T49868 | H82597 | T47161 | S54309 | A85076 | QQBE07 | T31663 | DOCTV6C | JN0498 |
| 01 | ~ | N | N | 7 | 7 | N | 7 | ~ | 7 | ~ | N | - | 7 | Н | 7 |
| 818 | 1043 | 240 | 324 | 392 | 392 | 393 | 1174 | 111 | 117 | 118 | 282 | 312 | 413 | 520 | 520 |
| 47.2 | 47.2 | 46.6 | 46.6 | 46.6 | 46.6 | 46.6 | 46.6 | 46.1 | 46.1 | 46.1 | 46.1 | 46.1 | 46.1 | 46.1 | 46.1 |
| 42 | 42 | 41.5 | 41.5 | 41.5 | 41.5 | 41.5 | 41.5 | 41 | 41 | 41 | 41 | 41 | 41 | 41 | 41 |
| 0 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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                                                     Gaps
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                                                                                           Score 52; DB 2; Length 1173; Pred. No. 5.6; 2; Mismatches 2; Indels
                                                                                             58.4%;
                                                                                      Query Match
Best Local Similarity 66.7.
Best Local Similarity 7.14
                                                                                                                             224 PGDDSPHREPPP 235
                                                                                                                     3 PGNKSPHRDPAP 14
                                                   A; Accession: T31421
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hypothetical protein APE1416 - Aeropyrum pernix (strain Kl)

C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000 C;Accession: G72619 R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takal awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; F DNA Res. G, 83-101, 1999 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy: A;Reference number: A72450; MUID:99310339; PMID:10382966 A; Accession: G72619
A; Status: preliminary
A; Molecule type: DNA
A; Residuae: 1-165 < KAW>
A; Residuae: 1-165 < KAW>
A; Residuaes: 1-165 < KAW>
A; Cross-references: DDBJ: AP000061; NID: G5104821; PIDN: BAA80413.1; PID: d1044199; PID: G510

C;Genetics: A;Gene: APE1416

C; Superfamily: Aeropyrum pernix hypothetical protein APE1416

Gaps 5; 56.2%; Score 50; DB 2; Length 165; 68.8%; Pred. No. 1.5; ive 0; Mismatches 3; Indels 11; Conservative Best Local Similarity Matches 11; Conserv Query Match

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2 LPGNK--SPHRDPAPR 15

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A, Accession: B33743
A, Molecule type: DNA
A, Residues: 1-729 < VAS>
A; Cross-references: GB: M32787; MID: G332983; PIDN: AAA46917.1; PID: G332985
A; Cross-references: GB: M32787; MID: G332983; PIDN: AAA46917.1; PID: G332985
A; Cross-references: GB: M32787; MUD: 94025614; PMID: 8212598
A; Title: Genomic organization and mapping of transcription and translation products of A; Reference number: A48472; MUID: 94025614; PMID: 8212598
A; Accession: D44472
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C.Species: Yershiia pestis
C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C.Accession: AG0157
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.I. R.; Parkhill, J.; Wutherford, R.; Simmonds, M.; Skelton, J.; Stevens, R.M.; Davis, P.; Dougan, G., il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A.Arittle: Genome sequence of Yersinia pestis, the causative agent of plague.
A.Accession: AG0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: parvovirus coat protein
C;Keywords: coat protein; glycoprotein
F;151-729/Product: coat protein VP2 #status predicted <VP2>
F;172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn) (covalent) #stat
Virology 173, 368-377, 1989
A;Title: Nucleotide sequence analysis of the capsid genes and the right-hand terminal
A;Reference number: A33743; MUID:90085785; PMID:2596019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable carbohydrate kinase YPO1291 [imported] - Yersinia pestis (strain CO92)
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N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: A60006
R;Sakurai, M; Nishimori, T:; Ushimi, C.; Nakajima, H.
Virus Res. 13, 79-86, 1989
Virus Res. 13, 79-86, 1989
A;Pitle: Nucleotide sequence of capsid protein gene of porcine parvovirus.
A;Reference number: A60006; MUD:89319168; PMID:2750278
A;Accession: A60006
A;Accession: A60006
A;Accession: A60006
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Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h
Similarity 61.5%; Pred. No. 29;
8; Conservative 2; Mismatches 3; Indels
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117 PGSKPPGKRPAPR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 PGNKSPHRDPAPR 15
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ses 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 399, 323-329, 1999
A;Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Recasion: C72417
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE001697; GB:AE000512; NID:g4980597; PIDN:AAD35210.1; PID:g498060
C;Genetics:
A;Gene: TM0116
C;Superfamily: xylulokinase
                                                                                                                                                                                                                                                                                                         sugar kinase, FGGY family - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-dun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: C72417
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Species: al-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: B33743, D48472
R;Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: porcine parvovirus
Cipacies: porcine parvovirus
Cipacie: 30-569-1991 #sequence_revision 30-5ep-1991 #text_change 12-Apr-1996
Cipacies 30-3302
Richarz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. virol, 70, 2541-2553, 1989
A; Fitle: Porcine parvovirus: DNA sequence and genome organization.
A; Fitle: Porcine parvovirus: DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.7%; Score 46; DB 1; Length 723;
61.5%; Pred. No. 29;
iive 2; Mismatches 3; Indels
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S.Superfamily: parvovirus coat protein
C;Keywords: coat protein
F;145-723/Product: coat protein VP2 #status predicted <VP2>
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A;Residues: 1-723 <RAN>
A;Cross-references: EMBL:D00623
C;Genetics:
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Cjaccesion: T48849
RjBevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; A; Reference number: 224492
A; Reference number: 224492
A; Accession: T48349
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A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable purine nucleotide-binding protein YBR270c - yeast (Saccharowyces cerevisiae) N;Alternate names: hypothetical protein YBR1738 C;Species: Saccharomyces cerevisiae C;Species: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002 C;Accession: 846151 R;Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F. submitted to the Protein Sequence Database, August 1994 A;Reference number: 845940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GH1 protein - soybean (fragment)
C;Species: Glycline max (soybean)
C;Species: Glycline max (soybean)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 20-Aug-1999
C;Accession: T05726
R;Hagen, G.; Guilfoyle, T.J.
A;Reference to the EMBL Data Library, July 1997
A;Reference number: Z15436
                                            ENZ protein - Arabidopsis thaliana
N;Alternate names: protein F12E4.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: ATP, P-loop, purine nucleotide binding; transmembrane protein E;259-266/Region: nucleotide-binding motif A (P-loop) F;313-337/Domain: transmembrane #status predicted <TWM>F;265/Binding site: ATP/GTP (Lys) #status predicted
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A;Cross-references: EMBL:AL162751
A;Experimental source: cultivar Columbia; BAC clone F12E4
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A;Introne: 83/3; 112/3; 149/3; 220/3; 282/3; 1169/3
A;Note: F12E4.10
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74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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Pred. No.
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8; Conservative
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939 HLPNNKSGYWDPS 951
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A,Cross-references: GDB:138310, OMIM:120260
A,Map position: 1p33-1p32.2
C,Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Molecular cloning of the human alpha-2(IX) collagen cDNA and assignment of the A,Reference number: $32436; MUID:93202262; PMID:8454052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen cDNA and assignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA
A,Readdues: 1-26, QT', 22, S, 31-32, 'LM', 35-561,'L', 563-578,'P',580-618 <PER2>
A,Gross-references: EMBL:195610; NID:g1054872
R,Diab, M.; Mu, J.J.; Eyre, D.R.
Blochem, J. 314, 327-332, 199
Blochem, J. 314, 327-332, 199
A,Title: Collagen type IX from human cartilage: a structural profile of intermolecular
A,Title: Collagen type IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Remidues: 123-133, P',135-137 <DIA>
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
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                                                                       A;Cross-references: GB:AL590842; PIDN:CAC90122.1; PID:g15979342; GSPDB:GN00175 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 2(IX) chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 15-Sep-2003
C;Accession: S32436; S34487; S64673
C;Accession: M.; Haenninen, M.; Haestbacka, J.; Elima, K.; Vuorio, E.
FEBS Lett. 319, 177-180, 1993;
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                                                                                                                                                                                                                                DB 2; Length 517;
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A; Regidues: 1-618 < PRR1>
A; Crose-references: EMBL:M95610; NID:91054872
A; Crose-references: EMBL:M95610; NID:91054872
Submitted to the EMBL Data Library, March 1993
A; Reference number: 634487
A; Reference number: 634487
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                                                                                                                                                                                                                                                           29;
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                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                               A;Gene: YPO1291
C;Superfamily: xylulokinase
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                                A; Molecule type: DNA
A; Residues: 1-517 < KUR>
preliminary
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R.Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Jun Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop. A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S35703
R;Borycki, A.G.; Lenormand, J.L.; Guillier, M.; Leibovitch, S.A.
Biochim. Biophys. Acta 1174, 143-;52, 1993
A;Title: Isolation and characterization of a cDNA clone encoding for rat CSF-1 gene. A;Reference number: S35703; MUID:93363632; PMID:8357831
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: C72631
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C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: S72961
A,Status: preliminary
A,Molecule type: DNA
A,Residus: 1-590 <SMI>
A,Coss-references: EMBL:U00021; NID:g467141; PIDN:AAA50916.1; PID:g467152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cross-references: EMBL:M84361; NID:g203640; PIDN:AAA03032.1; PID:g203641; Superfamily: macrophage colony-stimulating factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 1; Length 552;
Pred. No. 44;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S72961
K; Smitt, D.R.; Robb. K.
submitted to the EMBL Data Library, November 1993
A; Description: Mycobacterium leprae cosmid L247.
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45.0%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                    colony-stimulating factor - rat
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                                    202 PASASPHQPPAP 213
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3 PGNKSPHRDPAP 14
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C,Superfamily: CTP synthase
C,Keywords: ligase
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Matches 9; Conserv
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A;Molecule type: mRNA
A;Residues: 1-552 <BOR>
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C; Species: Mus musculus (house mouse)
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A31401; UN0294; A26575; A23166; A25883
C; Accession: A31401; UN0294; A26575; A23166; A25883
R; Ladher: M. B:, Martin. G.A.; Noble, J. A.A.; Wittman, V.P.; Warren, M.K.; McGrogan, M.; St Proc. Natl. Acad. Sci. U.S.A. 85, 6706-6710, 1988
A; Title: cDNA cloning and expression of murine macrophage colony-stimulating factor from A; Reference number: A31401; MUID:88320507; PMID:2457916
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A, Molecule type: mRNA

A, Kesidudes: 1-552 cLADA.

A, STA CASA CLADA.

A, CTOGS-references: GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1; PID:g309199

A, CTOGS-references: GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1; PID:g309199

R, Harrington, M.A.; Edenberg, H.J.; Saxman, S.; Pedigo, L.M.; Daub, R.; Broxmeyer, H.E.

Game 102, 165-170, 1991

A, Title: Cloning and characterization of the murine promoter for the colony-stimulating

A, Fitle: Cloning and characterization of the murine promoter for the colony-stimulating

A, Reference number: JN0294; MUID:91340149; PMID:1874443
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A;Rolecule type: DNA
A;Rolecule type: DNA
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A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule Acids Res. 15, 2389-2390, 1987
A;Title: Nuclecule sequence of a cDNA encoding murine CSF-1 (macrophage-CSF).
A;Rolecule type: A26575; MUID:87174763; PMID:3494232
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A; Residues: 1-5, R', 7-245, A', 247-552 < DEL>
A; Residues: 1-5, R', 7-245, A', 247-552 < DEL>
R; Ben-Avram, C.M.; Shively, JE.; Shadduck, R.K.; Waheed, A.; Rajavashisth, T.; Lusis, Proc. Natl. Acad. Sci. U.S.A. 82, 4486-4489, 1985
A; Reference number: A23166; MUD: 85242709; PMID: 3925458
A; Accession: A23166
A; Molecule type: protein
A; Residues: 33-39, CC', 42-57 < REN>
R; Rajavashisth, T.B.; Eng, R.; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively, J.E Proc. Natl. Acad. Sci. U.S.A. 84, 1157-1161, 1987
A; Title: Cloning and tissue-specific expression of mouse macrophage colony-stimulating farerence number: A25883; MUID: 87147232; PMID: 3493488
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                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-339 <HBG.
A;Residues: 1-339 <HBG.
A;Cross-references: EMBL:AF016633; NID:g2388688; FIDN:AAB70005.1; FID:g2388689
A;Experimental source: cultivar Wayne
C;Genetics:
A;Gene: GH:
C;Superfamily: auxin-induced protein aux28
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                                                                                                                                                                                                                                                                                                                          Length 339;
                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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N,Alternate names: colony-stimulating factor 1; M-CSF
                                                                                                                                                                                                                                                                                                                    Score 44; DB 2;
Pred. No. 27;
3; Mismatches
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Best Local Similarity 63.6%;
Matches 7; Conservative
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62 LPGSQSPEREP 72
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Matches 7; Conserva
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             A; Accession: T05726
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A Map position: 12q13-12q13
A Junizons: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
A Junizons: 16/3; 77/7; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc C; Keywords: ATP; hormone receptor; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>F;1-16/Domain: anti-muellerian hormone type II receptor #status predicted <MAT>F;17-11/Domain: extracellular hormone binding #status predicted <ELB>F;142-167/Domain: transmembrane #status predicted <TWM>F;142-167/Domain: protein kinase homology <KIN>
                                                                                                  Rivisser, J.A.; McLuskey, A.; van Beers, T.; Weghuis, D.O.; van Kessel, A.G.; Grootegoed Blochem. Biophys. Res. Commun. 215, 1029-1036, 1995.
Ajfille: Structure and chromosomal localization of the human anti-muellerian hormone tyt A;Reference number: JC4335; MUID:96028015; PMID:7488027
                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-573 <VIS.
A;Cross-references: GB:X91156; NID:g1107671; PIDN:CRA62593.1; PID:e198046; PID:g1107672
C;Comment: This is a receptor for anti-mullerian hormone (see PIR:WFHUM). It plays a cri
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A;Introns: 33/2; 130/1; 189/2; 238/1; 355/2; 388/3; 473/1; 540/2; 587/3; 670/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F16D3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z78062; PIDN:CAB01499.1; GSPDB:GN00019; CESP:F16D3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F16D3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T21021
                              C;Species: Homo sapiens (man)
C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 04-Mar-2000
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anti-mullerian hormone type II receptor precursor - human
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65;
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A;Reference number: Z19361
A;Accession: T21021
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Pred. No. 6
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Best Local Similarity 61.5%
Local Similarity 61.5%
Local Similarity
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A; Residues: 1-779 <WIL>
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A, Gene: CESP: F16D3.2
                                                                                  C; Accession: JC4335
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                           A, Residues: 1-105 <KAW>
A, Residues: 1-105 <KAW>
A; Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80505.1; PID:d1044291; PID:g510
A; Experimental source: strain K1
C; Genetics:
A, Gene: APE1506
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C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot
F;21-400/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
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A; Title: Nucleotide sequence and deduced functions of a set of cotranscribed genes of A; Reference number: S25840; MUID:92406871; PMID:1527048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:AL031035; PIDN:CAA19886.1; GSPDB:GN00070; SCOEDB:SC6A9.01c; Seperation of source: strain A3(2); Genetics:
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Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
Accession: S25841
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C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35432
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A;Reference number: Z21578
A;Accession: T35432
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-280 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable aldehyde dehydrogenase - Streptomyces coelicolor (fragment)
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48.3%; Score 43; DB 2; Length 407;
Best Local Similarity 46.7%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 6; Indels
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Pred. No. 31;
1; Mismatches 4; Indels
                                                                                                                                                                                                       Score 43; DB 2; Length 105;
Pred. No. 11;
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Similarity 58.3%;
7; Conservative
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HIPGRLLPQTDPSTR 73
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HNPGNATPDRFPA 14
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Best Local Similarity
Matches 7; Conserv
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A;Gene: SCOEDB:SC6A9.01c
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Best Local Similarity
Matches 8; Conserv
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A;Status: preliminary
A;Molecule type: DNA
   A; Molecule type: DNA
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RESULT 17

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Gaps

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RESULT 18

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JC4335

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3-isopropylmalate dehydrogenase (EC 1.1.1.85) - Sphingomonas aromaticivorans plasmid phaseoies: Sphingomonas aromaticivorans
C,Species: Sphingomonas aromaticivorans
C,Bate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C,Accession: T31128
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, B.C.; Sensen, C.W.;
submitted to the EMBL Data Library, July 1998
A,Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromat
A,Reference number: Z20992
A,Accession: T31128
A,Accession: T31128
A,Scatus: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 1.2e+02;
2; Mismatches 2; Indels
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Pred. No. 44;
0; Mismatches 5; Indels
A;Reference number: S25353; MUID:92327849; PMID:1626432 A;Contents: annotation
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Matches 7; Conservative
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Yeast 7, 867-872, 1991
A;Title: The product of the YCR105 gene located on the chromosome III from Saccharomyces A; Reference number: S40914; MUID: 92160395; PMID:1789009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003
C;Date: 16-Feb-1994 #sequence_revision 18.Nov-1994 #text_change 15-Sep-2003
C;Date: 16-Feb-1994 #sequence_revision 18.Nov-1994 #text_change 15-Sep-2003
C;Date: 16-Feb-1994 #sequence_revision N.G.; Gilbert, D.J.; Chu, M.L.; Jenkins, N.A.; Uit Genomics 16, 733-739, 1993
A;Fitle: CDNA cloning and chromosomal mapping of the mouse type VII collagen gene (Col7a A;Reference number: A45748; MUID:93315168; PMID:8325648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-1049 <GOF>
A; Cross_references: EMBL:X59720; NID:g1907116; PIDN:CAA42328.1; PID:g1907154; GSPDB:GN0d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-1049 <PUR>
R;Skala, J:; Purnelle, B.; Goffeau, A.
R;Skala, J:; Purnelle, B.; Goffeau, A.
X;Pant B, 409-417, 1992
A;Tille: The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of K genes.
                                                                                                                                                                                      A;Residues: 1-781 <WOO>
A;Cross-references: EMBL:AL023794; PIDN:CAA19355.1; GSPDB:GN00068; SPDB:SPCC70.05c
A;Experimental source: strain 972h-; cosmid c70
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ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein YCR011c; protein YCR105
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-Jan-2001
C;Accession, A.; Purnelle, B.; Skala, J.
R;Goffeau, A.; Purnelle, B.; Skala, J.
A;Reference number: S19420
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A.Note: sequence extracted from NCBI backbone (NCBIN:135000, NCBIP:135001)
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A, Cross-references: GB: S63654; NID: 9386656; PIDN: AAB27492.1; PID: 9386657
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 2; Length 781;
Pred. No. 90;
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                                                                                                      A,Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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A45748
collagen alpha 1(VII) chain - mouse (fragment)
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53.8%;
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A;Molecule type: nucleic acid
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                       A; Reference number: Z22001
A; Accession: T41551
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Best Local Similarity
77 Conserve
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A,Gene: SPDB:SPCC70.05c
A,Map position: 3
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Indels

Length 522;

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A;Title: DNA sequence of gene VI of cauliflower mosaic virus Japanese strain S (CaMV S-; A;Reference number: S06092; MUID:90016879; PMID:2798138
A;Accession: S06092
A;Molecule type: DNA
A;Residues: 1-522 <TAK>
A;Cross-references: EMBL:X14911; NID:g58828; PIDN:CAA33037.1; PID:g58829
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X71916; NID:g453177; PIDN:CAA50731.1; PID:g453178
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP
F;199-510/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Č;Species: Rattus norvegicus (Norway rat)
Cjātes: 13-Jan-1955 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
Cjācession: 841627
R;Baarends, W.M.; van Helmond, M.J.L.; Post, M.; van der Schoot, P.J.C.M.; Hoogerbrugge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: A novel member of the transmembrane serine/threonine kinase receptor family is A;Reference number: 841627; MUID:94163972; PMID:8119126
A;Accession: 841627
A;Status: preliminary
                                                                                                                                                                                A, Gene: VI
C, Superfamily: caulimovirus inclusion body matrix protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
47.2%; Score 42; DB 2;
Best Local Similarity 61.5%; Pred. No. 91;
Matches 8; Conservative 1; Mismatches
                                                                                                                                                                                                                                                  Score 42; DB 2;
Pred. No. 85;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable anti-mullerian hormone receptor - rat
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Best Local Similarity 61.55
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  228 GTKKPSSDPAPK 239
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                                                                                                                                                                                                                                                                           Best Local Similarity 58.3
Matches 7; Conservative
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A;Residues: 1-557 <BAA>
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                      A;Cross-references: EMBL:AF079317; NID:g3378261; FID:g3378269; PIDN:AAD03852.1
C;Genetics:
A;Genome: plasmid pNL1
A;Note: orfo4; orfo4; 3-isopropylmalate dehydrogenase
C;Superfamily: 3-isopropylmalate dehydrogenase
C;Keywords: oxidoreductase
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C;Species: cauliflower mosaic virus
C;Date: 28 Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
C;Accession: 806092
AsiTakahashi, H.; Shimamoto, K.; Suzuki, M.; Ehara, Y.
Nucleic Acids Res. 17, 7981, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 6 - cauliflower mosaic virus (strain Strasbourg)
C;Species: cauliflower mosaic virus
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 23-Jul-1999
C;Accession: A04162
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C;Species: cauliflower mosaic virus
C;Date: 31-Oct-1980 #sequence_revision 05-Apr-1983 #text_change 30-Jun-1993
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84;
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R;Guilley, H.
submitted to the Nucleic Acid Sequence Database, October 1982
A;Reference number: A94613
A;Reference number: A94613
A;Molecule type: DNA
A;Residues: 1-522 <GUI>
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A;Title: Nucleotide sequence of cauliflower mosaic virus DNA. A;Reference number: A90799; MUID:81001865; PMID:7407912
A;Accession: A04162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.2%; Score 42; DB 1; 58.3%; Pred. No. 85;
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Pred. No. 84;
1; Mismatches
                                                                                                                                                                                                     Score 42; DB
Pred. No. 57;
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Best Local Similarity 58.3%;
Matches 7; Conservative 1
                                                                                                                                                                                                     47.2%;
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 7; Conserv
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          A, Residues: 1-355 < ROM>
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4; Indels

Length 557

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A,Map position: 15
C,Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
F,197-508/Domain: protein kinase homology <KIN>
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                                                                                                                               A;Wolecule type: DNA
A;Residues: 1-568 <MIS>
C;Comment: This receptor in involved in the sexual differeatiation.
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Pred. No. 92;
1; Mismatches
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62;
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61.5%; Pred. No. 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
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89 PGDKAPPHRPPEP 101
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Matches 8; Conserv
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C96194
Dypochetical protein [imported] - Arabidopsis thaliana
C;Species Arabidopsis thaliana (mouse-ear-ress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C86194
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A;Introns: 18/2; 30/1; 53/1; 83/2; 135/1; 174/2; 221/2; 273/1; 308/2; 352/3; 377/3; 504/
A;Note: DJ430N08.2
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C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C; Accession: T13172
R; Sheen, F; Levis, R.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 12510-12514, 1994
A; Title: Transposition of the LINE-like retrotransposon TART to Drosophila chromosome
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submitted to the EMBL. Data Library, April 1998
A; Description: The Bequence of Homo sapiens PAC clone DJ430N08.
A; Reference number: Z14672
A; Accession: T02436
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Ctaus: preliminary;
A; Molecule type: DNA
A; Cross-references: EMBL: AC004542; NID: G3041846; PIDN: AAC12954.1; PID: G3041848
C; Genetics:
                                                                                                                                                                                                                                                                                            Species: Homo Bapiens (man)
Date: 05-Mar-1999 #sequence revision 05-Mar-1999 #text_change 05-Nov-1999
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A;Residues: 1-1043 <SHE>
A;Cross-references: EMBL:U14101; NID:g603662; PID:g603663; PIDN:AAC46493.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 2; Length 818; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: 217629; MUID:95107987; FMID:7809068
A;Accession: T13172
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                                                                                                                                                                                                                                             proline-rich protein DJ430N08.2 - human (fragment)
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A;Mobile element: transposon TART-B1
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Best Local Similarity 50.0%;
Matches 7; Conservative
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Local Similarity
nes 9; Conserv
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lmbI protein - Streptomyces lincolnensis
C;Species: Streptomyces lincolnensis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Oct-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Oct-1999
C;Caccession: S69818; S44956 #I.Z.; Piepersberg, W.
R;Peschke, U.; Schmidt, H.; Zhang, H.Z.; Piepersberg, W.
Mol. Microbiol. 16, 1137-1156, 1995
Mol. Microbiol. 16, 1137-1156, 1995
A;Fittle: Molecular characterization of the lincomycin-production gene cluster of Strept
A;Reference number: S69805; MUID:96020646; PMID:8677249
A;Accession: S69818
A;Accession: S69818
A;Accession: preliminary; nucleic acid sequence not shown; translation not shown
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NiAlternate names: core polyprotein
NiAlternate names: core protein p12; core protein p24
NiContains: core protein p12; core protein p15; core protein p24
NiContains: core protein p12, core protein p15; core protein p24
NiContains: core protein p12, core protein p15, core protein p24
NiNote: host Bos sp. (cattle)
A;Note: host Bos sp. (cattle)
C;Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text_change 31-Mar-2000
C;Accession: A94063; A93812; A3311; A03942
R;Asqata, N.; Yasunaga, T.; Tsuzuku-Kawamura, J.; Ohishi, K.; Ogawa, Y.; Ikawa, Y.
Proc. Natl. Acad. Sci. U.S.A. 82, 677-681, 1985
A;Title: Complete nucleotide sequence of the genome of bovine leukemia virus: its evolutivacession: A94063; MUID:85140159; PMID:2983308
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A.Residues: 1-324 <PED.>
A.Residues: 1-324 <PED.>
A.Residues: 1-324 <PED.>
A.Residues: 1-324 <PED.>
A.Residues: 1-324 <PED.>
A.Residues: EMBL:X79146; NID:9499194; PIDN:CRAS5755.1; PID:9581692
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
C.Genetics:
A.Gene: lmbl
A.Start codon: GTG
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A;Residues: 1-240 <STO>
A;Cross-references: GB:AE005172; NID:g6850322; PIDN:AAF29399.1; GSPDB:GN00141
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A;Residues: 1-392 <SAG> -
A;Residues: 1-392 <SAG> -
A;Cross-references: GB:K02120; NID:g210767; PIDN:AAA42784.1; PID:g210768
A;Cross-references: GB:K02120; NID:galoyflated basic gag product
A;Note: core protein pl5 is a phosphorylated basic gag product
A;Note: core protein pl2 is a genome-binding protein with repeated sequences
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Pred. No. 45;
3; Mismatches 3;
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R;Rice, N.R.; Stephens, R.M.; Burny, A.; Gilden, R.V.
Virology 142, 357-377, 1985
A;Title: The gag and pol genes of bovine leukemia virus: nucleotide sequence and analysi
A;Reference number: 829356; MUID:86045859; PMID:2997990
A;Accession: 229356
A;Status: preliminary
A;Molecule type: DNA
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R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, Briones, M.R.S.; Bloorny, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, B.E.; Laig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: T49868
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related to suppressor protein SPT23 [imported] - Neurospora crassa
N;Alternate names: protein B24P11.240
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                 A, Residues: 1-393 <RIC>
A, Cross-references: EMBL:M10987; NID:g210784; PIDN:AAA42794.1; PID:g210785
C, Superfamily: mammalian retrovirus gag polyprotein II
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A,Experimental source: BAC clone B24F11; strain OR74A
                                                                                                                                                                                                                                                                                                                              Length 393;
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Best Local Similarity 37.5%; Pred. No. 2.3e+02;
Matches 9; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                              Score 41.5; D
Pred. No. 76;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 HTPGPKMPGPROPAPK 341
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
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A; Residues: 1-1174 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: NCSP: B24P11.240
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         A;Note: the authors translated the codon TAT for residue 7 as Thr and TAC for residue 43 R;Oroszlan, S.; Copeland, T.D.; Henderson, L.E.; Stephenson, J.R.; Gilden, R.V. Proc. Natl. Acad. Scl. U.S.A. 76, 2996-3000, 1979 A;Title: Amino-terminal sequence of bovine leukemia virus major internal protein: Homold A;Reference number: A93812; MUID:79223918; PMID:223166
                                                                                                                                                                A,Accession: A93812
A,Molecule type: protein
A,Residues: 110-164 <0RC>
R;Copeland, T.D.; Morgan, M.A.; Oroszlan, S.
R;ESB Lett. 156, 37-40, 1983
A;Title: Complete amino acid sequence of the nucleic acid-binding protein of bovine leuk
A;Reference number: A91311; MUID:83210199; PMID:6303852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Coulston, J.; Naif, H.; Brandon, R.; Kumar, S.; Khan, S.; Daniel, R.C.W.; Lavin, M.F. J. Gen. Virol. 71, 1737-1746, 1990
A;Title: Molecular cloning and sequencing of an Australian isolate of proviral bovine le A;Reference number: JQ0554; MUID:90362060; PMID:2167927
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C;Species: bovine leukemia virus, BLV
C;Date: 13-Jan.1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
C;Accession: S29356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gag polyprotein - bovine leukemia virus (strain Australia)
N;Alternate names: core polyprotein
N;Contains: core protein p1; core protein p15; core protein p24
C;Species: bovine leukemia virus, BLV
C;Species: 31-Mar_1993 #sequence_revision 31-Mar-1993 #text_change 28-Jul-2000
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;Superfamily: mammalian retrovirus gag polyprotein II
;Reywords: core protein; duplication; phosphoprotein; polyprotein
;1-109/Product: core protein p15 #status predicted <P15>
;110-323/Product: core protein p24 #status predicted <P24>
;324-392/Product: core protein p12 #status experimental <P12>
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C; Superfamily: mammalian retrovirus gag polyprotein II
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56.2%; Pred. No. 75;
tive 1; Mismatches
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Best Local Similarity 56.2%;
Matches 9; Conservative
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A;Residues: 324-392 <COP>
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nes 9; Conserv
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Matches
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S29356
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Cypothetical 13.2K protein - fowl adenovirus 1

C;Species: Aviadenovirus gall (fowl adenovirus 1, CELO)

C;Date: 08-Jul-1995 #sequence_revision 14-Feb-1997 #text_change 28-Jul-2000

C;Date: 08-Jul-1995 #sequence_revision 14-Feb-1997 #text_change 28-Jul-2000

C;Accession: S54309

R;Hess, M.; Cuzange, A.; Chroboczeck, J.; Ruigrok, R.; Jacrot, B.

submitted to the EMBL Data Library, February 1995

A;Abecription: The sequence of the two fibers of an avian adenovirus (CELO) and organiss

A;Reference number: S54125

A;Accession: S54109
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.R.b.uthors: Marting, E.M.F.; Matsukuma, A.Y.; Menck, C.R.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J.; de Nor, de Nor., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, A.M.; Silva D.F., W.A.; da Silva, M.A.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; verjovski-Almeida, S.; Vettore, A.L.; ZA;Contents: annotation
C;Genetics:
A;Gene: XF2103
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T47161
hypothetical protein DKFZp762A1712.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47161
R;Ansorge, W.; Wikher, U.; Mewes, H.W.; Weil, B.; Wiemann, S.
R;Ansorge, W.; Wikher, U.; Mewes, H.W.; Weil, B.; Wiemann, S.
R;Ansorge, W.; Wikher, U.; Mewes, H.W.; Weil, B.; Wiemann, S.
R;Ansorge, W.; Wikher, U.; Mewes, H.W.; Weil, B.; Wiemann, S.
A;Accession: T47161
A;Status: preliminary
A;Accession: T47161
A;Status: preliminary
A;Residues: 1-117 cAAA>
A;Residues: 1-117 cAAA>
A;Residues: 1-117 cAAA>
A;Residues: 1-117 cAAA>
A;Residues: adult melanoma (MeWo cell line); clone DKFZp762A1712
C;Genetics:
A;Note: DKFZp762A1712.1
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A; Residues: 1-118 <HES>
A; Cross-references: BMBL:X84724; NID:g780165; PIDN:CAA59209.1; PID:g780170
A; Cross-references: EMBL:X84724; NID:g780165; PIDN:CAA59209.1; PID:g780170
B; Hess, M.; Cuzange, A.; Ruigrok, R.W.H.; Chroboczek, J.; Jacrot, B.
J. Mol. Biol. 252, 379-385, 1995
A; Title: The avian adenovirus penton: two fibres and one base.
A; Reference number: S59067; MUID:96025073; PMID:7563058
A; Rontents: annotation
C; Superfamily: Aviadenovirus gall hypothetical 13.2K protein
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46.1%; Score 41; DB 2; Length 118;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 2; Length 111; Pred. No. 25; Mismatches 4; Indels
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Matches 7; Conserval
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Search completed: March 2, 2004, 16:08:07 Job time: 3.125 sec8
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3 PGNKSPHRDPAPR 15

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March 2, 2004, 15:51:42 ; Search time 6.25 Seconds
(without alignments)
757.244 Million cell updates/sec
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                                                                                                                                                                                                                                                                                         1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                           - protein search, using sw model
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sp_vertebrate:*
sp_unclassified:*
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89
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Maximum DB :
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Q63624 rattus norv Q9yc35 aeropyrum p Q9yc35 cucumis sat Q9wxx1 thermocoga Q9blt0 leishmania Q7yx42 rhodopirell Q7yx8 canis famil Q9trz5 oryctolagus Q87db2 xylella fas Q7x93 griffithsia Q7x83 griffithsia Q7x83 griffithsia Q7x35 synechococc Q91115 oryza sativ Q9y215 homo sapien Q86x52 homo sapien Q8n683 homo sapien 063624 09YC35 09YC35 09WXX1 09BLT0 07UX42 07TX88 09TX5 087DB2 09TX39 09L115 09L115 08X50 086X52 Q8N683 Query Match Length DB 53.9 53.9 52.8 51.7 50.6 50.6 50.6 Result

| Q9s814 arabidopsis | Q8t917 toxoplasma | Q814g8 oryza sativ | Q93jd6 streptomyce | Q8t2z8 trypanosoma | O22465 glycine max | Q8a0k9 bacteroides | 052719 klebsiella | Q8gqm5 escherichia | Q83eh5 coxiella bu | Q8kz56 uncultured | Q9u252 caenorhabdi | Q9eqh1 rattus norv | Q9r1x3 mus musculu | O921s8 mus musculu | Q94527 drosophila | | | | | | Q8tv81 methanopyru | | | | Q89i54 bradyrhizob | | | Q8rve5 oryza sativ |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|--------|--------|--------|--------|--------------------|--------|--------|--------|--------------------|--------|--------|--------------------|
| Q9S814 | Q8T9L7 | Q8L4G8 | 93JD6 | 28T2Z8 | 022465 | QBA0K9 | 052719 | OBGONS | Q83EH5 | Q8KZ56 | Q9U252 | Q9EQH1 | Q9R1X3 | Q9Z1S8 | 094527 | Q9YBU3 | Q8BW91 | Q8BLG7 | Q8BW77 | Q8L479 | QBTVB1 | 6HSN6C | Q9LDK8 | QBVJI2 | Q89154 | Q8CJQ9 | Q7U5S7 | QARVES |
| 10 | s | 10 | 16 | 2 | 10 | 16 | 8 | 0 | 16 | ~ | 2 | 11 | 11 | 11 | S | 17 | 11 | 11 | 11 | 10 | 17 | 4 | 10 | 16 | 16 | 16 | 16 | 10 |
| 1294 | 1687 | 625 | 128 | 274 | 339 | 426 | 487 | 487 | 494 | 520 | 613 | 999 | 999 | 999 | 971 | 105 | 142 | 182 | 184 | 193 | 208 | 211 | 281 | 292 | 481 | 511 | 653 | 670 |
| 50.6 | 50.6 | 50.0 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 | 48.3 |
| 45 | 45 | 44.5 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 |
| 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

REMBL, BC008803; F:growth factor activity; IEA.
InterPro; IPR008996; Cytok Iil_like.
InterPro; IPR008996; Cytok Iil_like.
InterPro; IPR002348; IIL_HBGF.
REMBL; PR00167; FGF; I.
REMBL; SW00441; FGF; I.
SRARRT; SW004442; FGF; I.
SRARRT; SW00442; FGF; I.
SRARRT; SW00442; FGF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 89; DB 4; Length 209; 100.0%; Pred. No. 3e-06; Arive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                  209 AA
                                                                                             Q8N683 PRELIMINARY; PRT; 20
Q8N883, 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2003 (TrEMBLrel. 22, Last sequer
01-0CT-2003 (TrEMBLrel. 25, Last annott Fibroblast growth factor 21.
Homo sapiens (Human)
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Best Local Similarity 100.'
Matches 15; Conservative
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TISSUE=Lung;
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RESULT 1
                                                        Q8N683
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145 HLPGNKSPHRDPAPR 159 RESULT 2 Q63624 ID Q6362 g

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PRELIMINARY;

963624

1173 AA.

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SEQUENCE FROM N.A.
MEDLINES-20267442; PubMed=10809445;
MEDLINES-20267442; PubMed=10809445;
Fujii N., Kamada M., Yamasaki S., Takahashi H.;
"Differential accumulation of Aux/IAA mRNA during seedling development
"Differential accumulation of Aux/IAA mRNA during seedling development
and gravity response in cucumber (Cucumis sativus L.).";
Plant Mol. Biol. 42:731-74(02000).
EMBL; AB026822; BAA85821-1;
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STRAIN=MSBB / DSM 3109;
MEDLINE=99287316; PubMed=10360571;
MEDLINE=99287316; PubMed=10360571;
MEDLINE=99287316; PubMed=10360571;
Maleson K.E., Clayton R.J., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garreth M.N.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
ENBL, AB001697; AAD35210.1; -.
                                                                                                                                                                                                                    Cucumis sativus (Cucumber).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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Pred. No. 16;
2; Mismatches 1; Indels
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CO; GO: 0006301; F: kinase activity; IEA.
CO; GO: 0004856; F: xylulokinase activity; IEA.
CO; GO: 0005455; F: xylulokinase activity; IEA.
CO; GO: 0005265; P: carbohydrate metabolism; IEA.
CO; GO: 0005997; P: xylulose metabolism; IEA.
InterPro; IPR004448; SASP.
InterPro; IPR006009; Xylulokinase.
Fam; PF00370; FGGY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005622; C:intracellular; IEA.
GO; GO:0006445; P:regulation of translation; IEA.
InterPro; IRR003311; AUX IAA.
Pfam; PFC2309; AUX IAA, 1.
SEQUENCE 355 AA; 39030 MW; C471B7622522BBD8 CRC64;
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                                                                                   Last sequence update)
Last annotation update)
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PRT;
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                                                             (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 24,
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      PRELIMINARY;
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NCBI_TaxID=3659;
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                                                         01-MAY-2000
01-MAY-2000
01-MUN-2000
CS-IAA2.
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Q9SSY2;
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MEDINES-9310.39; Funket-1025.00;
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishidima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
orenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL; APO00061; BAA80413-1; -.
PIR; G72619; G72619.
PIR; G72619; G72619.
SEQUENCE 165 AA; 18858 MW; D73D0855F4D7A378 CRC64;
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Yuryev A., Patturajan M., Litingtung Y., Joshi R.V., Gentile C.,
Yuryev A., Patturajan M., Litingtung Y., Joshi R.V., Gentile C.,
Gebara M., Corden J.L.;
"The C-terminal domain of the largest subunit of RNA polymerase II
interacts with a novel set of serine/arginine-rich proteins.";
Proc. Natl. Acad. Sci. U.S.A. 93:6975-6980(1996).
EMBL; U9956; AAC52657.1; -.
PIR; T31421; T31421.
SEQUENCE 1173 AA; 124775 MW; 2F5209A6435F6770 CRC64;
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Desulfurococcaceae; Aeropyrum.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APR1416.
                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches 8; Conservative
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                                                                                                                                                                          Rattus norvegicus (Rat).
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Best Local Similarity
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RESULT 3

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RESULT 4 Q9SSY2

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MEDLINE=22735913; PubMed=12835416;
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SEQUENCE
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NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zimmermann W., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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Planctomycetaceae, Pirellula.
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Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                   Query Match 53.9%; Score 48; DB 16; Length 492; Best Local Similarity 53.3%; Pred. No. 23; Matches 8; Conservative 3; Mismatches 4; Indels
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EMBL; AL583933; CAC32260.1; -.

EMBL; AL583933; CAC32260.1; -.

EMBL; PRO04867; F:serine protease inhibitor activity; IEA. InterPro; IPR006105; Try/amyl inhib.

PROSITE; PS00426; CEREAL TRYP_AMYL INH; 1.

SEQUENCE 574 AA; 61489 MW; C22D8283F006965E CRC64;
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                                      TIGREAMS; TIGRO1312; XylB; 1.
PROSITE; PS00933; PGGY KINASES 1; 1.
PROSITE; PS003045; PGGY KINASES 2; 1.
PROSITE; PS003045; PGGY LINASES 2; 1.
Kinase; Complete proteome.
SEQUENCE 492 AA; 54405 MW; 0F66A3AB451DB8E1 CRC64;
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Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible monocarboxylate transporter protein.
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2; Mismatches
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Best Local Similarity 57.4.
8; Conservative
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                Pfam; PF02782; FGGY_C; 1
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STRAIN=1;
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Q7UX42;
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MEDIINE=96181606; PubMed=8601571;
MEDIINE=96181606; PubMed=8601571;
MEDIINE=96181606; PubMed=8601571;
MEDIINE=96181606; PubMed=8601571;
MEDIINE=FEPAIR TELHYLIVENSFERASE AS A MOLECULAR DEVICE for preventing mutation and cancer.";
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula sp.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OGT-2003 (TrEMBLrel. 25, Last annotation update)
0(6)-methylguanine-DNA methyltransferase (EC 2.1.1.63).
0ryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pissipedia, Canidae, Canis.
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                                                                                                                                      Proc. Natl, Acad. Sci. U.S.A. 100:8298-8303(2003).

EMBL, BX294135; CAD72170.1; -.
Aminoacyl-tRNA synthetase; Ligase; Complete proteome.

SEQUENCE 601 AA; 68668 MW; 0C6B526B11FF4CD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-007-2003 (TrEMBLrel. 25, Created)
01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 2.1e+02;
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HSSP, P06134; 1SFE.
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Pred. No. 28;
0; Mismatches
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Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity bb...
8; Conservative
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us-10-060-765-8.rspt

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STRAIN=cv. Nipponbare;
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Best Local Similarity
Matches 6; Conserv
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Q7U8Z9
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MEDLINE=22421331; PubMed=12533478;
MEDLINE=22421331; PubMed=12533478;
MIJAKI C.Y., Furlan L.K., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
MIJAKI C.Y., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tasi S.M.,
Goldman M.H.S., Goldman G.H., Lemos M.V., El-Dorry H., Tasi S.M.,
Gortinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
Marino C.L., Gigiloti E., Abreu I.L., Alves L.M., oder Marino C.L., Gigiloti E., Abreu I.L., Alves L.M., Abara G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
Geoni S.G., Oliveira A.R., Rosa V.B. Jr., Sassaki F.T., Sasna J.A.D.,
Ge Souza A.A., Truffi D., Tgukumo F., Yanai G.M., Zaros L.G.,
Kitajima J.P., Almeida N.F. Jr., Setubal J.C.,
Kitajima J.P.,
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GO; GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. . .; IEA. GO; GO:0006281; P:DNA repair; IEA. InterPro; IPR008332; MethylG_Mtase. InterPro; IPR01497; Methyltransf_1.
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                                                                                                                                                                                                                                                                                                                           Xylella fastidiosa (strain Temeculal / ATCC 700964).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales;
Xanthomonadaceae; Xylella.
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Pred. No. 14;
2; Mismatches 4; Indels
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InterPro; IPR010437; Prok lipoprot S.
PROSITE; PS010013; PROKATEIPOPROTEIN; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 111 AA; 13336 MW; 492CB96C4507E840 CRC64;
                                                                                       00374; MGMT; 1.
181 AA; 19397 MW; 12DF60974AA41A16 CRC64;
                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last sequence update)
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Pred. No. 16;
1; Mismatches
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                                              Pfam; PF01035; Methyltransf 1; 1.
Pfam; PF02870; Methyltransf 1; 1.
TIGREAMS; TIGRO0589; ogt; 1.
PROSITE; PS00374; MGY; 1.
SEQUENCE 181 AA; 19397 MW; 12D1
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity 66...
8; Conservative
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01-OCT-2003 (
01-OCT-2003 (
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SEQUENCE FROM N.A.
MEDLINE3-2285-697; PubMed=12917641;
MEDLINE3-2285-697; PubMed=12917641;
Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
Duffrenne A., Partenaky F., Webb E.A., Waterbury J.;
The genome of a motile marine Synechococcus.";
Nature 424:1037-1042(2003).
REMBI, BX569690, CARG6975.1;
BROUP ENSESSON, CARG6975.1;
SEQUENCE 326 AA, 35270 MW; EDC4DBDC51EE3526 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (OSJNBa0086F08.1 protein).
Oryza sativa (Rice).
Spraryota; Virialiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spraracophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Serine palmitoyltransferase (Fragment).
Griffithsia japonica.
Bukaryota, Rhodophyta; Florideophyceae; Ceramiales; Ceramiaceae;
Griffithsia.
Griffithsia.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative glycosyltransferase family 4 protein (BC 2.4.1.-).
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50.6%; Score 45; DB 16; Length 326;
Best Local Similarity 57.1%; Pred. No. 44;
Matches 8; Conservative 1; Mismatches 5; Indels
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Liu C., Lee Y., Lee H.;
Submitted (1907-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS42030; AAP80840.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                          NON TER 178 178 SEQUENCE 178 AA; 20056 MW; 4264182D29A597FF CRC64;
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NCBI_TaxID=84588;
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114 HIPGPRTPHDQPS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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TIGRFAMB; TIGR01312; XylB; 1
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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STRAIN=KIMS / Biovar Mediaevalis;
STRAIN=EXIST 863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
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MEDLINE=21470413; PubMed=11566360;
MEDLINE=21470413; PubMed=11566360;
MEDLINE=21470413; PubMed=11566360;
MEDRINE=21470413; PubMed=11566360;
Parkhil J., Waren B.W., Tanemson N.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Chillingworth T., Cronin A., Davies R.W., Varilyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quall M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Fyrzinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Enterobacteriaceae; Yersinia.
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                                                                                                                                            STRAIN=CV. Nipponbare;
Sasaki I., Matsumoto I., Yamamoto K.;
Sasaki I., Matsumoto I., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
"Oryza sativa nipponbare(GA3) genomic Matsubases.
Glone:OSJNBa0086608.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001539; BAA92224.1;
EMBL; AP001539; BAA92224.1;
EMBL; AP001539; BAA91192.1;
GRAMENDE, OSJ115;
SEQUENCE 352 AA; 39614 MM; B238C55E4707835B CRC64;
    Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0708G02.";
                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 10; Length 352;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
putative carbohydrate kinase (Putative xylulose kinase).
                                                                    Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0004865; F:kinase activity; IEA.
GO; GO:0005975; F:carbohydrate metabolism; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005977; F:GGY kin.
InterPro; IPR006000; Xylulokinase.
Pfam; PF00370; FGGY; I.
Pfam; PF00370; FGGY; I.
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"Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
EMBL; AJ41417; CAC90122.1; -.
EMBL; AE013892; AAM86444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 HLCAPGEESPDRSPIPK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HL--PGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                          50.6%;
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Matches 9; Conservative
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MEDLINE-99246063; PubMed=10231032;
Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
Mryajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:63-70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJNE=11486534; PubMed=11514575;

Kitagawa H., Uyama T., Sugahara K.;

"Molecular Cloning and Expression of a Human Chondroitin Synthase.";

J. Biol. Chem. 276:38721-38726 (2001).

EMBL; AB03207; BAA76834.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                   Score 45; DB 16; Length 517;
Pred. No. 71;
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                                                                                                                                                                           Indels
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Pfam; PP05679; CHGN; 1.
Hypothetical protein.
SEQUENCE 802 AA; 91729 MW; 9115C204FAF298D7 CRC64;
PROSITE; PS00933; FGGY_KINASES_1; 1.
PROSITE; PS00445; FGGY_KINASES_2; 1.
Hypothetical protein; Kinase; Complete proteome.
SEQUENCE 517 AA; 54066 MW; C836FB87C12BB111 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (Trembirel. 12, Created)
01-NOV-1999 (Trembirel. 12, Last sequence update)
01-OCT-2003 (Trembirel. 25, Last annotation update)
Hypothetical protein KIAA0990 (Chondroitin synthase)
KIAA0990 OR CHSY.
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                Pred. No. 71;
2; Mismatches
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                                                                                                                              53.3%;
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                                                                                                   Query Match
Best Local Similarity 50...
Best Conservative
8; Conservative
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939 HLPNNKSGYWDPS 951
 1 HLPGNKSPHRDPA 13
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                                                                                                                                                                                    NCBI_TaxID=5811;
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Matches
                                                          RESULT 18
QBT9L7
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                                                                                                                                                                                                                                                                                 Arabidopsia thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCNI_TAXID=3702;
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                Alonso J.M., Hirayama T., Roman G., Nourizadeh S., Ecker J.R.; "EIN2, a Bifunctional Transducer of Ethylene and Stress Responses in
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd S.,
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1294;
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Similarity 61.5%; Pred. No. 1.9e+02;
8; Conservative 2; Mismatches 3; Indels
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                                                                           Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBU databases.
                   Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC046247; AAH46247.1; -. SEQUENCE 802 AA; 91784 MW; SB4C02670332FA0E CRC64;
                                                                                                                                                                                                                                01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                           50.6%; Score 45; DB 4; L
63.6%; Pred. No. 1.1e+02;
tive 3; Mismatches 1;
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GO; GO:0005215; F:transporter activity; IBA.
GO; GO:0006810; P:transport; IBA.
                                                                                                                                                                                                          PRT; 1294 AA
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99316073; Pubmed=10381874;
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EMBL; AF141203; AAD41077.1;
EMBL; AF141202; AAD41076.1;
EMBL; AL16275.1; CAB83384.1;
EMBL; AB349; T48349.
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PRINTS; PR00447; NrRESASSCMP.
ProDom; PD01861; Nramp; 1.
SEQUENCE 1294 AA; 140955 MM
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                                                                                                                                                                                                                                                                                                                                                                                                                     Science 284:2148-2152(1999)
                                                                              Query Match 50.6
Best Local Similarity 63.6
Matches 7; Conservative
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519 LPGSKSEHKEP 529
                                                                                                                           2 LPGNKSPHRDP 12
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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             rissum=Brain;
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Gaps

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Int. J. Parasitol. 0:0-0(2002).
EMBL; AV059630; AAL27793.2; -.
EMBL; AV059630; AAL27793.2; -.
EQ; GO:0005737; C:Cytophasm; IEA.
GO; GO:000524; F.ArP binding; IEA.
GO; GO:0016874; F.Riges activity; IEA.
GO; GO:0016874; F.Riges activity; IEA.
GO; GO:0006875; P:rigrame activity; IEA.
GO; GO:0006807; P:rigrame activity; IEA.
GO; GO:0006807; P:rigrame metabolism; IEA.
GO; GO:0008807; P:rigramidine base biosynthesis; IEA.
                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCTT-2003 (TrEMBLrel. 25, Last annotation update)
Carbamoyl phosphate synthetase II (EC 6.3.5.5).
Toxoplasma gondii.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fox B.A., Bzik D.J., "Novel organization and sequences of glutamine-dependent carbamoyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1687;
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60.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1687 AA; 185865 MW; FA9979489DCCC509 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006220; Anth synthii.
InterPro; IPR006275; CarA_Lglu.
InterPro; IPR006274; CarA_synth.small.
InterPro; IPR005483; CPase_L_D:
InterPro; IPR005480; CPase_L_D:
InterPro; IPR005480; CPase_L_D:
InterPro; IPR005481; CPase_L_D:
InterPro; IPR001341; CPase_L_D:
InterPro; IPR001341; CPase_L'D:
InterPro; IPR002474; CP synthGATase.
InterPro; IPR002474; CP synthsmall.
InterPro; IPR002474; CP synthsmall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGRO1368; CPSaselIsmall; 1.
TIGRPAMS; TIGRO1369; CPSaselI_lrg; 1.
PROSITE; PSO0866; CPSASE_1; 2.
PROSITE; PSO0867; CPSASE_2; 1.
PROSITE; PSO0442; GATASE_TYPE_1; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21848414; PubMed=11859373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00098; CPSASE.
PRINTS; PR00099; CPSGATASE.
PRINTS; PR00096; GATASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxoplasma gondii.";
Nature 415:926-929(2002).
      PRELIMINARY;
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les 9; Conserv
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339 AA; 36477 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2003 (TrEMBLrel. 24, GH1 protein (Fragment).
                                                                                                                        Query Match
Best Local Similarity 66.7.
8; Conservative
                                                                                                                                                                                                                                                                      91 PRATSPHTDPAP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                3 PGNKSPHRDPAP 14
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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194 DKSPHNDPLP 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Soybean)
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CL Brener;
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01-JUN-2002
01-JUN-2002
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Glycine max
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TCClJ12.7.
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                                                                                                                                                                    01-JUN-2003 (TrENBLEE]. 24, Last annotation update)
P0676G08.4 protein (OSJNBB0093M23.16 protein).
P0676G08.4 OR OSJNBB0093M23.16.
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 44.5; DB 10; Length 625; 50.0%; Pred. No. 1e+02; ive 2; Mismatches 4; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Nipponbare; Saski T., Matsumoto K.; Saski T., Matsumoto T., Yamamoto K.; Chromosome 1, BAC "Cryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:OSJNBb0099M33."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAINER, STRAINER, NIPPONDATE; SARALI T., MAISHUNCLO T., Yamamoto K.; Sasaki T., Matsuncto T., Yamamoto K.; Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AFCOLOGY, Grantegral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR004655; C4dc/mal_transpt.
Pfam; PP03595; C4dic_mal_tran; 1.
Pfam; PP03595; C4dic_mal_tran; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
11-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative secreted protein.
SCOS991 OR STBACIGH6.26 OR SCBACI6H6.26.
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                                                                                                                                                       Last sequence update)
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                                                                                         625 AA.
                                                                                                                                     Created)
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                                                                                           PRT;
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                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
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                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone: P0676G08."
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                                                                                                                 Q814G8;
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                                                                                             Q8L4G8
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                                                   RESULT 19
                                                                         Q8L4G8
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Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                 Gaps
"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
BMBL; A1939125; CAC44605.1; -.
Complete proteome.
SEQUENCE 128 AA; 12736 MW; CD0FC3CFAE94821E CRC64;
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                                                                                                                                                                              Score 44; DB 16; Length 128; Pred. No. 24;
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Hagen G., Guilfoyle T.J.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016633; AAB70005.1; -.
PIR, T05726; T05726.
TRANSPAC; T04524; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005645; P:regulation of translation; IEA.
InterPro; IPR003311; AUX IAA.
Pfam, PF02309; AUX IAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andersson B., Bontempi E.J.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AC096945; AAL90893.1; -.
SEQUENCE 274 AA; 28374 MW; 76636EA2BA24A09D CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                 0; Mismatches
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Created)
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                                                                                                                                                                                                                                                                                                               336 YLSGERTPHNDPDAR 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HLPGNKSPHRDPAPR 15
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Best Local Similarity 46...
7, Conservative
                                                                                                                                                                                                                                                              Local Similarity 46.7 conservative
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylulose kinase.
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                                                                                                                                                                                                                  Кіпаве.
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RX MEDILINE-22560858; PubMed=12663928;

RX MEDILINE-22560858; PubMed=12663928;

RA XU J., Biquesell M.K., Himrod J., Deng S., Carmichael L.K.,

RA Chiang H.C., Hooper L.V., Gordon J.I.;

RY Grience 299:2074-2076(2003).

RE EMBI, ABG16943; AAO79117.1;

BR GO; GO:000520; C:membrane; IEA.

BR GO; GO:000520; C:membrane; IEA.

BR GO; GO:0005810; P:ATP-binding; Cassette (ABC) transporter acti. ..; IEA.

BR GO; GO:0006810; P:ATP-binding; Cassette (ABC) transporter acti. ..; IEA.

BR GO; GO:0004009; P:ATP-binding; Cassette (ABC) transporter.

CR GO; GO:0004009; P:ATP-binding; Cassette (ABC) transporter.

RM ATP-binding; Complete protecome.

RM ATP-binding; Complete protecome.

RM ATP-binding; Complete RA; 48748 MW; 635D2514F7FBEF8 CRC64;

RGC GO:0004009; P:AA; 48748 MW; 635D2514F7FBEF8 CRC64;

COTORDINGE 426 AA; 48748 MW; 635D2514F7FBEF8 CRC64;
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MEDLINE=97464425; PubMed=9324246;
Heuel H., Turgut S., Schmid K., Lengeler J.W.;
Hauel H., Turgut S., Schmid K., Lengeler J.W.;
Heuel H., Turgut S., Schmid K., Lengeler J.W.;
Heuel H., Turgut S., Schmid K., Lengeler J.W.;
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
                                    0
                                                                                                                                                                                                                    Bacterides thetalotaomicron.
Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=818;
                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ABC oligo/dipeptide transport, ATP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%; Score 44; DB 16; Length 426; 88.9%; Pred. No. 83; 1; Indels 1; Indels
            DB 10; Length 339; 66;
                                    Indels
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Last annotation update)
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                                                                                                                                               426 AA
                                     3; Mismatches
               Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                               PRT;
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                         ilarity 63.6%;
Conservative
                49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                PRELIMINARY;
                                                              2 LPGNKSPHRDP 12
                                                                                   62 LPGSQSPEREP 72
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               Query Match
Best Local Similarity
Matches 7; Conserv
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052719
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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MEDLINE-98304087; PubMed=9639934;
Henel H., Shakeri-Garakani A., Turgut S., Lengeler J.W.;
"Genes for D-arabinitol and ribitol catabolism from Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kane P.M., LaFayette P.R., Parrott W.A.;

Kane P.M., LaFayette P.R., Parrott W.A.;

"Cloning and characterization of the arabitol operon.";

"Cloning and characterization of the arabitol operon.";

"Cloning and characterization of the arabitol operon.";

"Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

"R GO; GO:0004856; P:Kinase activity; IEA.

"R GO; GO:0004856; F:Xylulokinase activity; IEA.

R GO; GO:0005975; P:Xylulokinase activity; IEA.

"R GO; GO:0005975; P:Xylulokinase."

"InterPro; IPR006007; FGGY_kin.

"InterPro; IPR006007; FGGY_kin.

"InterPro; IPR005077; FGGY_Ci. I.

"TIGRPAMS; TIGR01312; Xylulokinase."

"Pfam; PF007782; FGGY_C; I.

"TIGRPAMS; TIGR01312; Xylulokinase."
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46.7%; Pred. No. 96;
tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%; Score 44; DB 2; Length 487; 46.7%; Pred. No. 96;
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Last annotation update)
                                                                                                   pneumoniae.";

pneumoniae.";

Microbiology 144:1631-1639 (1998).

EMBL; APC45245; AAC26499.1;

GO; GO:00016301; F:Kinase activity; IEA.

GO; GO:0005975; F:Carbohydrate metabolism; IEA.

GO; GO:0005997; P:carbohydrate metabolism; IEA.

GO; GO:0005997; P:carbohydrate metabolism; IEA.

InterPro; IPR0006000; Xylulose metabolism; IEA.

InterPro; IPR0006000; Xylulose metabolism; IEA.

InterPro; IPR0006000; Xylulose metabolism; IEA.

InterPro; IPR000500; Xylulose metabolism; IEA.

InterPro; IPR000500; Xylulose metabolism; IEA.

ITGRFAM; PR00370; FGGY kin.

ITGRFAM; PR03370; FGGY kin.

PROSITE; PS00933; FGGY KINASES.1; I.

PROSITE; PS00445; FGGY KINASES.2; I.
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SEQUENCE FROM N.A.
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Q9U252
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EMBL, AE008920, AAM48617.1; -...

GO, GO:0016730; F:oxidoreductase activity, acting on iron-sul. ..; IEA.

GO, GO:0015995; P:chlorophyll biosynthesis; IEA.

GO; GO:0006118; P:electron transport; IEA.

GO; GO:0019685; P:photosynthesis, dark reaction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-21822632; PubMed=11832943;
Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
Hamad T., Eisen J.A., Fraser C.M., DeLong E.F.;
"Unguspected diversity among marine aerobic anoxygenic phototrophs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                STRAINE-NINE Mile phase I / RSA 493;
MEDLINE=22608657; PubMed=12704232;
Seahadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E., Seahadri R., Paulsen I.T., Tettellin H., Davidsen T.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J., Thompson H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A., Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F., "Complete genome sequence of the Q-fever pathogen, Coxiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
Light-independent protochlorophyllide reductase, B subunit.
BCHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 494;
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                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                            GO: GO: 0016301; F: kinase activity; IEA.
GO: GO: 0004856; F: xylulokinase activity; IEA.
GO: GO: 0005975; P: carbobydrate metabolism; IEA.
GO; GO: 000597; P: xylulose metabolism; IEA.
InterPro; IPR00600577; FGGY kin.
InterPro; IPR006000; Xylulokinase.
Pfam; PF02702; FGGY C; 1.
Pfam; PF02702; FGGY C; 1.
IGRFAMS; IIGR01312; XylE; 1.
                                                                                                                                                                                                                                                                  burnetii.";
Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
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46.7%; Pred. No. 97;
rative 3; Mismatches 5,
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                494 AA
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PROSITE; PS00933; FGGY_KINASES_1; 1.
PROSITE; PS00445; FGGY_KINASES_2; 1.
Kinase; Complete protecome.
                                      Created)
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                PRT;
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337 YLSGERTPHNDPYAR 351
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                                     01-UTN-2003 (TrEMBLrel. 24, 01-UTN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25, Xylulokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uncultured proteobacterium.
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                PRELIMINARY;
                                                                                                                    Coxiellaceae; Coxiella.
NCBI_TaxID=777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 7; Conserv
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                               Coxiella burnetii
                                                                                     XYLB OR CBU0346.
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                             Q83EH5
                  Q83EH5
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Matches
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      Q83EH5
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KONG M., Mounier C., Wu J., Posner B.I.;

KONG M., Mounier C., Wu J., Posner B.I.;

"Identification of Eabl as the major motion in rat hepatocytes.";

induced PI3-kinase activation and DNA synthesis in rat hepatocytes.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

-I. SIMILARIY: CONTAINS I PH DOWAIN.

-I. SIMILARIY: CONTAINS I PH DOWAIN.

INTERPRO; IPR001849; PH.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                              Length 520;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 283:2012-2018(1998).
EMBL, AL132864; CAB63392.1; -.
Wormbep; V53HAA.1; CE22431.
SEQUENCE 613 AA; 68897 MW; B55ABCA6062C338D CRC64;
InterPro; IPR000510; Oxred_nitrognsel.
InterPro; IPR00569; Protochl_reductB.
Pfam; PF00148; oxidored his i.
TIGREDAMS; TIGR01278; DPOR Bach8; 1.
SEQUENCE 520 AA; 57358 MW; CB71D34682586EEI CRC64;
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LYAR-2001 (TrEMBLrel. 16, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0MR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Y53HAA.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 5; Le:
Pred. No. 1.2e+02;
0; Mismatches 5;
                                                                                                                                                 49.4%; Score 44; DB 2;
61.5%; Pred. No. 1e+02;
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                                                                                                                                                                                                    1; Mismatches
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                                                                                                                                                                           Best Local Similarity 61.5%;
Matches 8; Conservative
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152 PGTQRPSRDPAVR 164
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cells, reveals a novel pathway for cytokine-induced gene activation.";
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Gu H., Pratt J.C., Burakoff S.J., Neel B.G.;
"Cloning of p97/Gab2, the major SHP2-binding protein in hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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-: SIMILARITY: CONTAINS 1 PH DOMAIN.

EMBL; AB018414; BAA76738.1; -.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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GG; GG:0005515; F:protein binding; IPI.
GG; GG:0016477; F:protein binding; IDA.
GG; GG:0007229; P:integrin-mediated signaling pathway; IDA.
InterPro; IPR001849; PH.
Fram; PR00169; PH; 1.
PROSITE; PS50003; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%; Score 44; DB 11; Length 665; 63.6%; Pred. No. 1.38+02; ive 2; Mismatches 2; Indels
                                                                                                                                                                             Score 44; DB 11; Length 665;
Pred. No. 1.3e+02;
2; Mismatches 2; Indels
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SMO0233; PH; 1.
E; PSS0003; PH DOMAIN; 1.
Free aa: 73208 MW; E8955EE638174085 CRC64; Tenath
                                                                 SMART; SM00233; PH; 1.
PROSITE; PS50003; PH DOMAIN; 1.
SEQUENCE 665 AA; 73328 MW; BEB170B69406063E CRC64;
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01-WAY-1999 (TrEMBLrel. 10, Last Sequence update)
01-CAT-2003 (TrEMBLrel. 25, Last annotation update)
PH domain containing adaptor molecule p97/Gab2.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches 7; Conservative
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                                       Pfam; PF00169; PH; 1.
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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

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RA Abril J.F., Agbayani A., An H.-J., Andrews-Prannkoch C., Baldwin D.,

RA Ballow R.M., Basu A., Baxendale J., Bryzaktaroglu L., Beasley E.M.,

Rabeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,

RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Rutis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Ra Durbin R.J., Evangelista C.C., Ferriera S., Pleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT--2003 (TrEMBLrel. 25, Last annotation update)
Rel/NF-kappa B homolog (Rel protein) (Transcription factor maternal isoform) (GH01881p).
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Rephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 11; Length 666;
Pred. No. 1.3e+02;
2; Mismatches 2; Indels
                                                                                                           MGD; MGI:1333864; Gab2.

GO; GO:005515; F:protein binding; IPI.

GO; GO:0015477; P:cell migration; IDA.

GO; GO:0007229; P:integrin-mediated signaling pathway; IDA.

InterPro; IPR001849; PH.

Pfam; PF00169; PH; 1.

SMART; SM00233; PH; 1.

SRART; SS50003; PH DOMAIN; 1.

SEQUENCE 666 AA; 73295 MW; D3B6D568CFCBA3F7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
MOI. Cell 2:720-740(1998).
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
EMBL; AF104244; AAD05166.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%;
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Best Local Similarity 63...
7; Conservative
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:||| |||: 59 NLPGGNSPHQPP 70

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Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Houstin D., Houston K.A., Hewland T.J., Wei M.-H., Ibegwam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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Rhe genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0014018; Rel. GO; GO:0005634; C:nucleus; NAS. GO; GO:0005634; C:nucleus; NAS. GO; GO:0003704; F:specific RNA polymerase II transcription fa. . .; NAS. GO; GO:0006963; P:antibacterial polypeptide induction; IMP. GO; GO:0006967; P:antifungal polypeptide induction; IMP. GO; GO:0006955; P:immune response; IEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Erokstein P., Hong L., Farfan D., Frise B., George R.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANK repeat; Alternative splicing; Repeat.

VARSPLIC 1 112 Missing (in isoform Maternal).

/FTIG=VSP 050089.

SEQUENCE 971 AA; 109775 MW; EAF607357381AD32 CRC64;
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49.4%; Score 44; DB 5; Length 971;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Maternal;
Isofa@09457-2; Sequence=VSP_050089;
Isofa AAB17-24.1; --
EMBL; AF186073; AAF07931.1; --
EMBL; AF186073; AAF07932.1; --
EMBL; AF086073; AAF07933.1; ALT_INIT.
EMBL; AX058264; AAL13493.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q94527-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSS0088; ANK REPEAT; 2.
PROSITE; PSS0297; ANK REP REGION; 1.
PROSITE; PSS0254; REL_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UnterPro; IPR002110; ANK.
InterPro; IPR002110; ANK.
InterPro; IPR007110; Ig-like.
InterPro; IPR000309; IPT TIG.
InterPro; IPR000401; NF Rel dor.
InterPro; IPR008967; F53-like.
Pfam; PP00023; ank; 5.
Pfam; PP00023; TIG; 1.
PRINTS; PR00057; NRMSTNSCPECT.
SMART; SM0048; ANK; 4.
SMART; SM0048; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P25799; IIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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The RANTON COMBORTIUM,
The RIKEN GENOME EXPLORATION Research Group Phase I & II Team;
the RIKEN GENOME EXPLORATION Research Group Phase I & II Team;
**Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                             Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi l Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Tucker Genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 17; Length 105;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AK053193; BAC35307.1; -...
MGD; MGI:2442914; E030030106Rik.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro: IRR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales;
Desulfurococcaceae, Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AP00061; BAA80505.1; -.
PIR, C72631; C72631.

Hypothetical protein; Complete proteome.

SEQUENCE 105 AA; 11568 MM; 5E33500281A43CC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Weakly similar to cyclin-dependent kinase 6 (Fragment).
                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE1506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.3%; Scor.
58.3%; Pred. No. 2c,
... 2; Mismatches
                          105 AA
                                                                                                                                                                                                                                                                                                                                                                                  crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=22354683; PubMed=12466851;
                          PRT;
                                                                                                                                                                                                                                                       MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 58.3
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HLPGNKSPHRDP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 HLPNNKASHKLP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxiD=10090;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                         Aeropyrum pernix.
                                                                                                                                                                                          NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E030030106RIK
                                                                                                                                                                                                                                           STRAIN=K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                            O9YBU3
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Matches
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RESULT 33
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ProDom; PD000001; Prot_kinase; 1

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Gaps

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Nature 420:563-573(2002).

EMBL; AKO54034; BAC3567.1; -

MGD; MGI:1914869; Noblp.

InterPro; IPR002861; DUF133.

InterPro; IPR005596; PINC.

SPROM; PD013236; DUF133; 1.

SMART; SMO6570; PINC; 1.

SEQUENCE 184 AA; 20995 NW; 7
50,770 full-length cDNAs.";
                                                                                                            Query Match
Best Local Similarity 50.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 LPDNROPHRRP 134
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                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=39947;
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STRAIN=CS7BL/6J; IISSUE=Oviduct;
MEDLINE=22354681; PubMed=12466851;
The FANTOM Consortium.
the RANTOM Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                      STRAILURE-2554683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Consortium,
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Than Iyais of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Malyais of the Mouse Lough.
Mature 420:653-573(2002).
EMBL: AK045260; BAC32285.1; -.
MOD; MOT:2442914; E030030106Rik.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006529; F:protein kinase activity; IEA.
GO; GO:0006648; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
Propon; PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                      48.3%; Score 43; DB 11; Length 142; 63.6%; Pred. No. 38; 1; Mismatches 3; Indels
                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Weakly similar to cyclin-dependent kinase 6 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20254 MW; 2CDCF1C442030048 CRC64;
       1
142 AA; 15111 MW; 5BD3BB72815111B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 63.6%;
tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ART-4 protein homolog. NOB1P OR 1700021109RIK. Mus musculus (Mouse).
                                            Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGSSVPHRQPA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 PGNKSPHRDPA 13
                                                                                             3 PGNKSPHRDPA 13
                                                                                                                    30 PGSSVPHROPA 40
                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI TaxID=10090;
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           NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8BW77;
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                                                                                                                                                                                                 Q8BLG7;
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                                                                                                                                                          RESULT 35
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Sasaki T., Mateumoto T., Yamamoto K.;
Sasaki T., Mateumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
clone:B1151A10.";
Submitted (MAR-2201) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2201) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003308; BAB91793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Oryza Bativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC clone:B1129G05.";
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Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
predicted serine protein kinase homologous to HPr protein kinase,
contains a Zn-ribbon.
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Pred. No. 53;
1; Mismatches 3; Indels
                                                 Score 43; DB 11; Length 184;
Pred. No. 50;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8L479; -.
193 AA; 20042 MW; A6F4D87037409BC0 CRC64;
705EEF164881F74E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 22, Last sequence update) (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                 193 AA.
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B1129G05.17 protein (B1151A10.8 protein).
B1129G05.17 OR B1151A10.8.
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                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created) 01-OCT-2002 (TrEMBLrel. 22, Last seq
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Local Similarity 63.6%;
Les 7; Conservative
                                                              48.3%;
                                                                                       50.0%;
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129 HLPSKVNPFRSPGP 142
                                                                                                                                                                1 HLPGNKSPHRDPAP 14
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1 HLPGNKSPHRDPAPR 15
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Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.S.,
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.S.,
Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.,
Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.,
Rosenthal A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
Remser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
B. Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databasee.
B. Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databasee.
B. GO; GO:0005109; F:electron transporter activity; IEA.
GO; GO:0006118; Pelectron transport; IEA.
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                                                                                                                                                                                                                                                                                                          Gaps
                                                                           Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.3%; Score 43; DB 4; Length 211; ilarity 46.7%; Pred. No. 58; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                              48.3%; Score 43; DB 17; Length 208; 50.0%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 AA; 22808 MW; CACBSSDOEB2DF1AE CRC64;
                                                                                                                                                                                                                                                        208 AA; 23128 MW; 2C5007356A714665 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA
                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                           SEQUENCE FROM N.A.
STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000923; BlueCu 1.
PROSITE; PS00196; COPPER_BLUE; 1.
                                                                                                                                                                                                                     InterPro; IPR003755; Hpr kinase.
Pfam; PF02603; Hpr kinase; 1.
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141 IPGPHHPHHDPSMR 154
                                                                                                                                                                                                                                                                                                                                   2 LPGNKSPHRDPAPR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRED59 protein (Fragment).
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0,
Best Tocal Similarity
7, Conservative
                                                                                                                                                                                                                                               Complete proteome
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Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                 NCBI_TaxID=2320;
         Methanopyrus
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SEQUENCE
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Gaps

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Gaps
                                                                                                  Oryza sativa (Rice).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
NCBL TaxID=4530;
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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki I., Matsumoto I., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare,
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.3%; Score 43; DB 10; Length 281; 66.7%; Pred. No. 78;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001859; BAA94790.1;
EMBL; AP001856; BAA92982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gramene; QGLDK8; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0006445; P:regulation of translation; IEA.
InterPro; IPR03311; AUX IAA.
Pfam; PF02293; AUX IAA; 1.
SEQUENCE 281 AA; 30298 MW; B9EB293680354BAO CRC64;
                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
ESTS AU08:004.
281 AA.
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PRT;
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PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 clone: P0485D09."
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